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(54) Title: HUMAN NUCLEIC ACID FRAGMENTS, ISOLATED FROM BRAIN ADRENAL TISSUE, PLACENTA OR BONE NARROW

(57) Abstract

This invention provides a nucleic acid fragment encoding a gene product or portion thereof and comprising any one of: (a) a sequence selected from SEQ ID Nos 1 to 1193 from the attached sequence listings; (b) an allelic variation of a sequence as defined in (a); or (c) a sequence complementary to (a) or (b). The invention includes uses of such fragments, and gene products corresponding thereto.

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HUMAN NUCLEIC ACID FRAGMENTS, ISOLATED FROM BRAIN ADRENAL TISSUE, PLACENTA OR BONE NARROW

This invention relates to new nucleic acid fragments encoding gene products or portions thereof, which fragments are obtainable from human nucleic acid populations, individual members of such populations being present in widely varying amounts.

Situations are increasingly arising in which it is necessary to study
5   complex nucleic acid or polynucleotide populations. For example, it is now widely appreciated that an invaluable resource could be created if the entire sequence of the genomes of organisms such as man were determined and the information available. The magnitude of such a task should not, however, be underestimated. Thus, the human genome may
10   contain as many as 100,000 genes [a very substantial proportion of which may be expressed in the human brain (Sutcliffe, Ann. Rev. Neurosci. 11:157 (1988))]. Only a very small percentage of the stock of human genes has presently been explored, and this largely in a piecemeal and usually specifically targeted fashion.
15

There has been much public debate about the best means of approaching human genome sequencing. Brenner has argued (CIBA Foundation Symposium 149:6 (1990)) that efforts should be concentrated on cDNAs produced from reverse transcribed mRNAs rather than on genomic DNA. This is
20   primarily because most useful genetic information resides in the fraction of the genome which corresponds to mRNA, and this fraction is a very small part of the total (5% or less). Moreover, techniques for generating cDNAs are also well known. On the other hand, even supposing near perfect recovery of cDNAs corresponding to all expressed
25   mRNAs, some potentially useful information will be lost by the cDNA approach, including sequences responsible for control and regulation of genes. Nonetheless, the cDNA approach at least substantially reduces the inherent inefficiencies resulting from analysis of repeated sequences or non-coding sequences in an approach which depends upon
30   genomic DNA sequencing.

Recently, the results of a rapid method for identifying and characterising new cDNAs has been reported (Adams, M.D. et al., Science 252, 1991, pp 1651-1656). Essentially, a semi-automated sequence
35   reader was used to produce a single read of sequence from one end of each of a number of cDNAs picked at random. It was shown, by comparing the nucleic acid sequences of the cDNAs (or the protein sequences produced by translating the nucleic acid sequence of the cDNAs) to each

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other and to known sequences in public databases, that each of the cDNAs picked at random, could be unambig. sly classified. The cDNAs could be classified as being either entir.ly new or as corresponding, to a greater or lesser extent, to a previously known sequence. cDNAs
5   identified in this way were further characterised and found to be useful in a variety of standard applic ions, including physical mapping. Unfortunately, such a process is insufficient. The longer the process is pursued with any given population of cDNAs the less efficient it becomes and the lower the rate of identification of new
10 clones. In essence, as the number of cDNAs which have already been picked rises, the probability of picking a particular cDNA more than once increases. This difficulty is exacerbated by the wide range of abundancies at which different cDNAs can occur, which abundancies can vary by several orders of magnitude. Thus, whereas some sequences are
15 exceedingly rare, a single cDNA type may comprise as much as 10% of the population of cDNAs produced from a particular tissue (Lewin, B. Gene Expression, Vol. 2: Eukaryotic Chromosomes, 2nd ed., pp. 708-719. New York: Wiley, 1980). The need to avoid missing rarer species in any given population presents a considerable problem.
20
Various approaches (so-called "normalisation" techniques) have been tried in addressing the problem of increasing the efficiency of examination of a mixed nucleotide population, for example, such a population as is to be examined in human genome sequencing.
25
Thus, a standard PCR protocol can be used to amplify selectively cDNAs which are present at extremely low levels, if there is information about the sequence of those cDNAs. If not, a primer specific to the desired cDNA cannot be constructed and the desired cDNA cannot be
30 selectively amplified. The standard PCR method is therefore inadequate if it is desired to characterise a number of unknown genes.

A second approach involves hybridization of cDNA to genomic DNA. At saturation, the cDNAs recovered from genomic/cDNA hybrids will be
35 present in the same abundance as the genes encoding them. This will provide a much more homogenous population than the original cDNA library, but does not entirely solve the problem. In order to reach saturation in respect of the very rare sequences, it will be necessary to use huge quantities of cDNA, which need to be allowed to anneal to
40 large amounts of genomic DNA over a considerable periods of time. Furthermore, cDNAs which are homologous to genes which are present in multiple copies in the genome will be over-represented.

A·third approach exploits the second order reassociation kinetics of
cDNA annealing to itself. After a long period of annealing, the cDNAs
which remain single stranded will have nearly the same abundance, and
can be recovered by standard PCR (see Patanjali, S.R. et al., PNAS USA

5   88, 1991, pp. 1943-1947; Ko, M.S.H., NAR 19, no.18, 1991, pp 5705-
5711). The methods disclosed in these two publications, however,
suffer from notable disadvantages. They are entirely dependent on the
stringent physical separation of single stranded and double stranded
DNA, require an elevated number of manual manipulations in each

10   reaction, and necessitate protracted hybridisation times (up to 288
hours in the method of Patanjali et al.)

Yet a further approach in "normalising" a nucleotide population is
described in co-pending British Patent Application No 91 15407.0, filed

15   17th July, 1991 by MRC, and involves a PCR process in which a mixture
comprising   a   heterogenous   DNA   population   and   appropriate
oligonucleotide primers is first formed and the DNA denatured, but
before effecting a conventional PCR protocol the conditions are altered
to allow the denatured strands of the more common DNA species to

20   reanneal together, whilst avoiding annealing of primers to the DNA
strands. By this means, rarer species can subsequently be amplified in
preference to the more common species.

This PCR normalisation method in general comprises the steps of:

25

(a)   preparing a mixture comprising a heterogenous DNA population and
oligonucleotide primers suitable for use in a PCR process, in which the
DNA is denatured;

30   (b)   altering the conditions to allow the denatured strands of the
more common DNA species to reanneal, while preventing the annealing to
the primers to the DNA strands;

(c)   further altering the conditions of the mixture in order to allow

35   the primers to anneal to the remaining single-stranded DNA comprising
the rarer DNA species; and

(d)   carrying out an extension synthesis in the mixture produced in
step (c).

40

Advantageously, the method consists of a cyclic application of the
above four steps.

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It will be appreciated that the conditions may be altered by the alteration of the temperature of the reaction mixture. However, any conditions which affect the hybridisation of complementary DNA strands to one another may be varied to achieve the required result.

5

Because the reannealing efficiency of any given DNA species will depend on the product of its concentration and time, the more abundant the sequence the greater the extent to which it will reanneal in any given time period. Once a DNA species has reached a certain threshold

10 concentration it will no longer be amplified exponentially, as a significant amount will have annealed to the double stranded form before the priming step. Thus, as each individual DNA species is amplified by the process to its threshold concentration, the rate of amplification of that species will start to tail off. Eventually,

15 therefore, all DNA species will be present at the same concentration.

The length of the reannealing step will determine how much DNA is present at the threshold concentration. Preferably, therefore, the duration of the reannealing step will be determined empirically for

20 each DNA population.

In the PCR normalisation process in general, the DNA primers may be adapted to prime selectively a sample of the total DNA population. By using primers which will only prime a sample of the population, only

25 that sample will be amplified and normalised. The total quantity of DNA generated will thereby be reduced, which means that the cycling times can be kept low. This ensures that the method is applicable to complex DNA populations such as cDNA populations. In addition, a first primer can be used which is adapted selectively to prime a sample of

30 the total cDNA population, and a second primer which is a general primer. Advantageously, the general primer is oligo dT (each primed cDNA will then be replicated in its entirely, as the oligo dT primer will anneal to the poly-A tail at the end of the cDNA).

35 In co-pending British Patent Application No 92 14873.3, filed by MRC 13th July, 1992, a new process is described which allows the study and identification of the individual members of a mixed or heterogenous population of nucleotide sequences perhaps of varying abundance. In preferred embodiments of the said process, the starting nucleic acid

40 population is treated by:

(a)   subjecting the nucleic acid to the action of a reagent,

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preferably an endonuclease which has its cleavage and recognition sites separated, which reagent cleaves the nucleic acid so as to produce double stranded cleavage products the individual strands of which overlap at cleaved ends to leave a single strand extending to a known
5   extent;

(b)   ligating the cleavage products from (a) with a population of adaptor molecules to generate adaptored cleavage products, each of which adaptor molecules has a cleavage product end recognition sequence
10   and the population thereof encompassing a range of adaptor molecules having recognition sequences complementary to a predetermined subset of the sequences of the cleavage-generated extending single strands; and

(c)   selecting and separating only those adaptored cleavage products
15   resulting from (b) which carry an adaptor of predetermined recognition sequence.

A preferred endonuclease for use in step (a) of the above process is Fok 1.
20

An important feature of this process is the use of adaptor molecules. The adaptors used must have "overhanging" fragment recognition sequences which reflect or are complementary to the extending cleavage-derived sequences which the adaptors are designed to react with. It is
25   also preferred that the adaptors used should end with a 5' hydroxyl group.   The avoidance of a 5' phosphate group removes the risk of inappropriate ligation involving the adaptors.

Adaptor molecules may also contain a portion permitting specific
30   sequence selection and separation (as in step (c) of the process) when a sequence is attached to the adaptor. For example, an adaptor can carry biotin, thereby permitting advantage to be taken of the biotin/avidin
reaction in selecting and separating desired adaptored molecules.
35   Additionally, adaptors preferably comprise a known and selected sequence such that specifically isolated adaptored molecules can be amplified by known techniques (such as PCR) using a primer complementary to the core sequence.

40   Preferably the adaptors are short double-stranded oligonucleotides which can be joined to the ends of cleavage products. They will have been chemically synthesised so that their sequence can be predetermined

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and so that large concentrations can be easily produced. They may also
be chemically modified in a way which allows them to be easily purified
during the process. As mentioned above, ideally their 5' ends will be
unphosphorylated so that once joined to fragments the adaptored end of
the latter will no longer be able to participate in further ligation
reactions.

It is preferred that the adaptor cleavage product end recognition
sequences are on the 5' end of the longest oligonucleotide strand
making up the preferred adaptor molecules, are at least 3 nucleotides
in length and with totally random bases at the single-stranded
position(s) two nucleotides in from the 5' end. This then allows
selection to be performed both during the joining reaction and during
subsequent priming reactions. Then, because the final degree of
selection is a result of the product of the degrees of selection
achieved at these two stages, maximum selection can be achieved per
adaptor/primer available.

Adaptor strand extensions on the 5' end of the longest oligonucleotide
also facilitate the use of modified oligonucleotides for separation
purposes. Preferably, the short oligonucleotide will be modified at
its 5' end. This has the double benefit of requiring just one modified
oligonucleotide for all possible single-stranded extensions that are
used, and also placing the modification at a position where it cannot
interfere with ligation or subsequent priming reactions.

Although only one type of adaptor is required per ligation reaction, it
is preferred that adaptors covering all possible reactions in a chosen
subset of sequences be present, because then the opportunity for
fragments in the chosen subset to ligate to each other is minimised.
It is also preferred that the chosen specific adaptor, carrying a
predetermined recognition sequence, should not only be different from
the other adaptors in its single-stranded extension, but also different
in the rest of its sequence since this allows orientation to be
introduced which is useful in subsequent steps. It is therefore also
preferred that this adaptor has a modified oligonucleotide to
facilitate its separation with the cleaving products to which it joins.

The above "adaptoring" process can be used to generate categories or
subsets of sequences by making some of the adaptors specific in some
way, and selecting and separating as in step (c). In this way subsets
of sequences can be provided depending upon the specific adaptor

chosen, e.g. for use in subsequent nucleotide sequencing. This
facilitates, for example, the identification of a large population of
sequences by permitting a rational approach to splitting such
populations into subsets, each of which subsets can be examined in
5   turn.

In the light of these developments, the present invention now provides
a nucleic acid fragment encoding a gene product or portion thereof and
comprising any one of:-

10

(a)   a sequence selected from SEQ ID Nos 1 to 1193;

(b)   an allelic variation of a sequence as defined in (a);   or

15   (c)   a sequence complementary to (a) or (b).

In another aspect, the invention provides a nucleic acid sequence as
set out in any one of SEQ ID Nos 1 to 1193, or a complement or allelic
variation thereof.   Preferred sequences exhibit no more than 90%
20   homology to a human sequence known per se.

In a further aspect, the invention provides a nucleic acid fragment
comprising a portion of a sequence as defined above of sufficient size
such that a probe of the same size and exhibiting complementarity to
25   said portion can hybridise to said sequence. Preferably, such portions
are at least 15 bases in length.   It will be appreciated that minor
mismatches in the aforesaid "complementarity" are not excluded provided
hybridisation can still occur.   In general, hybridisation conditions
are within the choice of the skilled person, but reference can be made,
30   for example, to the following: Melting temperature of hybrids -
Bolton, E. T. and McCarthy, B. J. Proc. Natl. Acad. Sci, 48 p1390
(1962).   Effect of formamide on lowering melting temperature - Casey,
J. and Davidson, N., Nucleic Acids Res. 4, p1539 (1977).   Effect of
imperfect homology - Bonner, T. I. et al., J. Mol. Biol. 81, p123
35   (1973).   General - Meinkoth, J. and Wahl, G. Anal. Biochem. 138, p267
(1984).   Oligo hybridization and washing - Lathe, R. J. Mol. Biol. 183,
P1 (1985).

The present invention also envisages DNA constructs comprising
40   fragments or sequences as referred to above with a control or
regulatory sequence.

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The invention includes such DNA constructs using a gene system known in
the art ligated to a sequence or fragment of the invention so as to
enable, upon expression, the provision of a fusion polypeptide.
Preferably, an endopeptidase recognition site is provided such that
5   when the sequence or fragment is expressed it is expressed in frame
with a known protein with the boundary being a cleavage site for an
endopeptidase with a rare cutting site. The known protein can then be
affinity purified, and the peptide corresponding to the fragment or
sequence in accordance with the invention may be released by the
10   endopeptidase. Alternatively, the whole protein can be used to raise
antibodies which can then be screened for those directed at polypeptide
corresponding to the fragment or sequence of the invention.

Since the present fragments and sequences can be used to produce, inter
15   alia, corresponding genes, whether by isolating them, by synthesis or
otherwise, such use and the resulting DNA fragments comprising genes
are further aspects of the invention.

Yet another aspect of the invention is an expression vector comprising
20   a fragment, sequence, gene-comprising DNA fragment, or DNA construct,
as above, positioned such that that nucleic acid sequence which
encodes the polypeptide corresponding to said fragment, sequence or DNA
fragment is in operable reading frame with a control or regulatory
sequence.
25

Other aspects of the invention are host cells incorporating a sequence,
or fragment, or gene-comprising DNA fragment, or DNA construct, as
above, as a heterologous part of the expressible genetic information of
the cell. The production of such modified host cells can be achieved
30   using methods known in the art. Such modified host cells can be used
to express corresponding proteins, and these materials lend themselves
in turn to the preparation of corresponding monoclonal or polyclonal
antibodies using standard techniques.

35   Also included in this invention are such antibodies. Reference can be
made, inter alia, to the following literature: Monoclonal antibodies,
Cambell, A. M. Laboratory Techniques in Biochemistry, and Molecular
Biology Ed. Burdon, R. H. and van Knippenberg, P. H. vol 13. Elsevier
Amsterdam 1984. Goding, J. W., Monoclonal antibodies: Principles and
40   Practice, 2nd Edition, academic Press, London 1986. Kipps, T. J. and
Herzenberg, L. A., Handbook of Experimental Immunology : Applications
of immunological methods in biomedical sciences, 4th edition Ed. Weir,

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D. M. et al., p108 Blackwell scientific Publications, Oxford. Harlow,
E and Lane, D. Antibodies, A Laboratory Manual, Cold spring harbor
Laboratory, Cold Spring, New York.

5   Expression in an appropriate higher eucaryotic host may be important to
     ensure correct protein folding and also activity. Expression to avoid
     copurification of toxic products can sometimes be better performed in
     organisms approved for human consumption, eg prokaryotic Bacillus
     subtilis, eurkaryotic yeast, mammalian cows milk vectors, and other
10   methods known in the art.

     The invention also includes novel gene products or portions thereof
     encoded by a fragment, sequence or gene-comprising DNA fragment of the
     invention.
15

     It will be appreciated that the sequences of the present invention
     collectively have utility based, inter alia, upon their common origin,
     and hence they can effectively be considered together rather than as
     separate entities. It is convenient to represent them as separate
20   sequences, because this is how they were produced and serves as
     "punctuation" between the different functional entities which each
     sequence represents. However, the sequences could just as easily have
     been presented as a continuous sequence derived by placing them end to
     end in the order in which they were produced, with a separate
25   indication of where the beginnings and ends of the component sequences
     are.

     In contrast to investigations hitherto, where gene fragments (sequence
     fragments) could only be identified through some known characteristic
30   [for example: their homology to a fragment which largely encodes amino
     acids identified by sequencing a previously isolated peptide or is the
     antisense of that coding sequence; or them having at least partial
     homology to previously characterised nucleic acids; or them having
     ability to encode expressed proteins which could later be detected by
35   functional assays of the cells expressing those proteins or by using
     antibodies which had been previously raised against the proteins to
     detect their expression, Sambrook J., et al., Molecular Cloning CSH
     Press 1989], the sequences and fragments described by the present
     invention are entirely underivable and unpredictable from the prior
40   art, but are nonetheless clearly of great value for various purposes.

     Thus, such sequences, by comparing them to sequence databases, can be

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used as a means for determining the existence of new members of existing gene fa lies, new human genes when previously only non-human genes were know and new genes when previously no genes were known (Karlin, S. and Altschul, S. F. Proc. Natl. Acad. Sci. 87 p2264-2268
5   (1980)). In all cases, this allows the isolation of the corresponding genes and their products, and hence enables the manufacture of molecules of potential biological interest by recombinant means. Screening libraries of known materials or hitherto unexplored source materials for biological efficacy is now an important industrial
10   activity in the search for new therapies and therapeutics. When new sequences have already been found to have counterparts in gene families or in non-human genes then knowledge about biological efficacy may already be apparant. For example, new receptors or receptor agonists/antagonists may exhibit differences to known instances of
15   these molecules, and such differences could make them more suitable as therapeutics by, for example, exhibiting binding characteristics which are more in keeping with avoidance of toxicity. Reference can be made, for example, to polymorphic dopamine receptors and the implications for mental health (Iversen, L. Nature 358, p109 (1992), and Van Tol, H. M.
20   M. et al., Nature 358, p149-152 (1992)). Where absolutely required, realisation of full length cDNAs for expression can be achieved by using the sequences to screen (by hybridisation) suitable cDNA libraries containing full length clones (D'Alession, J. M., et al., Focus (Gibco B.R.L) 9 p1 (1987)). Alternatively, the sequences can be
25   used to design primers suitable for obtaining the missing sequences by PCR or other amplification methods (Frohman, M. A., Dush, M. K. and Martin, G. R., Proc. Natl. Acad. Sci. 85 p8998-9002 (1988)).

Appropriate use of the sequence fragments in antisense or triple helix
30   (Griffin et al., Science 245 p967-971 (1989)) applications will be useful for identifying manipulable targets related to disease. For example, viruses have been inhibited by antisense RNA to their mRNAs (Chang, L-J., and Stoltfuz, C. M. J. Virol. p921-974 (1987)). A similar effect could be achieved by targetting the expression of
35   cellular proteins which are essential for growth or maintenance of the virus.

Partial or full length cDNAs have great utility once expressed. The manner of expression can be selected by one skilled in the art to suit
40   the intended application. Expression of full length cDNAs is typically required for biological activity. Procaryotic, and lower or higher eucaryotic hosts may be selected as the host for expression and higher

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eucaryotes may be preferred to ensure correct modifications, for example, glycosylation in vivo, when this proves to be important. Expression can be ensured by situating the cDNA appropriately to signals for expression (Amann, E. and Brosius, J. Gene 40 p183 1985),

5   Shimuzu, Y et al., Gene 65, p141 (1988), Straus, D. and Gilbert, W. Proc. Natl. Acad. Sci. 82, p2014 (1985)). Such signals may include a promoter for transcription, which may itself be regulatable.

The proteins thus-expressed can be screened for activities of

10 therapeutic or commercial value. It may be that the proteins have to be first isolated for this purpose or can be assayed in situ. It may be desirable that some means of stabilising the expressed protein is employed. This can be achieved, for example, (and as indicated earlier) by expressing in frame as part of a fusion polypeptide (Smith,

15 D. B., et al., Proc. Natl. Acad. Sci. 83 p8073 (1986)).

Useful antibodies can be raised against the expressed proteins. It is commonly not an absolute requirement that full length proteins are produced, although this may influence the quality of the antibodies

20 produced. Peptides as short as 8 or 9 amino-acids in length can be used as antigens (Germain R., N. Nature 353 pp605-607 (1991), Rudensky, A., Y., et al., Nature 353 p622-627 (1991)). Immunogenic peptides could simply be synthesised using the amino-acid sequence translated from a sequence or fragment of this invention. It is desirable,

25 although not absolutely required, that some means of producing purified antibodies is adopted. When fusion polypeptides are used to raise antibodies, an affinity matrix specific for the generic part of the protein allows the fusion polypeptide to be immobilised (Smith, D. B., et al., Proc. Natl. Acad. Sci. 83 p8073 (1986)). The immobilised

30 polypeptide can then be used to affinity purify the antibodies. Antibodies to both the generic part of the fusion polypeptide and the part of interest are produced. When these need to be discriminated between, a different affinity column can be used to remove only those antibodies specific for the generic part of the polypeptide.

35 Alternatively, and as mentioned earlier, it can be arranged that the boundary between the two separate protein components of the fusion polypeptide has the recognition sequence for an endopeptidase with a rare cutting site. The peptide of interest can then be released from the affinity purified polypeptide by the action of the endopeptidase

40 (Nagai, K., and Thogersen, H., C. Methods Enzmol. 153 p461-481 (1987). Another alternative is raise monoclonal antibodies against the purified protein.

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The antibodies can be used for localising in situ, or quantifying in samples through, for example, ELISA or RIA assays, peptides against which they were raised. These uses are particularly beneficial when the results of the assays can be correlated to a disease condition, eg
5   cancer. For example tumour markers may be found and used to target therapeutic agents. The antibodies can also be used to detect or monitor markers of undifferentiated growth, infection, cardiovascular or immune disease or a therapeutic response. When the antibodies recognise cell surface proteins they can be used in isolation or in
10   combination to isolate particular populations of cells. These in turn can be used to isolate yet more cDNAs which will be enriched for yet more of such surface markers for the population, which, if similarly screened, will permit yet further subdivision of the population. Ultimately, panels of antibodies which can describe particular disease
15   states will accrue. Such antibodies could be tailored for forensic applications as well as diagnostic purposes and disease monitoring.

The sequences or fragments can also be used for genetic analysis and mapping, for example, to diagnose the likelihood that a given
20   individual is predisposed towards a given genetic disease. In the event of a sequence co-locating, genetically, with a disease gene, it can be used for the derivation of new disease therapies bases upon precise genetic knowledge. Such therapies can include, for example, the techniques of so-called "gene therapy" (Dusty Miller, A. Nature 357
25   p455-460 (1992)).

Antibodies can be produced against the protein of a genetic disease with sufficient discriminating power to discriminate between diseased and non-diseased states (Caskey, T. Genome Sequencing Conference,
30   Hilton Head, S. Carolina (1991)). This would be useful for reducing the dependence of such tests on nucleic acid-based screens. Such antibodies also have the advantage of allowing detection of faulty expression of the protein, for example levels of expression which may be important for development of the disease in slow onset conditions.
35
Also very important is that not all cDNAs are likely to be found by conventional means, whereas the present sequences are, in one sense, "comprehensive". The use of the class of cDNAs which corresponds of necessity to truncated clones increases the chances that part of a cDNA
40   will be cloned free of any sequences that could otherwise compromise it from being cloned. Sequence obtained can then be used to generate PCR primers from which the remainder can be obtained without having to

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clone.

This invention will now be further described and illustrated by means
of the following Examples.

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All oligonucleotides used in these Examples were synthesised Trityl on
using an ABI 380B DNA Synthesizer according to the manufacturers
instructions.   Purification was by reverse phase HPLC (see, for
example, Becker, C., R., et al., J. Chromatography 326, p293-299
10   (1985)).

Example 1

Human brain and adrenal tissues were obtained from a mixture of 12 to
15   15 week menstrual age foetuses and then snap frozen in liquid nitrogen
before storing in bijou bottles in a -80°C freezer. The two types of
tissue were used separately, directly from the freezer, to prepare cDNA
from which restriction fragments were generated for sorting into
subsets. 1g portions of each of the separate tissues were homogenised,
20   using an Ultra-Turrax T25 Disperser (Janke and Kunkel, IKA-
Labortechnik), on ice in the presence of 4M guanidinium isothiocyanate
to solubilise macromolecules. RNA was isolated from each homogenate by
using centrifugation to sediment it through caesium trifluoroacetate.
This was performed using the Pharmacia kit according to the
25   manufacturer's instructions, except that centrifugation was performed
for 36 hours and the RNA obtained was finally desalted and concentrated
by performing two ethanol precipitations in succession with two 70%
ethanol washes after each precipitation. In each case, polyA⁻ (mRNA)
was isolated from 200 to 400 µg of the total RNA by binding it to
30   magnetic oligo-dT coated beads (Dynal). Solution containing unbound
material was removed from the beads, which were washed, and then mRNA
eluted directly for use. mRNA isolation was performed in accordance
with the manufacturer's instructions. Yields of RNA from the beads
were between 1 and 3% of the total RNA. 2 to 4 µg of the eluted RNA
35   were used for cDNA synthesis. cDNA synthesis was performed according
to the method of Gubler, U and Hoffman, (B. J. Gene 25 p263 (1983)
using a Pharmacia kit according to the manufacturer's instructions.
OligodT was used to prime the first strand cDNA synthesis reaction.
The cDNA was purified by extracting twice with phenol/chloroform and
40   then low molecular weight solutes including nucleic acids below ca. 300
bases were removed by passing the cDNA reaction mixture through a
Pharmacia S400 spun column used according to the manufacturer's

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·instructions. Running buffer for the column comprised 10 mM TrisHCl, 1 mM EDTA, 50 mM NaCl @ pH 7.5.

5   The column eluate was adjusted to 10 mM Mg^{2+} and then the purified cDNA was restricted by the action of 1 unit per 10 μl of the endonuclease Fok I at 37°C for 1 hour, so that it would be able to accept adaptors to enable fragment sorting.

10   The cDNA fragments were purified by two successive phenol/chloroform extractions followed by passing them through S400 spun columns as described above.

     The adaptors used were oligonucleotides 5' N$_4$N$_4$N$_4$N$_4$TCCTTCTCCTGCGACAGACA (SEQ ID: 1194) with the complementary strand 5' TGTCTGTCGCAGGAGAAGGA
15   (SEQ ID: 1195) and 5' AAN$_4$N$_4$TCTCGGACAGTGCTCCGAGAAC (SEQ ID: 1196) or 5' TTN$_4$N$_4$TCTCGGACAGTGCTCCGAGAAC (SEQ ID: 1197) each with the complementary 5' biotinylated strand GTTCTCGGAGCACTGTCCGAGA (SEQ ID: 1198). These were added to 25% of the eluted material by incubating together 200 pmoles of the mixture of double-stranded adaptors in the elution buffer
20   to which had been added MgCl$_2$ to 10mM, ATP to 10mM and 0.025 units/μl of T4 DNA ligase. The oligonucleotide 5' biotinylated GTTCTCGGAGCACTGTCCGAGA, (SEQ ID: 1198) and whichever of the complementary oligonucleotides with which it was used, each comprised 1/32 of the molar proportion total adaptors. The final reaction volume
25   was 90 μl which was heated to 65°C for 3 minutes and then cooled to room temperature before the ligase was added. Ligation was performed for 16 hours at 12°C.

     Two successive phenol/chloroform extractions were performed to remove
30   the ligase. The final aqueous phase was passed through an S400 spun column (Pharmacia) as described above except that the column was used with 10 mM Tris pH 8.3/50 mM NaCl.

     The column eluate was adjusted to 25mM Mg2+, 0.5mM dNTPs in a final
35   volume of 200 μl. The mixture was placed in a thermocycler (Techne MW2) and heated to 78°C for 5 minutes. At this point 10 units of cloned Taq DNA polymerase (AmpliTaq, Perkin Elmer) were added. This was followed by an incubation at 72°C for 10 minutes to fill in the unligated strand of the adaptor. After the second incubation 200 μl of
40   streptavidin coated magnetic beads (Dynal) prepared according to the manufacturers instructions were added to bind cDNA ligated to that of· the oligonucleotides which was complementary to the 5'

.GTTCTCGGAGCACTGTCCGAGA (SEQ ID: 1198) biotinylated adaptor.   Bead
binding was allowed to proceed at 28°C for 30 minutes with mixing every
10 minutes.

5   Un-biotinylated cDNAs were washed from the beads with 400μl each of 2M
       NaCl twice, fresh 0.15 mM NaOH four times at 28°C for 5 minutes each,
       water twice and finally a buffer comprising 20 mM Tris pH 8.3, 50 mM
       NaCl, and 25mM Mg^{2+}.   The beads were then resuspended in 240 μl of the
       final buffer including additionally 0.5 mM dNTPs and divided into 4x60
10   μl.

       Four of the 60 μl aliquots, two from each tissue, were processed
       further specifically to prime and copy a subset of the immobilised,
       adaptored fragments.   2 pmoles of the primer 5' CTGTCTGTCGCAGGAGAAGGAA
15   (SEQ ID: 1201) were added to each of two aliquots, one from each
       tissue.   2 pmoles of the primer 5' CTGTCTGTCGCAGGAGAAGGAG (SEQ ID:
       1202) were added to each of the other two aliquots.   2.5 units of Taq
       DNA polymerase were added to each reaction and 16 cycles of alternate
       denaturation at 95°C for 30 seconds, annealing at 63°C for 2 minutes
20   and polymerisation at 72°C for 3 minutes was performed to accumulate
       the selected single-strands in solution.

       On completion of the DNA synthesis reactions a further 30 μl of
       resuspended beads were added to each reaction to remove the
25   biotinylated fragments.   The reaction was incubated at 28°C for 30
       minutes mixing every 10 minutes to ensure that the biotinylated strands
       were bead bound.   Each aqueous phase containing the newly synthesised
       strands was then removed and extracted with phenol/chloroform twice to
       remove the enzyme before being further purified by passing through an
30   S400 spun column equilibrated with 10 mM Tris pH 8.3/50 mM NaCl as
       described above.

       Rounds of PCR amplification of subsets of the selected fragments were
       performed by using the original primer in each case, together with one
35   of the primers 5' GTTCTCGGAGCACTGTCCGAGAG (SEQ ID: 1199) or 5'
       GTTCTCGGAGCACTGTCCGAGAC SEQ ID: 1200).   This simultaneously rendered
       the fragments double-stranded and increased the amounts of available
       material. It was not known how many cycles of amplification would be
       required at this stage, since each primer pair would be expected to
40   behave differently.   It was therefore necessary directly to determine
       a suitable number empirically by using standard agarose gel
       electrophoresis to examine the reaction products after a given number

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·of cycles. In some cases, to avoid the accumulation of non-specific
products, it was necessary to perform an initial 5 cycles of
amplification with both of the primers present at 2 pmoles each. All
reactions were performed using 8 μl or 12.5 % whichever was the larger
5   but not exceeding 12 μl of the column effluent above.   Reaction
conditions were adjusted to 20 mM Tris pH 8.3, 50 mM NaCl, 25mM Mg^{2+},
0.5mM dNTPs and 2.5 units of Taq DNA polymerase in a final volume of 40
μl.   Apart from when an initial amplification with 2 pmoles of each
primer was performed, 20 pmoles of each primer were used. Cycles of
10   amplification were performed at 95°C for 30 seconds, 65°C for 1 minute
and 72°C for 3 minutes.

For the purposes of cloning, selected cDNA was amplified as described
immediately above, except that the reaction was not monitored.
15   Instead, the number of cycles which had previously been shown to just
give rise to all observable products plus another 4 cycles were
performed.   In addition, an extra 72°C for 10 minutes incubation was
performed after the last cycle.

20   The products of the reaction were then prepared for directional
cloning. Water was added to adjust the final reaction volume to 60 μl.
Enzyme was removed by two successive phenol/chloroform extractions.
The final aqueous mixture was passed through an S400 column as
described above, except that it had been equilibrated with 10 mM Tris
25   HCl pH 7.5, 50mM NaCl.

For directional cloning, advantage was taken of the different known
sequences introduced at each end of the selected cDNAs by the adaptors
in a modification of the method of Aslandis, C. and de Jong, P. J.
30   (Nucl. Acids Res. 18, p6156 (1990)).   Different cohesive ends were
produced on each end by using the exonuclease activity of T4 DNA
polymerase to resect from the 3' end, to the first T in each case. To
75 μl or 75 % of the column eluate, whichever was least, were added
9.5 μl of 100mM TrisHCl pH7.4, 100 mM MgC12, and 9.5 μl of 0.5 mM dTTP.
35   16 units of T4 DNA polymerase were added and the reaction incubated in
a water bath at 37°C for 30 minutes. The enzyme was removed by
extracting with phenol/chloroform, twice successively. The salt of the
final aqueous phase was adjusted by passing it through an S300 column
(Pharmacia) equilibrated with 10 mM TrisHCl pH 7.4, 1 mM EDTA as
40   described above.

The E.coli plasmid cloning vector pBluescript KS+ (Alting-Meese, M. A.

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··and Short J. M., Nucl. Acids Res. 17 p9494) was prepared for accepting the resected cDNA by restriction cleavage at the BamHI and HindIII sites and then adaptoring the resultant cohesive ends using the specific adaptors produced by the oligonucleotide 5' AGCTCGGCTCGAGTCTG
5   (SEQ ID: 1203) with its partially complementary oligonucleotide 5' GCGACAGACAGCAGACTCGAGCCG (SEQ ID: 1204) and the oligonucleotide 5' GATCCGGCTCGAGT (SEQ ID: 1205) with its partially complementary oligonucleotide 5'·CCGAGAACACTCGAGCCG (SEQ ID: 1206). Preparation of the vector and adaptoring were performed according to standard
10   procedures. Insertion of the cDNA was performed between the BamHI and HindIII restriction sites. ·Recombinant vectors were transformed into the host XL1-Blue (Bullock, W. O. et al Biotechniques 5 p376-378 (1987)) by the method of Hannahan, D. J. (Mol. Biol. 166 p577-580 (1983)). Suitable standard controls for the ligations and
15   transformations were also included.

Post transformation procedures were as described in "Molecular Cloning", 2nd Edition (Sambrook J., Fritsch, E. F., and Maniatis, T. CSH Press (1989)). Colonies were produced by plating onto X-gal/IPTG
20   L-agar plates containing 50μg/ml ampicillin and 10μg/ml tetracyclin. Clear colonies were picked, each into a separate well of a microtitre plate, containing 100μl of L-broth and 50μg/ml ampicillin. Growth was allowed to occur for 16 hours at 37°C. 100μl of 50% or 30% glycerol was added to plates which were archived at -20°C or -80°C,
25   respectively.

Bacteria corresponding to those archived were used for preparing templates for sequencing by the dideoxy method (Sanger, F. Milklen, S. and Coulson, A. R. Proc. Natl. Acad. Sci. 74 p5463-5467 (1977)).
30   Bacteria for this purpose were either grown on L-agar plates containing 50μg/ml of ampicillin, prepared at the same time as they had been grown in liquid culture, or after plating out from the archive. Alternatively, fresh liquid cultures were inoculated from the archive.
     In all cases, cDNA inserts were amplified for sequencing by PCR
35   (Saiki, R. K. et al Science 239 p487-491 (1988)). PCR was either performed using bacteria directly added to the reaction, by a toothpick, or PCR was performed using 1/50th of the plasmid isolated by preparative methods (Holmes, D. S. and Quigley, M. Anal. Biochem. 114 p193 (1981)) from the bacteria in the liquid cultures or from the
40   plates.

20 pmoles of each of the PCR primers 5' biotinylated GTAAAACGACGGCCAGT

(SEQ ID: 1207) and 5' CGAGGTCGACGGTATCG (SEQ ID: 1208) were used in 40μl reactions containing 2.5mM Mg^{2+}, 50 mM KCl, Tris-HCl pH 8.3 and 0.25 units of Amplitaq (Cetus). Reactions were performed at 95°C, for 1 minute, followed by 35 cycles at 95°C for 30 seconds, 60°C for 30
5   seconds and 72°C for 40 seconds. After the cycles, a final incubation at 72°C for 5 minutes was performed.

After PCR, standard agarose gel electrophoresis was used to determine which reactions had been successful. The biotinylated strands of
10   successful reactions were then recovered for single-stranded sequencing by binding them to steptravidin coated beads (Dynal) and then washing, all according to the manufacturers instructions, except that the washing steps were either performed manually or performed automatically in the 96 well microtitre plate format using a Biomek robotic work-
15   station attached to a side-arm loader (Beckman).

Dideoxy chain termination sequencing reactions were performed using the immobilised, biotinylated strands as templates and 2 pmoles of the oligonucleotide 5' CGAGGTCGACGGTATCG (SEQ ID: 1209) as primer.
20   Reactions were performed using fluorescently-labelled terminators (Du Pont) or a fluoroscein-labelled primer (Pharmacia) according to the manufacturers instructions. Reactions were analysed using automated DNA sequencers. A Genesis 2000 was used for the "Du Pont" reactions and an A.L.F. for the "Pharmacia" reactions. Bases were assigned for
25   the Genesis 2000 reads using the manufacturers Base Caller software. Files of called bases were then transferred to a SUN Network from an Apple Macintosh computer which had been used for base calling. Raw data from the A.L.F. reads was directly transferred to a SUN network where bases were called using the public domain "trace editor software"
30   (TED). In both cases, files of called bases were entered into a Sybase™ database. Entering data entailed automatically removing vector and adaptor or linker sequences, but not editing ambiguous bases. After removal of the unwanted bases, files were automatically compared to other sequences in the cDNA database and the latest versions of the
35   publically available databases, GENBANK and SWISSPROT. Searches were performed with the "basic local alignment search tool" (BLAST) (Karlin, S. and Altschul, S. F. Proc. Natl. Acad. Sci. 87 p2264-2268 (1990)).

Sequences SEQ ID Nos 1 to 610, given hereinafter, were obtained by the
40   above procedure.

Example 2

·· A second method of preparing cDNA libraries for obtaining gene fragments of the invention took advantage of the PCR normalisation process described above. Standard procedures were used to prepare mRNA from RNA that had been isolated by standard caesium chloride bouyant

5 density gradient methods from a full term human placenta. The oligonucleotide LNotdt, sequence 5' TACGTTCGACAAGCTTGAATTCGCGGCCGC(T)$_{26}$, (SEQ ID: 1210) was used at 1 μM with AMV reverse transcriptase, to prime first strand cDNA synthesis under standard conditions from 0.5 μg of the placental mRNA. Temperatures above 65˙C were used to inactivate

10 the reverse transcriptase and then the volume of the reaction made up to 100 μl with water.

PCRs were then performed in reactions containing 1 μl of the diluted cDNA, 10 mM Tris-HCl pH 8.3, 40 mM KCl, 1.5 mM MgCl$_2$, 0.01% gelatin, 200

15 μM dNTPs, 10 uCi a^{32}P dCTP, 1 μM each of the primers 11AD1, sequence 5' GCC(TA)(GC)CGCCGA (SEQ ID: 1211), and LNotdT and Taq DNA polymerase. An initial denaturation period of 95˙c for 90 seconds was followed either by 35 cycles of standard PCR, comprising 95˙C for 30 seconds, 45˙C for 30 seconds and 72˙C for 30 seconds or alternatively 3 cycles

20 of the standard PCR already described followed by 27 cycles of Cot PCR during which an additional step of 72˙C for 16 minutes was placed between all of the 95˙C and 45˙C steps of the standard PCR. The standard PCR was followed by a single 72˙C for 3 minutes step while the Cot PCR was followed by one standard PCR cycle except that the 72˙C

25 incubation was performed for 3 minutes.

Products of the PCR reaction were end repaired by adding 5 units of T4 DNA polymerase to the reaction and then incubating at 37˙C for 10 minutes. Enzymes were removed by phenol extraction. The cDNA was

30 precipitated by 70% ethanol, dried and then resuspended in NotI buffer. 20 units of NotI were used to digest the cDNA under standard conditions. cDNA was again phenol extracted and ethanol precipitated. 10% of the purified NotI cut DNA were ligated to the vector pBluescript lting-Meese, M. A. and Short J. M. Nucl. Acid Res. 17 p9494 which had

35 been prepared as standard to receive this DNA by restricting with the enzymes NotI and EcoRV. Transformation and processing of clear colonies was performed as described above except that the host E.coli strain DH5a was used in place of XL-1 Blue.

40 Preparation of clones for sequencing, sequencing and sequence analysis of cDNAs in clones thus-produced were performed as described in Example 1.

··Sequences SEQ ID Nos 611 to 772, given hereinafter, were obtained by
the above procedure.

Example 3

5

cDNA libraries corresponding to adult brain cortex (Clontech
Laboratories, Inc., Cat No. HL10036) and adult bone marrow (Clontech
Laboratories, Inc., Cat No. HL10586) prepared in lambda gt11 phage were
transfected into E.coli Y1090 and plated out for colour selection of
10   recombinant plaques ("Molecular Cloning", 2nd Edition Sambrook J.,
Fritsch, E. F., and Maniatis, T. CSH Press (1989)). 192 lambda Zap
clones, corresponding to rhabdomyocarcoma cDNAs and a gift from C.
Cooper, ICR, Sutton, were similarly plated except that the host XL-1
Blue was used.

15

Clear plaques from each library were resuspended in 5 μl of Tris-HCl pH
8, 1 mM EDTA. 2 μl of the r⸱ ⸱ltant phage suspensions were added
directly to PCRs for the purpos⸱ of amplifying the cDNA inserts for
sequencing. PCR was performed as described in Example 1, except that
20   the oligonucleotides used as primers for the lambda gt11 clones were 5'
GGTGGCGACGACTCCTGGAGCCCG (SEQ ID: 1212) and 5' TTGACACCAGACCAACTGGTAATG
(SEQ ID: 1213). Whichever of the oligonucleotides was to be used to
prime the strand which would serve as the sequencing template was used
in biotinylated form.

25

Preparation of clones for sequencing, sequencing and sequence analysis
of cDNAs in clones thus-produced was performed as described in Example
1, except that 2 pmoles of the primers that were unbiotinylated in the
PCR were used as sequencing primers.

30

Sequences SEQ ID Nos 773 to 1193, given hereinafter, were obtained by
the above procedure.

The following are the SEQUENCE LISTINGS which comprise sequences SEQ ID
35   Nos 1 to 1213 referred to hereinbefore. Certain of these sequences are
preferred, and are listed as such after the main SEQUENCE LISTINGS.

··(1) GENERAL INFORMATION

(i) APPLICANT
(A) NAME: MEDICAL RESEARCH COUNCIL
(B) STREET: 20 PARK CRESCENT
(C) CITY: LONDON
(E) COUNTRY: ENGLAND
(F) POSTAL CODE: W1N 4AL

(ii) TITLE OF INVENTION: HUMAN GENOME SEQUENCES

(iii) NUMBER OF SEQUENCES: 1213

(iv) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: DISKETTE
(B) COMPUTER: IBM PC COMPATIBLE
(C) OPERATING SYSTEM: MS-DOS
(D) SOFTWARE: EXTRACT

(2) INFORMATION FOR SEQ ID :1:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 264 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :1:

GCCGATTCGT GACCAAGAAG GCTCTGTGCA TTCGGGTTTT CCAGGAGACT   50

CAAAAGCTGA AGAAGCGAAG AAGAGCCTTA AAGGCTGCAG CAGCAGCTCA   100

ATAAACAAGC AAAGCGGAGG AACCCAGACA GCCCTTGTCC AAAGCCATAC   150

CAATATGATC TATCTTCTAA TGTATCCATG TTGTAATTAT ATATGTGTCT   200

GTGTGTGTCG AAATCTCTAG ACATACAGAT ATATATTCAT ATATCATATA   250

22

TATATATATA CACA   264

(2) INFORMATION FOR SEQ ID :2:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 124 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID :2:

AGGAACATGT GTTTATTCAT CCAGCAGTGT TGCTCAGCTC CTACCTCTGT   50

GCCAGGGCAG CATTTTCATA TCCAAGATCA ATTCCCTCTC TCAGCACAGC   100

CTGGGGAGGG GGTCATTGTT CTCT   124

(2) INFORMATION FOR SEQ ID :3:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 333 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID :3:

ACAGAGCCGA TTCTGCATCC ACTGTGGTCA ACATTTAGGA AGTTTTAAGC   50

TAAGATTTGC CAAATTGTAG CCTACTGGAT TCCGGTTCTC TTGACATCTC   100

TTTCTAGTAG CCATGTCTTG CACTTCCCGA GTATAAACGA ACTGAGATGC   150

AAATTAAAAA AGGGAGGATT TAGAATAATG AAAAGAGAAA AGTCAAGAAA   200

GCACAATCAC TAGTGTAGAG ATAACAGAAT TTCTGAATTC CCTGAAAGCA   250

ATCTATATAA ATGCATGTGA AATAATACAC CAGCATCTGT GGCCCATACG   300

TCACATATTA GGAACTGATA ACATAAGGTA AAC   333

5   (2) INFORMATION FOR SEQ ID :4:

              (i) SEQUENCE CHARACTERISTICS:
                  (A) LENGTH: 200 base pairs
                  (B) TYPE: nucleic acid
10   (C) STRANDEDNESS: double
                  (D) TOPOLOGY: linear

15   (xi) SEQUENCE DESCRIPTION: SEQ ID :4:

         AGGGAGAAAG GAACATCCGC GAACAGCCAA AGAAATCTCA GAAGAGTCCC   50

         GGAGCTCAAG GATCAGAGTA ACACAATTTT CACTTTTTCT GTCTTTATGT   100
20
         AAGAAGAAAC TGCCTAGATG ACGGGGCCTC CTTCTTCAAA CAGGAATTTC   150

         TGTTAGCAAT ATGTTAGCAA GAGAGGGCAC TCCCAGGCCC CTGCCCCCAT   200

25   (2) INFORMATION FOR SEQ ID :5:

              (i) SEQUENCE CHARACTERISTICS:
                  (A) LENGTH: 213 base pairs
                  (B) TYPE: nucleic acid
30   (C) STRANDEDNESS: double
                  (D) TOPOLOGY: linear

35   (xi) SEQUENCE DESCRIPTION: SEQ ID :5:

         ACAGAGCCAT TTGCATCCAC TGTGGTCAAC ATTTAGGAAG TTTTAAGCTA   50

         AGATTTGCCA AATTGTAGCC TACTGGATTC CGGTTCTCTT GACATCTCTT   100
40
         TCTAGTAGCC ATGTCTTGCA CTTCCCGAGT ATAAACGAAC TGAGATGCAA   150

24

ATTAAAAAAA GGGAGGATTT AAGAATAATG AAAAGAGAAA AATCAAGAAA   200

GCACAATCAC TAG   213

(2) INFORMATION FOR SEQ ID :6:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 345 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID :6:

CGCAGGAGAA GGAACAGAGC CATTGTGCAT CCACTGTGGT CAACATTTAG   50

GAAGTTTTAA GCTAAGATTT GCCAAATTGT AGCCTACTGG ATTCCGGTTC   100

TCTTGACATC TCTTTCTAGT AGCCATGTCT TGCACTTCCC GAGTATAAAC   150

GAACTGAGAT GCAAATTAAA AAAAGGGAGG ATTTAGAATA ATGAAAAGAG   200

AAAAATCAAG AAAGCACAAT CACTAGTGTA GAGATAACAG AATTTCTGAA   250

TTCCCTGAAA CAATCTATAT AAATGCATGT GAAATAATAC ACCAGCATCT   300

GTGGCCCATA CGTCACATAT TAGGAACTGA TAACATAAGG TAAAC   345

(2) INFORMATION FOR SEQ ID :7:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 159 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID :7:

TCCATTTGAC ATCGCATTTC CATAGAAATG GCCAAAGAAA GAAGGTCCTG   50

GGGTTTTTTA TAGAAAGCTC AAAAAGTTCA ACCTTTGATG CTATCCCCCA   100

GCCCAATACA AAATATATAG AAAAAGCGAT TATTACAATA ACGCTTCAAT   150

TTCTTTTCC   159

(2) INFORMATION FOR SEQ ID :8:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 124 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: double
            (D) TOPOLOGY: linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID :8:

ATATTTCAAT CGAACAAAAA GGAAACTTTT TTTGAACTTA TTGAGGCTCT   50

ACTTAAGTAC ATCGAAACCC TTAATGCTTC TGGGGCTGTG TTGATTTCCT   100

TGCCTGGCTG GGGGTTTGAT TCGC   124

(2) INFORMATION FOR SEQ ID :9:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 259 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: double
            (D) TOPOLOGY: linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID :9:

CCGATACAAA TGTACGGAAT GTGTGAGTCC CTCTGGGAGC CCAACATGGA   50

TCCGGATCAC CTGTTTGAAA CCATCTCCCA AGCCATGCTG AATGCTGTGG   100

ACCGGGATGC AGTGTCAGGC ATGGGAGTCA TTGTCCACAT CATCGAGAAG   150

GACAAAATCA CCACCAGGAC ACTGAAGGCC CGAATGGACT AACCCTGTTC   200

CCAGAGCCCA CTATATATTA TTTCTACTTC ATCTATATAT TGCAAAAATA   250

GAAAATAGA   259

(2) INFORMATION FOR SEQ ID :10:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 216 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID :10:

GTCACCAAGA CCGAGGCCAA ACTGGGCACC TTCCCCAGGG CCCTCAAGAA   50

GCTCCTGCAC ACAATAAACG CGCCCTCGTT CTTTAGCAAG TCTGCTCCCT   100

CGAGGCCACA GCAAGCCGGC TACGGAGCCC CCGTTCTGTT TTGAGCCGAA   150

GACTACTTTA TTGGATGCGG TGAAAGGCCT CAGCTCTGAC ACTCTGATCA   200

CTGTGACAAG GGGCCC   216

(2) INFORMATION FOR SEQ ID :11:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 205 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID :11:

27

CACACTTCTT AAGATACATC AAGTACTAGT GATCTTTGCT AGCAGTTATG   50

CCTGTTTCGT GTTACAGATT TGGCCATATA TTGACTAAAC AGCCCCTGTA   100

AAGTTGAAAG AAAAAGTTTA TAACAGTGAA CTTCTGAGGT TTACGTTACT   150

GCAGGCTTTG TTGAGAAGAG ATTGTTACAG TGTGATTTAT GGATGATCAG   200

GGATG   205

(2) INFORMATION FOR SEQ ID :12:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 267 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID :12:

TGCATCTGAA GAGTTGATGA TCGAGACTAC AGCTGCACTA TCAGACTGTC   50

AGGCAGCTCC CTCAGAAACA GCTTCAACAG ACTGGCTGCT GAGCAGACAT   100

CACCGTCCTT CCGAGCTCCA CGGCGACTCC ACTCTCGAAC TTCAGTCGAA   150

GTTGTTCCAC CACCTTCACG TTACCATTCA CCCTAAAAGA CCTTCTTGGG   200

TAAGTCCATG CTGCGTCAAA TATTCCACTA TATTCCACAC TACTGCTGGA   250

TATGCCATTC TCGGTGA   267

(2) INFORMATION FOR SEQ ID :13:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 116 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

· (xi) SEQUENCE DESCRIPTION: SEQ ID :13:

GCCTCATCAG GTTTGCCCAG ATGCTGGAGA AGGTGTGCGT GGAGACGGTG   50

GAGAGTGGAG CCATGACCAA GGACCTGGCG GGCTGCATTC ACGGCCTCAG   100

CAATGTGAAG CTGAAC   116

(2) INFORMATION FOR SEQ ID :14:

       (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 296 base pairs
          (B) TYPE: nucleic acid
          (C) STRANDEDNESS: double
          (D) TOPOLOGY: linear

       (xi) SEQUENCE DESCRIPTION: SEQ ID :14:

TTCGAACTTA CCAGCATCAT GTTTGGTCTC TTCGTATGGT CAAACTTCAA   50

CTTTATAAAA ATAGTGAATA CCACTTATTG AGTGCTTAGA GTGTACCAGG   100

CATGGTGCTA AATACTCTCT ATCCATTATC TCATTAAATC ACATGACACT   150

ATGAGAAATG TACTATTCTT ATACCCACGT TGCCCAGGGT CATACATCTA   200

AGGGGTGCAA GGACCAGGCT TTGATTTCAA ATTATAATCT AATGCTCACT   250

CTCCAGGCCT GATGTCACGC AGCTCCTCAT TCTTATACTT AACATA   296

(2) INFORMATION FOR SEQ ID :15:

       (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 123 base pairs
          (B) TYPE: nucleic acid
          (C) STRANDEDNESS: double
          (D) TOPOLOGY: linear

29

(xi) SEQUENCE DESCRIPTION: SEQ ID :15:

CGTCAGTGTG CTACTTCACA TCATTAGCGA GGCCCAGAAA CTTGAACAGG   50

AAGTCCGGCA CTACCAACAT GCCGCCACTC ATACAACTCA ACTCTTCCTC   100

CAAACTCGAT TCAAAGAGCA ATA   123

(2) INFORMATION FOR SEQ ID :16:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 262 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: double
            (D) TOPOLOGY: linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID :16:

CAACACATTA GTGCATCAAT ATGAATTACT TGTTTAAAAA ATCAAATGCT   50

GGCATTGTCA GAAAAATTTA ACAGGTTTAT TTATAATTAT CATAAAGTTG   100

ACGCTGAAAC TTGTTCACTG AAACATTTTA ACTTGCATTA ATGCTTTACG   150

TCTCCGCATT TATATTAAAA ATTCACACAC AAATGAAATG GAAAAACTGC   200

CAATACCTGA TTTCTGTCCC TATTTTTCAC TCGCAATCAT ATACTTAGTA   250

CTTTTGACTC TA   262

(2) INFORMATION FOR SEQ ID :17:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 169 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: double
            (D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :17:

TAGCCAAATT CTAGGGCATC CAGATGCATT TGAGCCAGTC GTAATCCAGG   50

AAATGTCAAA AAAGCCCCAA TGAATGAACA GAAAATAGCC AGGAAAAATT   100

TGAAAGTAAG TTTTGAAACA GGACTCGTGG AGATTCTAAA CCTTGCATTT   150

TCAAGAAACG TGCATCAGC   169

(2) INFORMATION FOR SEQ ID :18:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 221 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: double
            (D) TOPOLOGY: linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID :18:

AGGGGCACCA TTACCATCCA TCTGACATCG CATTTCCATA GAAATGGCCA   50

AAGAAAGAAG GTCCTGGTAG GTTTTTCATA GAAAGACTCA AAAAGTTCAA   100

CCTTTGATGC TATGCCCCAG CCCAATACAA AACTACACAG AACAAAGCAA   150

TTATTAAAAT ACTGGCTTCG GTTTCTTTTT TTCCTTTGCA AAGTTTCCTA   200

CATATATGTC TTTTACAGTA T   221

(2) INFORMATION FOR SEQ ID :19:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 135 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: double
            (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :19:

TAGGCTCTGT GACGGCATAG TTTTCAGTAG CTTTATCACA ATATTCACAA   50

TGGAGAATTA TATGACATGG TAGCAGAAAT AGGCCCTTTT ATGTGTTGCT   100

TCTATTTTAC CTGAAATTGT AGATATAGGG TAATC   135

(2) INFORMATION FOR SEQ ID :20:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 314 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :20:

GTTATCTATC TATCTTGCAG TTTACCTATC TGATCTGATC TCTGTAATTA   50

TAGTTCTGTC ATTTAAAATA TACTATTTAA ATCTAATTTT TACATTTCAA   100

AAATTATCTT CAGTAGTAAC TAAGTATATT TTCTGTGGAT TCTGAGAATG   150

TTATTTTTCA GAATGTGAGA GTACATATGT ACATTTATAA TCTTGTGACT   200

TTAAAGTCTG TTTTCAGATA CAGTATGTAA ATACTTGTAA AAAAAATTGT   250

ATAATTTTGT GATAATGTAG TTTCCCAAAA CACATTTAGA AAGCATTATG   300

TTATTAGTAA ATGA   314

(2) INFORMATION FOR SEQ ID :21:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 178 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

32

    (xi) SEQUENCE DESCRIPTION: SEQ ID :21:

```
          TCTTCGCATC ACGCAGTACA GATACTCTTT CTGTACTTGC TTAATCTGCT          50
 5
          TTTTGGCATC AGTCAGTTCT CTTTCAGGTC AGCATAATCT TCTTCCTTCC          100

          TCTGAAGATC TGCTTTCAGA TTCTGGGTAC GAGCAGAGCT TACAGAGAGT          150

10        TCCTCTTTCA ATATTTCTGT TTCTTGCC                                178
```

    (2) INFORMATION FOR SEQ ID :22:

        (i) SEQUENCE CHARACTERISTICS:
15   (A) LENGTH: 188 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: double
            (D) TOPOLOGY: linear

20

    (xi) SEQUENCE DESCRIPTION: SEQ ID :22:

```
          ACATCTGATA TCCACCTCCA TGACAGACTG ATCACACCTC CTTCTATACT          50
25
          ACTTCTGTTC TTTGTAAATA CTTAGTATTT TCCAAGGGAG TGTGAGAGAA          100

          GAAATGCTAG GTTCATGAAG GGTCTCTAGG TTAAACTTTC TTTCTTTTTT          150

30        TTTCTTAAAA CAACACACTT ATTATCTTAC AAATCTGT                    188
```

    (2) INFORMATION FOR SEQ ID :23:

35   (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 152 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: double
            (D) TOPOLOGY: linear

40

33

(xi) SEQUENCE DESCRIPTION: SEQ ID :23:

TTCCANCTAA ACATCCAATA TNTCNTTTAN TGCTTTTATA TTTTTNAAAT   50

GTTAAAACCC CTATACCACC TTTTGGGAAT GTTTTAAATT CTCCAATTTT   100

TCGTTATATA GGATCAACCA ACTAAGAAAA GATTTTATCA ATTGAATTGA   150

GG   152

(2) INFORMATION FOR SEQ ID :24:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 83 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :24:

ACAATACAGA GGACAAAGAC CCCTCACAGA ATGCTTTTCA ACCAACTTCA   50

ACTTTTGCAC ACTTTTTCAA CGGTCCCACC ACA   83

(2) INFORMATION FOR SEQ ID :25:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 176 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :25:

AAATGTCCAT TGCTGTATTG CGTGACCGTG GTCCTTGCCT GTCAAATNCA   50

ACAATGACCA AATGATGATG CGCCCTTAAT ACCAGGATGA GACCAAACCT   100

34

ACACATCTCC CAAGTGCCGA ACAAAAACCT GAACAAAAAC CATNTGCACC   150

CTACATCTGG CTGACATTTA CATTTT   176

(2) INFORMATION FOR SEQ ID :26:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 232 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID :26:

AAATGTATGA TCAGAAAATA GGTACGCTTT TAAAATATTT GAACAGAAAA   50

GCTACAAATA AATNGAGCAA TGCTTTTAAA ATCATCTTTG TTTTATAGAC   100

TTTTTCTCGC ATGAATTACA TTTTACAATT TCATNNGGCA TATTCGCACT   150

TTAAGTACTG ACGAAGAAGA CTAAAACAAT CATTTTTTAA CAATATTTAA   200

AAGGATCATA TAGTCGACTT TTAAAACANC CC   232

(2) INFORMATION FOR SEQ ID :27:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 192 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID :27:

GAGAAAGTCC TTGCCATTCT AAAAGCCACC CCACTTCTCT AAGGAGAATG   50

GCCCAATCTT CCCAAGTCCA CACAGGAGGG AAACATTGTT TGCGTAAATA   100

CGCAATGCAA AATTTNNTAT CTTGGCTTAA TACNNCGACG TTTTATTTCG   150

AATGATGAGC CTTCTGCCCC CCCTTCCCCT TTNNNCTCCC CC   192

(2) INFORMATION FOR SEQ ID :28:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 201 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: double
            (D) TOPOLOGY: linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID :28:

TAACACTTTA ANCATCTCTC CAAGCCAAGG AGGCTATGAC ANTGTAGCTT   50

TTATACTGTC CCCATCGGCC ACAATAACAA ACTTTTAACC CTCATAAAAT   100

GAATGAAATC ATCTTTCTAA GAATCTATAC CTACAATTCT CTGAACTAAT   150

CAATGAAAAA GATGATCAAT TCTGACTAAC AAAGATATAT CGATTCCATT   200

T   201

(2) INFORMATION FOR SEQ ID :29:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 275 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: double
            (D) TOPOLOGY: linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID :29:

AACCTAAGGC AGTTGACCCC ACCTTCCAAC ATGTTTTCAC TTTATTGGCC   50

CCTCCCTACA TTCGGGTTAG GTTCCATTTG ATTTGCACAA TAATGACTTT   100

36

ATTTCTCTTT GATCAGGATT TGGCACATAA AATCCTTTTA TCATAGAACT   150

AACTATTTTA ATTACATATA ATGTAACTAA TGGAGAGATT TATAGAGAAT   200

TTTGTTTTTT TGTCATATAC TCCATTTCGA AGACAGATAT GATAGAACTA   250

GAAATTAAGT TGCATTTCTG CAAGT   275

(2) INFORMATION FOR SEQ ID :30:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 122 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID :30:

GTAAATNTAC AAAGATAACG TCGCAATTTT CTTAGATTTA AATCAAAGAC   50

ATTCATCAAC AAGATTTCGA ATGGAATATT CCAGAAATTT CTGAGCCATC   100

TGATCACAAC AACCGTCTTT GA   122

(2) INFORMATION FOR SEQ ID :31:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 197 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID :31:

GGATTTGNAG CTTGAAGTTC AGAGCTGGTT TACCCAAAAA GGGAGCCAAT   50

AGAGATCTTC CCAATGAACC TCAATACACG ATCGTAATAC TCGCACAATG   100

AAATGTTAAG TATGATTCTA GACTTCACTG ACTATCACAA TGATATTTTC   150

TCGATCGCAC TAGTGCACAA CAAAACACGA TGAGTGCAAT GTGAAAC   197

(2) INFORMATION FOR SEQ ID :32:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 97 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: double
            (D) TOPOLOGY: linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID :32:

ACAAAAGTCT GAAGAAATCA CCAACNACAA GACGATTAGA AAATATGTTG   50

TTGGGGTCAC AACTAAAAAG TCCCTGATCT ACATTGNNTT TCNACTC   97

(2) INFORMATION FOR SEQ ID :33:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 260 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: double
            (D) TOPOLOGY: linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID :33:

CAAATAAAAC AANTNTTGTA AAGCTACAAT AGTTATATAC CAAAGCAATA   50

CCTATTACAT GCTTTACACA ATCCCATGAA AAAATAATTT AATAGCTCCT   100

AATCCCTGAT GCAAGGCACT TCAAAGCACC CGCACAAAAC TCCATGAAAC   150

AACATACAAT ACATCATTTA AATAACATAA ACGACTTTCA CACACTTGAC   200

CTAGGAAAAA ATAAAATCCA TACAACCACA GCTAAAAACA TGTTAAGATT   250

38

CACAATAAGA   260

(2) INFORMATION FOR SEQ ID :34:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 168 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: double
            (D) TOPOLOGY: linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID :34:

GGACNTGCGC NNNANNNANA GCCANTGAAC NCAGCCACCA NTGCAAGAAG   50

ACTGCCTCTT NCCAGGCAAG ATTTTACTGG AGCAACANAA CCGGAGGTGT   100

GATCCAAAAT ACCTTCCTTN CCAAGCCCGG GGTNNNNGAT AAGGTGTGGA   150

NTTNGGTTAA AGACAAGG   168

(2) INFORMATION FOR SEQ ID :35:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 173 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: double
            (D) TOPOLOGY: linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID :35:

CTCGNACACT GTGGAGAGCC TGCGNNNNNN NNGGTNTACT CAGGGGGACG   50

AAAAGGAGNN GAANAAGTGA CACNGCNGNT AGCAGAGNGC ACAGAGCTGT   100

GCTNNNGTGG TCCCTTAGNA GCCGAGNAGG TGGGCGCGAG GTGAANAAGG   150

TGCNNGTGCG AGAGTGCGTG ATT   173

(2) INFORMATION FOR SEQ ID :36:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 134 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID :36:

AGCAAGTNNN NNNNNNCATC CTGAAAGTCA AAATGGAATT TGTGTTTATA   50

CAACTAATAA TGATTTTTAT TTGCTCAGTA CAGACTNATT TACAATGAAA   100

GTTTTGCTAA CCTTGGTAAG CTTGTTTACC GTTT   134

(2) INFORMATION FOR SEQ ID :37:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 160 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID :37:

TGGCGCCTGT CCGAGAGCAA GTNGNNNNNN NNCCTGAAAG TCAAAATGGA   50

ATTTGTGTTT ATACAACTAA TAATGACCTT TTATTTGCTC AGTACAGACN   100

GATTTACAAT GAAAGTTTTG CTAACCTTGG TAAGCTTGTT AACCGTTTAC   150

ATGACTTCTT   160

(2) INFORMATION FOR SEQ ID :38:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 140 base pairs

40

(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :38:

CTAGTTTAAT GAATCTGAGG GGCTACTATA AACAATCCCA CCCTCACACG   50

ATTTTTTACC TTCNTTACTT NGCCCTTCAT TAGGCAACCC TAGCAGCACT   100

CCACCTCTAT TCTCGCACTG TCCAAGAGGC CCACCTAATC   140

15   (2) INFORMATION FOR SEQ ID :39:

            (i) SEQUENCE CHARACTERISTICS:
                (A) LENGTH: 203 base pairs
                (B) TYPE: nucleic acid
20   (C) STRANDEDNESS: double
                (D) TOPOLOGY: linear

25   (xi) SEQUENCE DESCRIPTION: SEQ ID :39:

AGCAAGTATC ANNNNNNNNN ATACATTTGA ATTCAAGTTG TTTTTTGTCA   50

AATTGTACAG TGTGTCAATT GATCTTCAAG CTGNNGGTGC CTAGAAATGG   100

30

GNCGGTGTCT GTAGCCCTGG CATGTGCACA CGGAGCATTT GCCACCACCG   150

CAAGCAAAAA GTCTGGGNGA AGTTCACCAA NGNCAAGAAN NATTANGGGA   200

35   AAA   203

        (2) INFORMATION FOR SEQ ID :40:

            (i) SEQUENCE CHARACTERISTICS:
40   (A) LENGTH: 170 base pairs
                (B) TYPE: nucleic acid
                (C) STRANDEDNESS: double

41

        (D) TOPOLOGY: linear

5   (xi) SEQUENCE DESCRIPTION: SEQ ID :40:

    GAAAAGCNNN NNNNNNNGGC TTAAAGAACA ATATGCTGAG ATGGAGAAGG   50

    ACCTAGCGAA ANTNNNAACC TTTTAAGAAC TTGAANNACA ACAATCACAA   100
10
    ACTAATGAGA AGATGTTCAC CTCTCTCCTG AAAACTATGC CCACCAGACC   150

    GTTTAGCCTC TGCTCAAGCT   170

15 (2) INFORMATION FOR SEQ ID :41:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 270 base pairs
            (B) TYPE: nucleic acid
20   (C) STRANDEDNESS: double
            (D) TOPOLOGY: linear

25   (xi) SEQUENCE DESCRIPTION: SEQ ID :41:

    GCTGCATGTT TCCTTGNATT TGAGCTTGAA AGTTCAGAGC TGTTTACCCA   50

    AAAAGGGAGC CAATAGAGAT CTTCCCAATG AACCTCAAAC ACGTCGTAAT   100
30
    ACTCGCACAA TGAAATGTCA AGTATGATTC TAGACTTCAC TGACTCATCA   150

    CAATGATATT TTCTCGATCG CACTAGGCAC AACAAAATAC GATGAGTGCA   200

35 ATGTGAAACA TCTACAAAGT AAATCACACA CTGTTTTTTT AAATNCATAG   250

    AAATTTGATT TGTAATAAAA   270

    (2) INFORMATION FOR SEQ ID :42:

40   (i) SEQUENCE CHARACTERISTICS:
                (A) LENGTH: 245 base pairs

42

        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID :42:

AGAGCTGCAT GTTTCCTTGA TTTGNAGCTT GAAGTTCAGA GCTGTTTACC   50

CAAAAAGGGA GCCAATAGAG ATCTTCCCAA CGAACCTCAA TAACGATCGT   100

AATACTCGAC AATGAAATGT TAAGTATGAT TCTAGACTTC ACTGACTATC   150

ACAATGATAT TTTCTCGGAA TCGCACTAGT GCACAACAAA ATAGATGAGT   200

GCAATGTGAA ACAATCTCAA AGTAAATCAT ATACTTGTTT TCTTA   245

        (2) INFORMATION FOR SEQ ID :43:

            (i) SEQUENCE CHARACTERISTICS:
                (A) LENGTH: 124 base pairs
                (B) TYPE: nucleic acid
                (C) STRANDEDNESS: double
                (D) TOPOLOGY: linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID :43:

TACACTGNGA AAATGTACAA AGAAAGTATC CCCAAATNAT TTACAAAGCC   50

TAAATGTCCT TGATACACAT ACACGGNAGT ATGCAGACAA CAAAGATTAA   100

ATGAAGACAC TTTACACTTT TCGG   124

        (2) INFORMATION FOR SEQ ID :44:

            (i) SEQUENCE CHARACTERISTICS:
                (A) LENGTH: 144 base pairs
                (B) TYPE: nucleic acid
                (C) STRANDEDNESS: double

43

(D) TOPOLOGY: linear

5   (xi) SEQUENCE DESCRIPTION: SEQ ID :44:

GAGTTCTCAC GAATACACAG GTTCAGAGAG ATGAGANGGA ANAACATAAG   50

GCAAATTCCT AACANNCGCT AATATAGGAG GCCGCTCGAT AGGATTTTAA   100

10

AAAAATAAAA ACAATCTTAA TAGTGGGACA AGGCCATCAG AAAA   144

(2) INFORMATION FOR SEQ ID :45:

15   (i) SEQUENCE CHARACTERISTICS:
               (A) LENGTH: 177 base pairs
               (B) TYPE: nucleic acid
               (C) STRANDEDNESS: double
               (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :45:

25   ACTGATTCNN NNTGAAAATA CCCCCTTTCT CCATTAGTGG CATGCTCATT   50

CAGCTCTTAT CTTTATATTC CAGTAAGTTA TTTTGCTCTC ACTGTTTTAA   100

CAAAAAAAAA AACAACAACA TAAAAATCCT TGCAAACCAT GTCAATTGGA   150

30

GAAATTTAAT GTTTTTCATA ACATGAA   177

(2) INFORMATION FOR SEQ ID :46:

35   (i) SEQUENCE CHARACTERISTICS:
               (A) LENGTH: 256 base pairs
               (B) TYPE: nucleic acid
               (C) STRANDEDNESS: double
               (D) TOPOLOGY: linear

40

44

(xi) SEQUENCE DESCRIPTION: SEQ ID :46:

ACTGATTCTG CGAAAATACC CCCTTTTTAT TAGTGGCATG CTCATTCACT   50

TTATCTTTAT ATTCAAATAA GTTATTTCGC TTTCACTGTT TTAACAAAAA   100

AAAAAAAAAA AAAAAAATAC AGCCCTCCCC AATCGAAGAT TTCAACTTTT   150

TAATTCACAC GGAAAAACCA AGACAATTTC ACAACTTCTG GACACAACCA   200

TCAACACAGG ACATTTTTTT TACAGGCAAA TCACTTAAAA CAAAAAAGAT   250

CCCAGA   256

(2) INFORMATION FOR SEQ ID :47:

     (i) SEQUENCE CHARACTERISTICS:
         (A) LENGTH: 155 base pairs
         (B) TYPE: nucleic acid
         (C) STRANDEDNESS: double
         (D) TOPOLOGY: linear

     (xi) SEQUENCE DESCRIPTION: SEQ ID :47:

GAGAAAAGTC NNNNNNNNNA GGTTAATCTA ACTTTTCTTG CTTATTTCAG   50

CTATGATCTG AAAGGATGGA AGACACAAAA TGTATGNNTA AGGTATTTTT   100

AACAAAGATA CATGGGTAAA TTAACAGCAG TAATGTAAAA AAGACTGAGG   150

AGCAA   155

(2) INFORMATION FOR SEQ ID :48:

     (i) SEQUENCE CHARACTERISTICS:
         (A) LENGTH: 68 base pairs
         (B) TYPE: nucleic acid
         (C) STRANDEDNESS: double
         (D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID :48:

GCTTATTTTA CTATATCTAA AGGATAAAGC ACAAAATGAT GAATAAGATA   50

TTTNNACAAA GATACACG   68

(2) INFORMATION FOR SEQ ID :49:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 244 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :49:

CCTGAAAGCA AAGCCATNNA AAGCTTAGAG ACAAGCACNT GAGATGCAGG   50

GGCCTAGCTA AATTTNGAAC CTGNTGGAAC TTGAACCACA ACGATAAAAA   100

ATTACAGAAG AGTTCACCTC TTTCTGAAAA CTATCCACAG ACCGTTTACC   150

TCTGCTTCAA GCTANCAATA TATCAATGGC ACTCTCATAN CAGAAGAAAG   200

AAGTTCCTAC TAGCTCCTGA TTATATTNAA GAAGATGCCC ATGG   244

(2) INFORMATION FOR SEQ ID :50:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 81 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :50:

ACTCGNNCAG CGATAGTCGG AGCTCACCAA CAAAAACNCT NNNNCAGAAA   50

46

GGANAAAGNG CCGCCCTACG TGGTACACAC A   81

(2) INFORMATION FOR SEQ ID :51:

(i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 223 base pairs
    (B) TYPE: nucleic acid
    (C) STRANDEDNESS: double
    (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :51:

GTACTTACTG CACTATGAAA AGCAATAGAT CGTCCATAAG TTATAACCAA   50

AATCTCTCCC TCAGGAATAT ATTCCATACT ACTAACAGAC ATATTAAAAT   100

TTAGAGATTT CACTTCTGTC ATAGTAGCAT GATCCCAAAG TCGAACAGTT   150

TTGTCATCAG CAGAAAGAAT CTGTTTATCT CACTGCACCA CAGAGCTTTT   200

TTATACCAGA AGNATGACCA CTG   223

(2) INFORMATION FOR SEQ ID :52:

(i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 49 base pairs
    (B) TYPE: nucleic acid
    (C) STRANDEDNESS: double
    (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :52:

TATGGTTTNT TGTAAAAAAG CTCANNNANA AAGGGANNGG CTTAAGAGA   49

(2) INFORMATION FOR SEQ ID :53:

(i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 213 base pairs

           (B) TYPE: nucleic acid
           (C) STRANDEDNESS: double
           (D) TOPOLOGY: linear

     (xi) SEQUENCE DESCRIPTION: SEQ ID :53:

     CAACGTCAGA GCACACNNNN NNCTCAGNGC ANAGGCATGA CAGGAGCTCA   50

     TANCNATAAG CCATATAANN NTGTTACCTG TATAGAATGA TGAATTATCT   100

     TTCTAGAGTC TATACCTACA GTTCTCTGAG CTAATCAATG GAAAAGATGA   150

     TCAATCTGAC TAACAAGAGN AATTGATTCA TTTTCTTCCA CNCCCCTTCA   200

     TTCAATAATC AAA   213

     (2) INFORMATION FOR SEQ ID :54:

           (i) SEQUENCE CHARACTERISTICS:
                (A) LENGTH: 166 base pairs
                (B) TYPE: nucleic acid
                (C) STRANDEDNESS: double
                (D) TOPOLOGY: linear

     (xi) SEQUENCE DESCRIPTION: SEQ ID :54:

     GCGTGTTGTG NGGAGTGGNN GTCTNGTCNT CCTGTTAAGG TTTTTGTGTG   50

     CGTNNTTGCG TANGGGGNGG GTTTNGGCAG GTGTTGCCGG TAGCNAAACN   100

     GTTGGCCCCA TNGCCNGNAT TGNNNCCCCN CNNGGGAANG GGGGGGGNGA   150

     CCNNAGNGGG AAAAAA   166

     (2) INFORMATION FOR SEQ ID :55:

           (i) SEQUENCE CHARACTERISTICS:
                (A) LENGTH: 75 base pairs

48

```
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear


 5


        (xi) SEQUENCE DESCRIPTION: SEQ ID :55:


    ACCTCATAGC GAACTCGTCN TATAGANNNN ANNTGAGTCG AGCTCGATGT        50
10
    NGNCGTTGTN GCTGCCAAGC GACAT                                    75


    (2) INFORMATION FOR SEQ ID :56:


15          (i) SEQUENCE CHARACTERISTICS:
              (A) LENGTH: 181 base pairs
              (B) TYPE: nucleic acid
              (C) STRANDEDNESS: double
              (D) TOPOLOGY: linear
20



        (xi) SEQUENCE DESCRIPTION: SEQ ID :56:


25  AATNNNNNCC TATTTTGTAA TTTTTTTGAA AAAAGTTCAA TGTTCAGTTT         50

    TCCTTAGTTT TTACCTTGTT TTCTCTATAG GTCATGATTT CTGTGAAGCA        100

    AAAAGATGCC TTTTACCATG AATTCTTGAG TTTACATCAA TAATATTGTA        150
30
    TATTAAGGGG ATCAGAAGTA GGAAGGAAAA A                           181


    (2) INFORMATION FOR SEQ ID :57:


35          (i) SEQUENCE CHARACTERISTICS:
              (A) LENGTH: 130 base pairs
              (B) TYPE: nucleic acid
              (C) STRANDEDNESS: double
              (D) TOPOLOGY: linear
40
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49

(xi) SEQUENCE DESCRIPTION: SEQ ID :57:

TCGAAGAGAC CTCAATCACC GTTTTTCAGG ATGTTTGATC ACAATACGAA   50

GATGACGNNA TCCAATTTCA GAACACCACA GGGCACTGGC ACACAGAGGG   100

GATTATTACA GAACCACTGA GATGACATTT   130

(2) INFORMATION FOR SEQ ID :58:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 157 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: double
            (D) TOPOLOGY: linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID :58:

GTNATTTTGA AGGTCTCACA AATNTAAAGA CTTATTGTAG CCCATGAACA   50

CATTGACAAG TACAAAAATT ACAAAAATAT GCAGAAATAT TGAATAACTA   100

GAACACAAGC CACTGTTTCA ACTCCAGAAA AAAGAAAGGC TTTACTTTTT   150

CCATGAA   157

(2) INFORMATION FOR SEQ ID :59:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 252 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: double
            (D) TOPOLOGY: linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID :59:

GAGGTGAAGT TGTTCTTTAT TGAATTGCAT TATNAATGNA TAGGCTGTGC   50

50

CTTTTTGNAC TCTCTATGAG TTCATGAATT TAACCAATAC GNCCACAAAT   100

GCTGCTGCTG TCACAGAGAG ATGCCGATAA AGGACACCCA CCACCAATTT   150

TTGAACAGGG AGGGGAGAAT CAACTCTGAA TGTGATGCAG TGACCAGGAG   200

AGAGGACCAT GTTAACAACA CCACACAAAT GCAAATGACT NGTTCTNAAA   250

CA   252

(2) INFORMATION FOR SEQ ID :60:

     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 198 base pairs
          (B) TYPE: nucleic acid
          (C) STRANDEDNESS: double
          (D) TOPOLOGY: linear

     (xi) SEQUENCE DESCRIPTION: SEQ ID :60:

GACCTCGTTT TTCATCCTAT TATGGCGTTT ANCAGGCTAG ACAGAAACAC   50

GCCTTAACTT TANTTGCCAC AAATCTTAAT ATTTTCTCCA CTAATATTAG   100

AAAGGAAGCA ACAAATAATG TCGCTTTTCA CCTGACGTCT GGTTCAACTT   150

TCCGCCCAGC CTATTCCTGN GTCTTCCTCC TGCCTTTCTA ATGTCCCA   198

(2) INFORMATION FOR SEQ ID :61:

     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 229 base pairs
          (B) TYPE: nucleic acid
          (C) STRANDEDNESS: double
          (D) TOPOLOGY: linear

     (xi) SEQUENCE DESCRIPTION: SEQ ID :61:

51

GAGGTGGCAT TATGTGAGAC AGCATTTGGT TAGGGAGTGC CAAGCATTCT   50

ACAGCATTTG ATGGTGGAAA TAGTCATGCT TTTTATTTCT GCTCTCTAGG   100

AATGTAAGGT GCACAGCAGG TCAGGGTACT GCTGTGTGAG ACAAAAGGTC   150

CAGGTAGAGG CAATTCCCCA GATGCAGGCA GGGCAGGTGC TCACTGGGCA   200

GAGTGCTTCT CATACACCTT CAGGAACCC   229

(2) INFORMATION FOR SEQ ID :62:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 181 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID :62:

CATCCTGGGC CCTGGCCGAT GTGCATATCA ACANAAAAAA GGGACTGAAG   50

AACATCGGCC ATATCATCCA CACAAGCCAA ATCTCACACC TTTACTTTAA   100

ACCGCTTAAT GAATTTCATG ACCTTGAGGG CTAAAGATCG TTCTTCGGGC   150

AAGAGCTTTT GGACTGTTTT TAGAACAGAA T   181

(2) INFORMATION FOR SEQ ID :63:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 180 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID :63:

52

GTTGATTGTG AATCATCCCT CTAACATATA ATCAANANTA TGAGTAGAGA   50

ATTTGGCAGA AACAAGAAAA GGACATGGGA TAACTTTTAG ATTTAAAGAG   100

GCAGGCTTGG AACACAAACT GGTATTCTGC TGACACACTG CTGCATATCA   150

TAAGGCTACT CCACAAGACC ATTAGAAGTC   180

(2) INFORMATION FOR SEQ ID :64:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 120 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: double
            (D) TOPOLOGY: linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID :64:

ACAATGTTCC AACATATATA TGGGGAGGGG AGAACANTTA TCTGTATAAC   50

AGGGAACTGT GATTATTTAA AAATANGCNA GAACTTATTT CANCTGTGCT   100

TTAGAAANAA NTGTATACGG   120

(2) INFORMATION FOR SEQ ID :65:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 70 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: double
            (D) TOPOLOGY: linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID :65:

CACATCGCTA TAATCCTTTC TGAGGACTTA AAACTTTATN CCACTTACCT   50

TTATGACTTT TAACAAGCCT   70

(2) INFORMATION FOR SEQ ID :66:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 240 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID :66:

```
TTTCGAGCAA AATGTTTACA TTTACATGGA AATACACACT AAAACAGAAT          50

ATTTTCCTAA TCATGAAACT TCGCCAAAGC AAAATACAAA CTTCCAACGG         100

GAGGTCCACT CAACTAACAA CAATGATCCC CAAGCAGGGC ACCAAGAAAC         150

CTGGGGGACC CTTTNCAAAA AACCTCCTTT CAAGAGACCC TAATACTCTN         200

TCCACACACC CACACGATTT AGGAACTTGG ACATGTTCCT                    240
```

(2) INFORMATION FOR SEQ ID :67:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 254 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID :67:

```
GGAAGCACTA CATTTCATCC AAAGCTGGGT TGAGTTATTT TTGAACACTT          50

TACGATATGC TTAGGTAGGC TTTTAACTTG CTCCTCCAAA CAATATCTNT         100

TGGGAAAACA AGCCCTGTGG AGAGATCCTT CCATCAAGTC GCTTCAATTT         150

AACCTATTTC TAGAGGACTA GACATGCAGA ATCGTCAACT ACAGGGAATG         200
```

54

AAAAGTTCAA AAAGTAGATC CTACAAGATG AACGAGTACT TTTCTAAACA   250

TAAG   254

(2) INFORMATION FOR SEQ ID :68:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 192 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID :68:

AGGCACCAAA GAAACACCAA GCAATAAAGT GAAAGACTAA CCAAGATTTG   50

ACATTGTATG NTTACTGTAT TCTTTAAGAA ACAACTACAA AAAGAAAATG   100

TCAACAAATN NNNACAACTG AGAACCTGGG AATTCCCGCA CGGAAGACAA   150

GAGATAACCT CTCCAATTTA ACACCGCTAG GNTTCTATNN TA   192

(2) INFORMATION FOR SEQ ID :69:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 112 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID :69:

AGCAGCGNNN NNNNTNNAAA CAAAAGACAG GAGCAGAGAG GCCTGAGAGC   50

AGGAGGCGAA TTCGATCTCT CCTCACAAAC AGCCCAGGAA AATATACACC   100

CCGGGGGAAG CC   112

(2) INFORMATION FOR SEQ ID :70:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 232 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID :70:

```
AAGGGTCTCC AATTTAATCC TTGGGTTGTT TTACCACTTC TTTCGTAAAT          50

TTATCAAGAT TTCTTTCGCA CAAATACTCT AGCGCCTCAC AACAAACCTG         100

ACCTTGCGCA GGAAGTCGAC CATCAGCACC CCCTTTACAA CATCGTTCAT         150

ATCACAATTG AGAAGATGAT GAATGAAGAT TCGCTTCCAA GTTCCAAGGG         200

CAGATTTATT CCTTTAACTG ACATTTCCAT GA                            232
```

(2) INFORMATION FOR SEQ ID :71:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 160 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID :71:

```
CNTGGATCCG NCCTTGTTAC GNCCAGGACG NCTGGACCGC AAAATGAATT          50

TTCACTTTTC GACCACCGCC AGAAGAGATG ATTTTCTCAT CATNAACAAG         100

GAACCTTTGA GGAGATCGAC TGAAAGACTA GCGNCCCNGT CAGATAAGAT         150

TTAGGGCTGA                                                    160
```

56

(2) INFORMATION FOR SEQ ID :72:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 182 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID :72:

AAGGAAGACT GGTTTGCCAT CCGAGATCAT TAAAAANGNC TGACCCTAAC   50

AATACGTACA AAAATATAAA ACGCAAATAA AAAATACAAA CAGATTCCTT   100

CTTAAAGTAC TTTTAAGAAA AAAAGCAGGN CCTTGGAAGT TTCGATTCTT   150

TTTTCCTCCC GTCGCAAATT CTATGTTTGG AT   182

(2) INFORMATION FOR SEQ ID :73:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 168 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID :73:

CAAGAGGCAG CTGCCCCTCC CACCTCGGAG GNCTGAGAGG GNCTGTGNCG   50

ATGAGCTGGA CGAGCACAGC ACTAAAAAGG CTTGCCCTNG CACAATAACA   100

CTGAGAGGAT GATGAGAACA CNCTTGAAAT GCTTCATNCA CATGGGCAGG   150

ANAGGCTGCA CAATGAAA   168

(2) INFORMATION FOR SEQ ID :74:

57

(i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 221 base pairs
    (B) TYPE: nucleic acid
    (C) STRANDEDNESS: double
    (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :74:

AACCTTTATT CATCCTCCTN TCCAAGACCT ATGAGAAGGT TCCAGGCCCC   50

AGGAACACAG GCTTCTTGGC CCCAGATGCA CCTCCCTGCA CCCCGGGGTT   100

GTATACCACA CCCCGGGCCC CTAATCCCAG GCCCCGAGAT AGGAAAGCCA   150

ACTAGTTCTT TNTNTGTGAT TCAGTAGGCC TGACCTATAG NTGGAATGTC   200

NCTNTCCCTN NAATAAATTN C   221

(2) INFORMATION FOR SEQ ID :75:

(i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 127 base pairs
    (B) TYPE: nucleic acid
    (C) STRANDEDNESS: double
    (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :75:

AGACTGNTTG GGTCATCCGA GATCATTAAA AATGNCTGAC CCTAACAATA   50

GGCACAAAAA TAAAAACGAA ATAAAAAACC TCCTTANNTT CGAAGTATCT   100

TAGAAAAAAA CAGGGCCTTG AGTTCTG   127

(2) INFORMATION FOR SEQ ID :76:

(i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 180 base pairs

58

        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

5

        (xi) SEQUENCE DESCRIPTION: SEQ ID :76:

    AAAAGAACAG CAGTTTCACA TTTCACATAT TTGAAAAACA TTTCAAAACC   50

10

    CTCTAATAAG TATTTAATGA AAATAAATTT ATCGAAGAGA AACAATGACC   100

    ACAAAATTAA TACTACCAAA TCATTACTGA GACTCTTGCA TTACAATATT   150

15 TGGAGAGTAG GTGAAGAAAA TNTAGACCGA   180

    (2) INFORMATION FOR SEQ ID :77:

        (i) SEQUENCE CHARACTERISTICS:
20   (A) LENGTH: 142 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: double
            (D) TOPOLOGY: linear

25

        (xi) SEQUENCE DESCRIPTION: SEQ ID :77:

    GATTAANNNN NNNGCACCCN NNATTACTGG CACAGCTGGT GAATATTTTC   50
30

    GTGGACTTTT GACTAGTGCA CCTGCGTGCG GGAAAACANT GATAAAACTG   100

    TCACTTTAGC CNCNAACTAC AAGACCNGTT AGACTAGAGA GC   142

35 (2) INFORMATION FOR SEQ ID :78:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 124 base pairs
            (B) TYPE: nucleic acid
40   (C) STRANDEDNESS: double
            (D) TOPOLOGY: linear

59

(xi) SEQUENCE DESCRIPTION: SEQ ID :78:

GGCCCTGAGA GCAGGACGGC GAATTCGATC TCCTCCTTCA CAAACAGCCC   50

ANGGAAANTA CACCCCGGGG AANNCCCCNC NCNNTTAGAA CCNNCAGGNT   100

CTGNCCCCCC CNNNGNCCCC CCCG   124

(2) INFORMATION FOR SEQ ID :79:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 171 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID :79:

AGGTATAGTG TTCCCTAATC ATGTACTTGT GAAGCACCCG GANTTTTTCA   50

TATAGTCTAA AAGCTAGAAG AACAAGAGTG TATTTCGTGG GTGGATGTAT   100

NGTCACTTGC TGAANNNNTT GAAATACCAT TATCCCCCTT GCTAACNCCT   150

TTAAGNAAAN GCCNTTTTAA G   171

(2) INFORMATION FOR SEQ ID :80:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 98 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID :80:

CTGAACAGTG TGGTCGAGCA TTCCAAGTCC GTGAAGGTGC AGGAGCGGTA   50

60

CGACAGTGCC GTGNGGGCA· ·ATGGCACCT NGACCACGGG CNCCTAAG   98

(2) INFORMATION FOR ·.Q ID :81:

(i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 108 base pairs
    (B) TYPE: nucleic acid
    (C) STRANDEDNESS: double
    (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :81:

CCTCAACAAG TGCGAGACCT GGGCGTCCAA CCTGCCTACA ACCACAGCCG   50

CGAAAGAAGA AGACCTGCTG CTTCAATACA ACACGGGAGG ACCTGGCCAT   100

CAACATCA   108

(2) INFORMATION FOR SEQ ID :82:

(i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 180 base pairs
    (B) TYPE: nucleic acid
    (C) STRANDEDNESS: double
    (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :82:

ACACATNACC CACNGCCAGT ATATCTCGAA CAAAGTCTCA GACGATACTC   50

CCT...AATTG TAAAGCTTAA TACAGGTTNT GGAAATCATT TAACACCCGA   100

GAATGTCCCA TCACAGTCTT CCGTCAAAAT TTAGCCTCAC AACAACAACA   150

ACGCCTACGA AATTCTAAAT TCAGAAGGAA   180

(2) INFORMATION FOR SEQ ID :83:

     (i) SEQUENCE CHARACTERISTICS:

          (A) LENGTH: 199 base pairs

          (B) TYPE: nucleic acid

          (C) STRANDEDNESS: double

5   (D) TOPOLOGY: linear

     (xi) SEQUENCE DESCRIPTION: SEQ ID :83:

10

    GGCTTCTGAT CGCCATCCTT GAACAGGGCA AAGGTGGCCT CACCAGCCTT   50

    CGATGCAGCT GCCATGCGCG CCAGAATCAG CGAAGGCATA CCCTTACGTC   100

15 GTTGGACGCA TGTTTAGATG CCTTTGAGAC CGCCCAGAGA AGTCCTTGTC   150

    CTTCTTAATA AACACCTCCT CGCCAACTGC GACGACCACA ATCACCGTA   199

    (2) INFORMATION FOR SEQ ID :84:

20

     (i) SEQUENCE CHARACTERISTICS:

          (A) LENGTH: 214 base pairs

          (B) TYPE: nucleic acid

          (C) STRANDEDNESS: double

25   (D) TOPOLOGY: linear

     (xi) SEQUENCE DESCRIPTION: SEQ ID :84:

30

    CTTCGGTAGT GCCGCCGTGG TGCCACACAC CGTTGAGGTT GGAGTGGGCA   50

    CAGGCATGGT ACCACCAGCC TCCCCGCTGG TACAGGGCAC AGTTACCTGA   100

35 GGGGAGAGAG AGAGTCCATG TCCTCTCACC AGAATAAAAG CCTCTACCTG   150

    CACCTCACAG TGCAAGGCTT TTGCCAGGCA TCCCCTGGCC CCTCCCATTT   200

    NACNGAATAC AACC   214

40 (2) INFORMATION FOR SEQ ID :85:

62

(i) SEQUENCE CHARACTERISTICS:

    (A) LENGTH: base pairs

    (B) TYPE: r. .eic acid

    (C) STRANDE:. ESS: double

5   (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :85:

10

CCTGGGCAAG CTGAATGTGA AGTTGACCAG GCTAACTGAG AAGCAAGCCC   50

AGTACCTGGG CATGTCCTGT GATGGCCCCT   80

15 (2) INFORMATION FOR SEQ ID :86:

    (i) SEQUENCE CHARACTERISTICS:

        (A) LENGTH: 210 base pairs

        (B) TYPE: nucleic acid

20   (C) STRANDEDNESS: double

        (D) TOPOLOGY: linear

25   (xi) SEQUENCE DESCRIPTION: SEQ ID :86:

GGGGATAGCT GGCTCATCCT CGGAAAACAG ACCCACATCT CTATTCTTGC   50

CCTGAAATAC GCGCTTTTCA CTTGCGTGCT CAGAGCTGCC GTCTGAAGGT   100

30 CCACACGGCA TTGACGGGAC ACAGAAATGT GACTGTTACC GGATAACACT   150

GATTAGTCAG TTTTCATTTA TAAAAAAGCA TGACAGTTTA TTACTCTGTT   200

35 TCTTTTAATG   210

(2) INFORMATION FOR SEQ ID :87:

    (i) SEQUENCE CHARACTERISTICS:

40   (A) LENGTH: 102 base pairs

        (B) TYPE: nucleic acid

        (C) STRANDEDNESS: double

        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID :87:

CACAAAAAGC ATGATCAGGG CTAGCCTCAA TACAGGGAGA AATCATGGAT   50

ATTTAAAAAT ACTTTTTTTG ATTCAGATTC CGGTATGACT GAAGANGCAA   100

CA   102

    (2) INFORMATION FOR SEQ ID :88:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 275 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: double
            (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID :88:

GATAGGCGCA TGCATACTAC GGCTAAGGAG AAACAATGTT CCTACATATT   50

ACGGGCAGTG AGAACATTAT CTGTATAACA GGAACTGTGA TTATTTAAAA   100

ATAGCAGAAC TTATCNGTCT GTGCTTTAGA AATAACTGTA TACAGTGTTA   150

TAAGTTGAAA AGAACTCAAA ATAACTAATA CAAATAAGAA CCTACGTATT   200

AGAATTCAAA AAAGCTGCTT TCTGTGAAGT CAATCAGCTA TATTAAAAAA   250

TGACACAAAT TCAAAACACG ATCAT   275

    (2) INFORMATION FOR SEQ ID :89:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 263 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

5   (xi) SEQUENCE DESCRIPTION: SEQ ID :89:

GCCTGATGGT ATATACTGTT TTGCAATTGC ATACAACTGT GCATTACAAA   50

TTAATAGTAA TTATGGTTTG GNNGTAAAAT CGAGTTTCAG AATAAAATNA   100
10

AAAACAATAA AATCCAAAGA ACGATGTAAA CAAAAAAGCT TTTGTTTTGT   150

TACAAAGTAT ATTAAGGATT TTCTGCTAAG ATTCAGTTTA AGAGTTTTCC   200

15   TCGTGAAAAC TAAGTAGAAA CACAATGCCA ACAGCTGGCC AGTAATCAGT   250

GCTGTGTACT CCA   263

(2) INFORMATION FOR SEQ ID :90:
20
          (i) SEQUENCE CHARACTERISTICS:
              (A) LENGTH: 108 base pairs
              (B) TYPE: nucleic acid
              (C) STRANDEDNESS: double
25   (D) TOPOLOGY: linear

          (xi) SEQUENCE DESCRIPTION: SEQ ID :90:
30
GCGTCCTGCC CAACATCCAG GCCGTACTGC TGCCCAAGAA GACGGAGAGC   50

CACCACAAGG CCAAGGGCAA GTGAGGCCGC CCGCCGCCCC CGAGGGACCC   100

35   CTTTGAGA   108

(2) INFORMATION FOR SEQ ID :91:

          (i) SEQUENCE CHARACTERISTICS:
40   (A) LENGTH: 206 base pairs
              (B) TYPE: nucleic acid
              (C) STRANDEDNESS: double

65

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :91:

GCCTTGGTGG AGGGCATGAG GCTATGATGA CTATTGGCTA TAATATGGAT   50

ATGGCTTTGG CTGATAGATT TGAAGAGACC TCAATTACGT TTTTCAGGAA   100

TGTTTGATCA TAGATACAGA GATGGTGGTC CAGTTTTCAG AGCACCACAG   150

GGCACTGTGT ACACATGAGG GGTTACCTTA CAGAGCCACT GAGAATATAT   200

TAATAA   206

(2) INFORMATION FOR SEQ ID :92:

     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 210 base pairs
          (B) TYPE: nucleic acid
          (C) STRANDEDNESS: double
          (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :92:

CCTTGGTGGA GGGCATGAGG CTATGATGAC TATTGGCTAT AATATGGATA   50

TGGCTTTGGC TGATAGATTT GAAGAGACCT CAATTACGTT TTTCAGGAAT   100

GTTTGATCAT AGATACAGAG ATGGTGGTCC AGTTTTCAGA GCACCACAGG   150

GCACTGTGTA CACATGAGGG GTTACCTTAC AGAGCCACTG AGAATATATT   200

AATAAANNNG   210

(2) INFORMATION FOR SEQ ID :93:

     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 189 base pairs

66

(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :93:

AGGACTTCAT CCCAGACTCA CTTGTTCTGT TACAGAAACT AACCTAAAAG   50

GCTGGAAATT AAAGGATACA ACCTAAGAGG TTATAACAGC AGACTGGTAA   100

AACATGGCGA AAGGAGCTCT CTCTTTCCCC GCAGTCTACC AAGCTCCTGT   150

GCATTTTCAC CACATAGATC TGCTAGCTTA CAAATGATG   189

(2) INFORMATION FOR SEQ ID :94:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 160 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: double
            (D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :94:

GAAGTGACAG GNAAGCTACA GGTGTATAAC AAATTTGTAA ACTAACCAAG   50

CACAATGTGG CAGGGCCTAG CTGCTACAAA GAAGACAATT TAACAAATAC   100

TCAACGCATG ACAAAAAACT CAGGACTGCA TTTGCACTAA TCGATAACGN   150

GTCATTTAAT   160

(2) INFORMATION FOR SEQ ID :95:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 171 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: double

67

                        (D) TOPOLOGY: linear

5   (xi) SEQUENCE DESCRIPTION: SEQ ID :95:

        TGCTTTATAC ATNATNAAAG GTAGGCACTT CATAAAATTT GCATTTTGGT   50

        AAAAGGCAAC AATTTGATGT CAGTATCTTA ATTGTGTCAT TAACTTTTTT   100
10
        AAGAGAACAG ATTATCAAAA TTTTACGAAG AAGAAAAAAA NTATAGTTTT   150

        TAAGGAAACT ACAGAAGGGA T   171

15   (2) INFORMATION FOR SEQ ID :96:

            (i) SEQUENCE CHARACTERISTICS:
                (A) LENGTH: 131 base pairs
                (B) TYPE: nucleic acid
20   (C) STRANDEDNESS: double
                (D) TOPOLOGY: linear

25   (xi) SEQUENCE DESCRIPTION: SEQ ID :96:

        GTGGATAAGA AGATGTGTAC TTGGGAACAA GGCTAAAGCC ATTGGCTGAT   50

        TTCCCCAACC TTTTTATTCG CGAAGAAACT CCAGTTGTTA ACTTTTTGAG   100
30
        AGTTTTTTTT GGCAAAAGAA CTNCATTTAN C   131

        (2) INFORMATION FOR SEQ ID :97:

35   (i) SEQUENCE CHARACTERISTICS:
                (A) LENGTH: 279 base pairs
                (B) TYPE: nucleic acid
                (C) STRANDEDNESS: double
                (D) TOPOLOGY: linear
40

(xi) SEQUENCE DESCRIPTION: SEQ ID :97:

GTCCTAATAT TTCTGTNCAG AAATTGTCAA CTTGACTTGA GAGTTGAGAA   50

GTAAAGTTAA GGCACTGACA ATATATCAGA ATGGAAGTCC TTAAGAGCAA   100

CTAACAGGTT CTTGATCAGA CTGACTATCT TTTCTTAAGT TCATAATATN   150

TTACTGTCCA GCCAACTATA CTTGGATCAA AATATCCTTC ATGAAGGGCC   200

ATAATGTATT GATGATCTGC TGTAACTTTG AGAAGCTTCC TGAAGCTCNT   250

TTTGAATAAA TTTATNGAAC TTATGAAGA   279

(2) INFORMATION FOR SEQ ID :98:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 266 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: double
            (D) TOPOLOGY: linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID :98:

GTGAGTCTTT CTTCAACTAG GGGAATGTTT CCAGGGCACG CCAGGCCTCA   50

CTCACGCAGG CCTCCGCGAC AACTGTTCAG CACTGACTGA GGATGAAGTG   100

AAATCCTGAA AGCTGAGAGC CAGCGCCCTC ACACGAGGGC TGGGACGTAA   150

CAAAAGCCCA TCAAGAGTTT TGCCCAGGGC TTTCTTGAGC CTTGAAGCAT   200

GACGAGACCA GGACCCTTTA GGATTAAGCA AGTTTTATGC GGTCTNAAAA   250

AACTCCAGGG CCTCCA   266

(2) INFORMATION FOR SEQ ID :99:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 206 base pairs

69

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :99:

GGGAACATTT ATTGACATGA AAAGGTGTTT CAGATATACT GATATGTCAA   50

ACAAATAGTA AAACAACATA GAGTAATGAT TCATTTTGGT AAAAAATATA   100

TATGTATATA TAGAAAAAAA TTCTGCAGGA CATATGCTAA ATTGGTAACA   150

GTGCTTACCC CTGGGAAGGG GGTATACGAT GTTGATTTAC TCTTTGGGTA   200

CGTATT   206

(2) INFORMATION FOR SEQ ID :100:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 73 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: double
            (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :100:

CGCAACTNTC NCTAAACATC CAGTTTTCTA ATNTAATAAA AAATGGCAGT   50

AATTATCCTC ACCTCTCAGG GAA   73

(2) INFORMATION FOR SEQ ID :101:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 108 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: double
            (D) TOPOLOGY: linear

70

(xi) SEQUENCE DESCRIPTION: SEQ ID :101:

GAGCACAATC ATGNGCAAGC GCAACAGCAC ACCTTTATCC GAGTGAGACC   50

ACTATGCAGC NGAACAGAGA CTTCTTATCT CTTCTTCTTG ATACTTGAAT   100

ACTGCCCC   108

(2) INFORMATION FOR SEQ ID :102:

     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 210 base pairs
          (B) TYPE: nucleic acid
          (C) STRANDEDNESS: double
          (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :102:

GAATTATCAA ACCATCNTTG CTGACATTAA TTTTCCAGCT TTGATCTTAN   50

NTCTNGCTTT AGTCCTCATA CAATGACTGT GTTTTTCTCA FACGATNTAT   100

CGTATAGGNA TCCTTCTAAG CAATCCTGCA CCCACAAAAA AGCTGCATCT   150

TCAATATAAC ANAAAAAGGN ATTTTGCAAA AAGTACAAGT TTTATGTCTN   200

CTGTTAACTG   210

(2) INFORMATION FOR SEQ ID :103:

     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 76 base pairs
          (B) TYPE: nucleic acid
          (C) STRANDEDNESS: double
          (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :103:

71

CGTAGTTCGA TTCGAGTGGT CTATACAATC ACACCAAGCT TGATGTTGAT   50

GTCACCAAAA TTTCTTTCCA AAAAAA   76

5   (2) INFORMATION FOR SEQ ID :104:

            (i) SEQUENCE CHARACTERISTICS:
                (A) LENGTH: 167 base pairs
                (B) TYPE: nucleic acid
10   (C) STRANDEDNESS: double
                (D) TOPOLOGY: linear

15   (xi) SEQUENCE DESCRIPTION: SEQ ID :104:

       CTTATGATTA ACTAAGCAAA TCTTTCATAG AAAGATATTA TCAAAGCTGA   50

       AGAAATGCAA ACTTNAACAA AGTGCCGTGA GATTCCGGAA AAACCCTTAA   100
20
       CCGATTGAAT GGTTTTTTAA GAATAAAAAA GAAGTCTGAT ACTGAACTAC   150

       AAGTCGCAAG GAACATC   167

25   (2) INFORMATION FOR SEQ ID :105:

            (i) SEQUENCE CHARACTERISTICS:
                (A) LENGTH: 122 base pairs
                (B) TYPE: nucleic acid
30   (C) STRANDEDNESS: double
                (D) TOPOLOGY: linear

35   (xi) SEQUENCE DESCRIPTION: SEQ ID :105:

       TATCTGCATA TCTAAACATA GAAAAGCACA ATAAAAACAC ATATCATAAC   50

       CTCACGGGAC CACCATCATA CAGCAATTTG TCATGATCAA AAGAAACATC   100
40
       ATTAGTCGTG CCATAACTGT AT   122

72

(2) INFORMATION FOR SEQ ID :106:

     (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 255 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

     (xi) SEQUENCE DESCRIPTION: SEQ ID :106:

GAATTCTTCA CTCCAGATTT CCAATGCCAA GATACATTGA TACTGAACAT   50

GGAGGCAACC AGGCCCGTTT CCTCCTTTCA AAGTCAACCC TCACAGACTC   100

ATAATAATAT GCATGCCTGG GGGCAGGAGT CTGGAGCACC TATTCTNACA   150

GATGATGTTA TTTACAAGTG TTTATGGATC ACTTGAAGAA ACTTGCTGTG   200

TCCAGTGCTG CTTGAAGTGC TAATAATGTT AAAGACACTT AAGAAGATGA   250

AATAA   255

(2) INFORMATION FOR SEQ ID :107:

     .(i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 227 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

     (xi) SEQUENCE DESCRIPTION: SEQ ID :107:

GGACGTGAAT TGGTGGAATA TTTACAAAGA AAACTGTTTT CTCAAAACAC   50

TGTTCATTGG TTGCAAGAAT GAATACTGAC TTCAGAACTC AAACAATGGA   100

AGAACTTGCA TTTTTATGGA ACTCAGTATT AAAAGAAAAT ATAATGTGAT   150

73

AGCACTTTGC AGATATGTCT AGACTGTGAT CTGAAGCATC GTAGTTTCCT   200

ATACCAAGAN ACANTTATGT GGTAAAT   227

5   (2) INFORMATION FOR SEQ ID :108:

            (i) SEQUENCE CHARACTERISTICS:
                (A) LENGTH: 162 base pairs
                (B) TYPE: nucleic acid
10   (C) STRANDEDNESS: double
                (D) TOPOLOGY: linear

15   (xi) SEQUENCE DESCRIPTION: SEQ ID :108:

GAAAAATNGC ATGAAAGAAG ACTCTTNNNN NGCCATACCA TGGTACAATA   50

ATCATNAAAA NACAANAACA AAAACAAACA CATAAAACCA CTCACATATA   100
20
CATGTAGATA CAACAACNAT ATAATATCAA TAAAAAAAAA ATAGNAAAAA   150

AAAAAAATAA CA   162

25   (2) INFORMATION FOR SEQ ID :109:

            (i) SEQUENCE CHARACTERISTICS:
                (A) LENGTH: 154 base pairs
                (B) TYPE: nucleic acid
30   (C) STRANDEDNESS: double
                (D) TOPOLOGY: linear

35   (xi) SEQUENCE DESCRIPTION: SEQ ID :109:

AATTAAAAAT ATTAAACAAA ACTACCACTC CTCCTTATTA AAGCCCATAA   50

AAATAAAAAA CGAAACCCGA GAACCAAAAT GAACGAAAAT CTTTCGCTTC   100
40
ATTCATCGTC CCCACAATNC CAGGCCTACC CCCCATACTG ATCATTCATT   150

74

GTTT   154

(2) INFORMATION FOR SEQ ID :110:

        (i) SEQUENCE CHARACTERISTICS:
                (A) LENGTH: 182 base pairs
                (B) TYPE: nucleic acid
                (C) STRANDEDNESS: double
                (D) TOPOLOGY: linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID :110:

ATGTGCCAAG TAAAAAATCA ATTNGTNGCC TTTTTCCATT NCGCGGACAC   50

CCATAGGCAC CAAAAAAAGG TGCTAATAAG TAACATGTTT TAAGATGCAG   100

AATAAGCTAT GGAAACAAGG AATGCTCCAA GTGTCCCAGT CTTTCTCCTT   150

GCACTCCTTG TTAATAACAA TACACTATAT CA   182

(2) INFORMATION FOR SEQ ID :111:

        (i) SEQUENCE CHARACTERISTICS:
                (A) LENGTH: 94 base pairs
                (B) TYPE: nucleic acid
                (C) STRANDEDNESS: double
                (D) TOPOLOGY: linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID :111:

GAAGGTGAGA ATAGGGTAGG GGAAACAGTA GGACAGGAAG TATTCACGTA   50

CNTCAAAACC AATGGTAGAA CATCACATTT CAAACTGCAA ACCA   94

(2) INFORMATION FOR SEQ ID :112:

        (i) SEQUENCE CHARACTERISTICS:
                (A) LENGTH: 92 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

5

    (xi) SEQUENCE DESCRIPTION: SEQ ID :112:

TAGGGCAGTG AAACCTAATC TGCCTGATGC TATAANTGAN TGAATTACAT   50

10

GNTCATTNGT TAAATTTTGT TCTAAACCCA TTAGGAAATT GT   92

(2) INFORMATION FOR SEQ ID :113:

15   (i) SEQUENCE CHARACTERISTICS:

        (A) LENGTH: 152 base pairs

        (B) TYPE: nucleic acid

        (C) STRANDEDNESS: double

        (D) TOPOLOGY: linear

20

    (xi) SEQUENCE DESCRIPTION: SEQ ID :113:

25   GATTGTTTTT GCATTGCGTG TGTCACACAG CAGCACAAAG ACAATATATG   50

TAAGCGTNNA TACACCAGAT TTGACACAAG AGATAGCGAA CACCACAAAG   100

ATTAGGACAG ACCGCGTATA GTAGCTCTGA GGAACTCCAA GAATCTAGAG   150

30

GG   152

(2) INFORMATION FOR SEQ ID :114:

35   (i) SEQUENCE CHARACTERISTICS:

        (A) LENGTH: 182 base pairs

        (B) TYPE: nucleic acid

        (C) STRANDEDNESS: double

        (D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID :114:

TTGGCACTGA CATCCAGGAC AACAAATGCA GCTGGCTGGT GGTTTCAGTG   50

TCTGCAACGG GCCACTCCAG AACAGTACCA ATCCTGAAGG AAAATACNTG   100

GCAGAAGGAG GCTGAGAAAG TGGCTCCGTG AAGGCNCTAT AGAGGGCTGA   150

TCTGCCAGCA TGTCTTCAAT ATGAGGAAGG CA   182

(2) INFORMATION FOR SEQ ID :115:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 182 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :115:

GGCACTGACA TCCAGGACAA CAAATGCAGC TGGCTGGTGG TTTCAGTGTC   50

TGCAACGGGC CACTCCAGAA CAGTACCAAT CCTGAAGGAA AATACNTGGC   100

AGAAGGAGGC TGAGAAAGTG GCTCCGTGAA GGCNCTATAG AGGGCTGATC   150

TGCCAGCATG TCTTCAATAT GAGGAAGGCA NT   182

(2) INFORMATION FOR SEQ ID :116:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 227 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :116:

GAGGTTCTTG AATATGTATT TTTTACTGAA AAAATCATTC ATAAANTAAC   50

ATACAAAAAT GTACAAACAC ATGAGTAAAT AATGTAATGA CAAAGGACTA   100

TTTTCGGAAA AGTGTTTTTT AAAACANNCT AGATTTCAGT GCAAAAATGT   150

ACCCCTGGCA CCTCTTAAAA CGTAAGAGCA AGCTCAAAAA CACGTAGTGA   200

TGGAAATAAG CTAGCTACGC TCAATGC   227

(2) INFORMATION FOR SEQ ID :117:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 172 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: double
            (D) TOPOLOGY: linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID :117:

CGAGAGATTG GTAATGAGGA AGCAATTTGG AGGGGNGGAA GCTACAANGA   50

NNNNGGGAAT TACAACAATC AGTCTTCAAA TTTTGGACCC ATGAAGGGAG   100

GAAATTTTGG AGGCAGAAGC TCTGGCCCCT ATGGCGGTGG AGGCCAATAC   150

TTGCAAAACC ACGAAACCAG GT   172

(2) INFORMATION FOR SEQ ID :118:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 210 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: double
            (D) TOPOLOGY: linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID :118:

AATGATGGAA GCAATTTTGG AGGTGGTGGA AGCTACAATG ATTTTGGAAT   50

TACAACAATA GTCTTCAAAT NNGGACCCAT GAAGGGAGGA AATTTTGGAG   100

GCAGAAGCTC TGCCCCTATG NCGTGGAGGC CAATACTTTG CAAAACCACG   150

AAACCAAGGT GGCTATGGCG GTTCCAGCAG CAGCAGTAGC TATGGCAGTG   200

GCAGAAGATT   210

(2) INFORMATION FOR SEQ ID :119:

     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 95 base pairs
          (B) TYPE: nucleic acid
          (C) STRANDEDNESS: double
          (D) TOPOLOGY: linear

     (xi) SEQUENCE DESCRIPTION: SEQ ID :119:

GGTAAACACA AAGAGTTTCT GATAGTGTCT GCACAACAGC AAACCAACAT   50

TTGGTGAGGA ATTAGCAATT TCTTGCCAAA GAAAATTGAT TCTGC   95

(2) INFORMATION FOR SEQ ID :120:

     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 168 base pairs
          (B) TYPE: nucleic acid
          (C) STRANDEDNESS: double
          (D) TOPOLOGY: linear

     (xi) SEQUENCE DESCRIPTION: SEQ ID :120:

GGAGTATTTN AANNTTTCAA ACTTTATTAC TTAATGAAAC AGTTTCTATA   50

TACTGCTTCC AATATACTTT AATCCTTTTT TTCTCGTTAA ATTTTTTTTG   100

79

TTGTTCTTCA GTTGAGCTGA GATACTTTTA ATTACTTTTT ATTAACTGCT   150

TCCAGAAACC GTAACAGG   168

5   (2) INFORMATION FOR SEQ ID :121:

                (i) SEQUENCE CHARACTERISTICS:
                     (A) LENGTH: 231 base pairs
                     (B) TYPE: nucleic acid
10   (C) STRANDEDNESS: double
                     (D) TOPOLOGY: linear

15   (xi) SEQUENCE DESCRIPTION: SEQ ID :121:

           GGAGTATTTA TCTTTCAAAC TCCNTACTNA GTGAAACAGT TTCTATACCA   50

           CTGCTTCCAA TTACTANCTN TTTTNTCNGT TAAATTTTCN NCTGTTTTTC   100
20
           AGTTGAGCTG AGATACTTTT AATATNNNGT NACTGCTTCC AGAAACCGTA   150

           ACAGGTGCAG GAATAATTGA TGATATCCAA GTAGAGGCTG ATGNCAGCTA   200

25   ATACATACTT CGGTGACNTT ATGCATCATG A   231

           (2) INFORMATION FOR SEQ ID :122:

                (i) SEQUENCE CHARACTERISTICS:
30   (A) LENGTH: 174 base pairs
                     (B) TYPE: nucleic acid
                     (C) STRANDEDNESS: double
                     (D) TOPOLOGY: linear

35

                (xi) SEQUENCE DESCRIPTION: SEQ ID :122:

           TCTATGGCAT GAATGTTTGC AACCAACNNN NNGGAAAGCC TTAAAGGAAT   50
40
           AGCTGTTCAC ATAGGAGACC GTGACAATGC TGTACGCAAT GCTGCACTAG   100

80

ACACCATTGT ACGGTGTACA ATGTCATGGG ATCAGGTGTT CAAACTGATT   150

GGAATCTTTC TGAAAGGAT ATGA   174

(2) INFORMATION FOR SEQ ID :123:

        (i) SEQUENCE CHARACTERISTICS:
                (A) LENGTH: 170 base pairs
                (B) TYPE: nucleic acid
                (C) STRANDEDNESS: double
                (D) TOPOLOGY: linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID :123:

CTNNACAGGA GAAGNAAGTA ATGATCATTC CCCAAAAATG TTCTGTTATC   50

AACTGNNTTT ATAAAAAATC GATTGTGGGT AGAAGCAGAG AAAAGGCACT   100

TAGTAAAGAT ACTACATGAN GAAAAANNTC TGCCCTTTGA ATTCTTANGA   150

AACATNNTNG NNGAATCAAT   170

(2) INFORMATION FOR SEQ ID :124:

        (i) SEQUENCE CHARACTERISTICS:
                (A) LENGTH: 157 base pairs
                (B) TYPE: nucleic acid
                (C) STRANDEDNESS: double
                (D) TOPOLOGY: linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID :124:

AAGTAATGAT CATTCCCCAA AAATGTTCTG TTATCAACTG NNTTTATAAA   50

AAATCGATTG TGGGTAGAAG CAGAGAAAAG GCACTTAGTA AAGATACTAC   100

ATGANGAAAA ANNTCTGCCC TTTGAATTCT TANGAAACAT NNTNGNNGAA   150

81

TCAATNT   157

(2) INFORMATION FOR SEQ ID :125:

5   (i) SEQUENCE CHARACTERISTICS:
                    (A) LENGTH: 169 base pairs
                    (B) TYPE: nucleic acid
                    (C) STRANDEDNESS: double
                    (D) TOPOLOGY: linear
10

               (xi) SEQUENCE DESCRIPTION: SEQ ID :125:

15   CAACTTGAAA TACATTATGA TGTCTGATAT GATTAAATAT CATTGAGNAT   50

       CTTGCAAACA AAAAAAGCAA AAAATTAAAT CTCCATATCA ATCTTAAATT   100

       CTTGGCATAT TTACTTCTGG TAAATATTAC TTCTGGTCCT TATTCTATAT   150
20
       GTGTTATTGA AATTGTGTT   169

       (2) INFORMATION FOR SEQ ID :126:

25   (i) SEQUENCE CHARACTERISTICS:
                    (A) LENGTH: 90 base pairs
                    (B) TYPE: nucleic acid
                    (C) STRANDEDNESS: double
                    (D) TOPOLOGY: linear
30

               (xi) SEQUENCE DESCRIPTION: SEQ ID :126:

35   GTTTNGTTNN NNNNTGTTCC ACCTTTTGTT GAATTTTAGT TGTTAGGCTG   50

       AACCTCCGAG CAGTTTNAGG ACTTGCCTGA GTTTTTCTTC   90

       (2) INFORMATION FOR SEQ ID :127:
40
               (i) SEQUENCE CHARACTERISTICS:
                    (A) LENGTH: 160 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :127:

TTTAGTTTAC TTCTGTTCCA CCTTTTATTG AAATATTAGT TGTTAGGCTG   50

AAAGCCTCCA GTTAAGAACT TGCTGAGTTT TTTTGTTCAG CAACTTGACA   100

TTTACTATGC GCATTATATA NCTCAATTAT GTCTGTTTTT TATGCTAAGT   150

AGGAAAACCA   160

(2) INFORMATION FOR SEQ ID :128:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 150 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :128:

GCCCACAACT TACATCCTCA TTATTGGCGC CTACAAACTC AACTACGAAC   50

ACACTCACAG TCGCATCATA ATCTTTTGAG GACTTCAAAC TTACTCGGCT   100

ACCGCTTTTT GATGACTTCT AGCAAGCCTC GCTAACCTCC CTTACCCCCC   150

(2) INFORMATION FOR SEQ ID :129:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 182 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

83

(xi) SEQUENCE DESCRIPTION: SEQ ID :129:

AGAGAGACAG ACACCATGGA GCCACAGGGG CAAGAGGNNG NTTTCCGAAG   50

CAGGGGANNG GCTATCACTC GGACGGACCN NNGCTCAACG AGTCCCACGA   100

GAACACACCA GAAATTTGTC ATTGCACTCA ACCAAAATCG ATATCAGCAA   150

TGAAAAACCC AAAACAGTTA CGANGCTAAT CC   182

(2) INFORMATION FOR SEQ ID :130:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 219 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :130:

GGACCATTCT GATCATCCTC ACTGGACGCC ACAGGGGCAA GAGGGTGGTT   50

TTCCTGAAGC AGCTGGCTAG TGGCTTATTA CTGTGACTGG ACCTCTGGTC   100

TCAATCGAGT TCCTCTACGA AGAACACACC AGAAATTTGT CATTGCCACT   150

TCAACCAAAA TCGATATCAG CAATGTAAAA ATCCCAAAAC ATNTTACCGA   200

TGCTTACTTC AAGAAGAAG   219

(2) INFORMATION FOR SEQ ID :131:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 181 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

84

(xi) SEQUENCE DESCRIPTION: SEQ ID :131:

AATAATTCAT CCACTTATGG AGGAGGAGGA GAATGTGGAA GAGGTAAAAA   50

GCTGGGCACA AGTTCATATG CCTATGAGTC AGTAAAGACT GAAGTAATGT   100

CCTATGTTGA GCTGGTTATT TTGATATATG ATAATAATTA TCTTTGTAGT   150

AGAACATCGT TAACGGAATC ACAGATATAT C   181

(2) INFORMATION FOR SEQ ID :132:

    (i) SEQUENCE CHARACTERISTICS:
       (A) LENGTH: 188 base pairs
       (B) TYPE: nucleic acid
       (C) STRANDEDNESS: double
       (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :132:

GACCAGCAGC TGTGGACATT ATGAGAAAGT GAAACCTGAG ATCCNCTGTT   50

GATTGAGAAA TGCAACACCT CAAAATGNGG GACAGCTCCT GATTACCAGG   100

TAGAAGATGN AAACAACTGG GGTGTCCATT CAGGAGGAAA CAATTGCAAG   150

CTAAGAACTG TTGAGAGTGA AGCTGCATTT TCTGNACC   188

(2) INFORMATION FOR SEQ ID :133:

    (i) SEQUENCE CHARACTERISTICS:
       (A) LENGTH: 190 base pairs
       (B) TYPE: nucleic acid
       (C) STRANDEDNESS: double
       (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :133:

GAGGTTGGGT CGTTGCATCC ATCATCAGGA GTTGACTTGT TCTGAGCAAC   50

TGAACAGAAC ACACCGCGAT GCTCTCGACA CTCCGCTCCT GGACTTCAGT   100

CACGAGTGAG TTGATGGTGA CTTGACCTGA GAGATTTCAC AGAAGCTCTG   150

TGACTTGGTT GTGGAAGAAA TCTGAACTGT TCAAGTTAAC   190

(2) INFORMATION FOR SEQ ID :134:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 235 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: double
            (D) TOPOLOGY: linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID :134:

ACATTACGAT CACTGATAGT TGGTGTGCGA CTGAAACCCA CATTNTGGTC   50

AATCTCCTCG TAGAGCTTCT TCTTCACCTG AGGATTGGCA GCAGGAAGGC   100

CAGGGTCCAT TTAACTAAGA GGTGGTGATC TCCACGCCAG CCCCAAAGAT   150

GTCCCCTATA TGGTGAGAAT GNGTCATCTG AAAGCAGCTC TGAGTCTTGA   200

TCTGGGCCAG CATTGCCATT ATTGAGTTTA TCTAG   235

(2) INFORMATION FOR SEQ ID :135:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 147 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: double
            (D) TOPOLOGY: linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID :135:

```
GAGAAACAGT ACCATCCANG ACACGATGTG GTGGAGGTTG ACNCCGCTGT        50

ACCCCAGAGG AGCNCCACCT GTCCAAGATG CAGCAGAACA CTACAAAATC       100

AACTATGTTT TTTAGCAGAT GCAGGACTAG ACCCCCACGC AGCTCTG          147
```

(2) INFORMATION FOR SEQ ID :136:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 171 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID :136:

```
GAAAAATGNG TTGANCCATT CATCCACAAA TTGACTTGCC TGAACAACCA        50

CCAAACAATA CACTAATGNT TCACACNTTT NCTTTTACTT GNACNTTAAG       100

NTCCCANTGA GTCACGGTGA CTTACCCTAA ACATCTCAAN NGTNNTCTGA       150

CTNAGAATGC GGAGGAGATC T                                       171
```

(2) INFORMATION FOR SEQ ID :137:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 159 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID :137:

```
ACATATATGT GGTAGGATAG AGAGATGGNN NNNGTGTATG ACATAGGTGT        50

TTCTCGTGTG ATGAGGGTTT ATGTGTTATG TGGGGTGAGT GAGCCCATTG       100
```

TGTTGTGGTA ATATGTGAGG AGTATAGGCT GTGACTAGTA TGTTGAGTCT   150

GTAAGTAGG   159

5   (2) INFORMATION FOR SEQ ID :138:

             (i) SEQUENCE CHARACTERISTICS:
                  (A) LENGTH: 179 base pairs
                  (B) TYPE: nucleic acid
10   (C) STRANDEDNESS: double
                  (D) TOPOLOGY: linear

15   (xi) SEQUENCE DESCRIPTION: SEQ ID :138:

        CCCACGACTT ACATCCTATN ACNCTTCGCC TAGCAAACTA AAACTACGAC   50

        NCACTCACAA TCGCTCATAA TCTCTTNAGG ACTTCAAACT NTCTCTNTGA   100
20

        NCCTTTTGAT GACTTCTACA AGCCTCGCTA CCTCGCCTTA CCCCNTGTNC   150

        TNCGGGAGAA CTCTCTGTGC TGTACCAGT   179

25   (2) INFORMATION FOR SEQ ID :139:

             (i) SEQUENCE CHARACTERISTICS:
                  (A) LENGTH: 177 base pairs
                  (B) TYPE: nucleic acid
30   (C) STRANDEDNESS: double
                  (D) TOPOLOGY: linear

35   (xi) SEQUENCE DESCRIPTION: SEQ ID :139:

        GACCTGGGAC GTAAATGATG AGACGGGTAC TTTGGCGGAC ATGAAGGAAC   50

        TGGCATATGG AACCTTGGCT GTGAAGCTGC AGACTATAAG ACAGCATGAG   100
40
        ACGACAATTC TGCTACTGCA ATGATGACAT CGTTTCAGAC CACAAAAAGA   150

88

AAGGCGATGA CCAGAGCCGC AAGGCNG   177

(2) INFORMATION FOR SEQ ID :140:

(i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 72 base pairs
    (B) TYPE: nucleic acid
    (C) STRANDEDNESS: double
    (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :140:

GTTTACAACA TTTACATCCT ATGAACTCAT GGATTATAAA ACATTTGTGA   50

CTTATACTGT CTNTGTCAGT TA   72

(2) INFORMATION FOR SEQ ID :141:

(i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 62 base pairs
    (B) TYPE: nucleic acid
    (C) STRANDEDNESS: double
    (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :141:

GTNGGCTGAA ATGAAANAAT AAAACCAAGA AACGAATTTA AGTATTNGTT   50

TTAGTACGNA AA   62

(2) INFORMATION FOR SEQ ID :142:

(i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 127 base pairs
    (B) TYPE: nucleic acid
    (C) STRANDEDNESS: double
    (D) TOPOLOGY: linear

· (xi) SEQUENCE DESCRIPTION: SEQ ID :142:

ACCAGTNNNT GATTGGTAAA TGGGAAATAT AATTGATTCT GATCACTCTT   50

GGTCAGCTTC TCTTTCTTTA TCTTTCTTTC TCCTTTTTTA AGAAAACGAG   100

TTAAGTTTAA CAGTTTTGCA TTACAGG   127

(2) INFORMATION FOR SEQ ID :143:

    (i) SEQUENCE CHARACTERISTICS:
       (A) LENGTH: 198 base pairs
       (B) TYPE: nucleic acid
       (C) STRANDEDNESS: double
       (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :143:

AATATAAAAG ACAGCAGTTT CACATTTCAC ATATTTGAAA AACATTTCAA   50

AACCCTCTAA TAAGTATTTA ATGAAAATAA ATTTATCGAA GAGAAACAAT   100

GACCACAAAA TTAATACTAC CAAATCATTA CTGAGACTTT TTGCATTACA   150

ATATTTGGAG AGTAGGTGAA GAAAATATAG AACAGAACAT GNACATTT   198

(2) INFORMATION FOR SEQ ID :144:

    (i) SEQUENCE CHARACTERISTICS:
       (A) LENGTH: 174 base pairs
       (B) TYPE: nucleic acid
       (C) STRANDEDNESS: double
       (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :144:

GTTTCTCTNT ACGTCATCCA CCTTGACATG ATGGGTCAGA AACAAATGGA   50

90

AATCCAGAGN CAAGTCCTCC AGGGTTGCAC CAGGGNNTAC CTAAAGCTTG   100

TTGCCTTTTC TTGTGCTGTT TATGCGTGTA GAGCACTCAA GAAAGTTCTG   150

5   AAACTGCTTT GTATCTGCTT TGNA   174

        (2) INFORMATION FOR SEQ ID :145:

            (i) SEQUENCE CHARACTERISTICS:
10   (A) LENGTH: 156 base pairs
                    (B) TYPE: nucleic acid
                    (C) STRANDEDNESS: double
                    (D) TOPOLOGY: linear

15

        (xi) SEQUENCE DESCRIPTION: SEQ ID :145:

GAGAAATAGT ACTTTAAAAT AAAACTAACA TGGTTTGATC AGCTTGAAAT   50
20
AAGATTCATA AAATGTACCT TTTTTGATTG TTTTGTTCTN GAGTTTTCGA   100

TTGAGANCAT TTGGTAAAGA TAAAGAGGTT TCCTGGGTGG CAAAAAATTA   150

25   TTTTGG   156

        (2) INFORMATION FOR SEQ ID :146:

            (i) SEQUENCE CHARACTERISTICS:
30   (A) LENGTH: 151 base pairs
                    (B) TYPE: nucleic acid
                    (C) STRANDEDNESS: double
                    (D) TOPOLOGY: linear

35

        (xi) SEQUENCE DESCRIPTION: SEQ ID :146:

AAGATTCNNN NNTCCATTGA ATGTTACCTG TGCCAGAATT AGAAAAGGGG   50
40
GTTGGAAATT GGCTGTTTTG TTAAAATATA TCTTTTAGTG TGCTTTAAAG   100

```
TAGATAGTAT ACTTTACATT TATAAAAAAA ATCAAATTTT GTTCTTTAAT        150

T                                                            151
```

5   (2) INFORMATION FOR SEQ ID :147:

            (i) SEQUENCE CHARACTERISTICS:
                (A) LENGTH: 177 base pairs
                (B) TYPE: nucleic acid
10   (C) STRANDEDNESS: double
                (D) TOPOLOGY: linear

15   (xi) SEQUENCE DESCRIPTION: SEQ ID :147:

```
CTTTATTTTT CTTATACAGA TTCAGAGAAG TAAAANNCAG TACCAAACTC         50

CAGGTAANNT GGTTTGATCT GATCGATTTG GCTGCATACT TTCGGTACGT        100
20
ATAACATTCT AAACTTAAAA TAGAAATTTT TATATTACAA AACGAGGAAG        150

TAAAATTTTA AAAGTTAAAG TACTAGC                                 177
```

25   (2) INFORMATION FOR SEQ ID :148:

            (i) SEQUENCE CHARACTERISTICS:
                (A) LENGTH: 148 base pairs
                (B) TYPE: nucleic acid
30   (C) STRANDEDNESS: double
                (D) TOPOLOGY: linear

35   (xi) SEQUENCE DESCRIPTION: SEQ ID :148:

```
GATTCNNNNN TCCATTGAAT GTTACCTGTG CCAGAATTAG AAAAGGGGGT         50

TGGAAATTGG CTGTTTTGTT AAAATATATC TTTTAGTGTG CTTTAAAGTA        100
40
GATAGTATAC TTTACATTTA TAAAAAAAAT CAAATTTTGT TCTTTAAT         148
```

92

(2) INFORMATION FOR SEQ ID :149:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 204 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID :149:

AGATTCNNNN NTGGNATTGA ATGTTACCTG TGCCAGAATT AGAAAAGGGG   50

GTTGGAAATT GGCTGTTTTG TTAAAATATA TCTTTTAGTG TGCTTTAAAG   100

TAGATAGTAT ACTTTACATT TATAAAAAAA ATCAAATTTT GTTCTTTATT   150

TTGTGTGTGC CTGTGATGTT TTTCTAGAGT GAATTATAGT ATTGACGTGA   200

ATCC   204

(2) INFORMATION FOR SEQ ID :150:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 93 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID :150:

AACATCGAGG TCGTAAACCC TATTGTTGAT ATGGATCTCT ATGAATAGGA   50

TTGCGCTGTT ATCTCTAGGG AACCTCACCG TTGGCAAGTT ATT   93

(2) INFORMATION FOR SEQ ID :151:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 151 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :151:

AATCGAGAGA AAAAATGATG ACACTGTAGC AATATCGTCG GANTCCACCT　　　　50

10

ACTTTGGGAT CAGCCTATCC ATCCGTGTCT TCCTATTTAA ATCGTCTATC　　　　100

CTCTATCCTT CCCCTGTCTT TTTNTGAAAA GGAAAAAAAC CAGGAAGGTG　　　　150

15　T　　　　　　　　　　　　　　　　　　　　　　　　　　151

(2) INFORMATION FOR SEQ ID :152:

(i) SEQUENCE CHARACTERISTICS:

20　　　　(A) LENGTH: 109 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :152:

TCTGAGAGGA ATACTNNTAA GTGCAATGAA TATTGCAAAT TTTCCCCCCT　　　　50

30

CTAAGTAATT CCCGATATTA GCAAANCANN NANATTAATG TCCCAGTGAA　　　　100

TGTAGCCTC　　　　　　　　　　　　　　　　　　　　　109

35　(2) INFORMATION FOR SEQ ID :153:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 136 base pairs

(B) TYPE: nucleic acid

40　　　　(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :153:

AAAATTATTT TCACAGTCCC CCCCAACTCT CATTGCGTCG TTAAAGTCCC	50
TCCAATCCTT TTTTAGTTGT GAAAAAATAA GGGGCCTTTA AAGGAGGAGG	100
AGGAAAAGGG GAAAAAAACC CATAATGGGC CTAAAA	136

(2) INFORMATION FOR SEQ ID :154:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 160 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :154:

CATCTTCATC ACCATCACAA TACTCATCAT CACCACCCTT CATNCACTAT	50
CATCTTCTAT GACTGCAAAC TTCTTATCTT TCTCTTCATT ATAGAAAGTT	100
TCAAGATGAG TATACGCATC TATCATTCGA ATTGTGTCAT TAATTTGTAG	150
GGCCTCATTG	160

(2) INFORMATION FOR SEQ ID :155:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 191 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :155:

ACCAGTNNNN NNNGGTCAAA TAGGGAAATA TAATTCGATC TCTCGAATCA	50

ACTCTCTGGG TCAGCTTTCT NCTTNTCTTC TATCTTTNCT TNTCTCCTTT   100

TTTTAAGAAA AACGAGTTAA GTCTTAACAG TTCTCGCATT ACAGGCTTGT   150

5   GACTTCATGC TTACTGTAAA GTGGAAGTTG AGATATTTTA A   191

(2) INFORMATION FOR SEQ ID :156:

    (i) SEQUENCE CHARACTERISTICS:

10   (A) LENGTH: 139 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: double
            (D) TOPOLOGY: linear

15

    (xi) SEQUENCE DESCRIPTION: SEQ ID :156:

CAACTGAACG CTTTGGTCAG GCTGCTACAA TGGAAGGAAT TGNGGGCNAN   50
20

TTGGTGGAAC TCCTCCTGCN NTCAACCGTG CAGCTCCTGG AGCTGAATTT   100

GCCCCAAACA AACGTCGCCG ATACTAATAA GTTGCAGTG   139

25   (2) INFORMATION FOR SEQ ID :157:

    (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 172 base pairs
            (B) TYPE: nucleic acid
30   (C) STRANDEDNESS: double
            (D) TOPOLOGY: linear

35   (xi) SEQUENCE DESCRIPTION: SEQ ID :157:

GGTACAGAGC ACTCTGTACC AACACACAGA ATTTACTGTT CTGCAAATGA   50

CCAATACTAA AAATTTATAA AGATGTGCAC AATTNNNNGC AGGCAATCTT   100
40

TCTTTTGTTT ACAAGATACA ACATTTAACA GTTATTAAAT GTAATCCTGA   150

AGCACCCGCA AATTTACCTT TG   172

(2) INFORMATION FOR SEQ ID :158:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 93 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID :158:

GGGTGGCTGT TNNGTATATC TCGTTAGTAA ATGTACATGC TCTTCAGGTT   50

CTAGGGCTCC TGTTAGGGGA GGGAGAAATG TTGGAAGNGG GGG   93

(2) INFORMATION FOR SEQ ID :159:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 102 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID :159:

GNATTTTTTT ATTGATATAT CATAGTTGTA CAAACATTTG GGAGTNCANG   50

TNGATACTTT GATACTATCG TGTNNNNNGG ATAATCACCA AATTGGATTC   100

CA   102

(2) INFORMATION FOR SEQ ID :160:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 205 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double

                        (D) TOPOLOGY: linear

5   (xi) SEQUENCE DESCRIPTION: SEQ ID :160:

    GCTTTTNNNN NNNNNNNNNC AGGTTTATAT TTACAATAAT TATCTTCCTA   50

    TAGAAGCAAT AANNCNAGTA TTCTCCAGTA ACAACACANN NNNATATTCT   100
10
    ACTCATCAGA GTTGGGAAAA ATAGGAATAA AGCAGATTCC ATACAGAAAT   150

    ACCGTACTCT GCATATGTAC AAATAAATTC AATATATTAA ATCATTTTGA   200

15 GCGGA   205

        (2) INFORMATION FOR SEQ ID :161:

            (i) SEQUENCE CHARACTERISTICS:
20   (A) LENGTH: 150 base pairs
                (B) TYPE: nucleic acid
                (C) STRANDEDNESS: double
                (D) TOPOLOGY: linear

25

            .(xi) SEQUENCE DESCRIPTION: SEQ ID :161:

    AACTTTTTTA ATGGGTCTCA AAATCTCTGA GACAAAATTA CTNNGNNNAA   50
30
    AGTTGTTTTC CATATAAAAA ANNNNNNTGA TTTTTAAAAA ACTAANNAAC   100

    TTAAAAACNT GCCACACGCA AAAAAAGAAA CCAAAAGTGG GNCACCAAAA   150

35 (2) INFORMATION FOR SEQ ID :162:

            (i) SEQUENCE CHARACTERISTICS:
                (A) LENGTH: 77 base pairs
                (B) TYPE: nucleic acid
40   (C) STRANDEDNESS: double
                (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :162:

TATTCAAAAG AAAAACATGG GTAAAAATGA TAGTGTTAAA TCTTGGCTCT   50

GTGTACATAG ATAGATACCT GTTACAG   77

(2) INFORMATION FOR SEQ ID :163:

        (i) SEQUENCE CHARACTERISTICS:
              (A) LENGTH: 182 base pairs
              (B) TYPE: nucleic acid
              (C) STRANDEDNESS: double
              (D) TOPOLOGY: linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID :163:

GAAAATTATT TTCACATCCC CCCCAACTTC TTGCTCTTAA TCCTCATCTT   50

TTAGTTGAAG AATAAGGCTT AAGAGAGAGA AAGGAAAAAC CATAATGGCT   100

AACTTAGCAG CACAACACGG TTCTTTTATC AAGGCGTNAT CATCATTTCT   150

CAAACTGACA TGCTACAGAA ATGTCTTCCA AA   182

(2) INFORMATION FOR SEQ ID :164:

        (i) SEQUENCE CHARACTERISTICS:
              (A) LENGTH: 182 base pairs
              (B) TYPE: nucleic acid
              (C) STRANDEDNESS: double
              (D) TOPOLOGY: linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID :164:

GAGGGAGCAA AGAGAGCCAT AAAGGCTCGT GCTGGGAAAG AAAGCTGTTA   50

TGCTTAGACT TCTCTAGGTG AACTCAGAGT CTTCAAAGAG GAAATGTTAC   100

99

AAATTGTCAC CCGCCAGCTT TCTGGCCAGT AAGCAGAATG CCAGGTTGCT   150

CAGATTCACA GACATTTGCA AAACAGAAGA TG   182

(2) INFORMATION FOR SEQ ID :165:

    (i) SEQUENCE CHARACTERISTICS:
       (A) LENGTH: 119 base pairs
       (B) TYPE: nucleic acid
       (C) STRANDEDNESS: double
       (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID :165:

GTATCTCCCT CTACATCCCT CCCGAAATAC TAGGAATACT TATTCTATAT   50

GAGACATATA TACCACCCAA GTTTTAACAC CATATCCCAT CGGCTGTTAG   100

TGTATATAAA AAGAAATAA   119

(2) INFORMATION FOR SEQ ID :166:

    (i) SEQUENCE CHARACTERISTICS:
       (A) LENGTH:.193 base pairs
       (B) TYPE: nucleic acid
       (C) STRANDEDNESS: double
       (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID :166:

GTACAAAGCC ACTCATCCTC GTGTGCCTAT CACGTTTTCC AAACACATAG   50

GATCCCATCT CAGGAGCAGG ACCAGTGTTT AGCTAGATTA AACTTCGCTG   100

GTGATCTTGT TGATGCATAT AAAGTAATCT GGCATATATG GTTAAATTCA   150

AGATGTTATG GCAGAAGTGA CTTGTTTTGC TCAACAAGCA TTG   193

100

(2) INFORMATION FOR SEQ ID :167:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 185 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID :167:

GTTCTGACTN AGAACTGAGC ACATAGCATT GACGCGGTAC CCTTGGAGAG   50

GGTGTGCTAG GAGGAGTGCT TGGCGAATTT GGACACGTAC TAATGTCTCT   100

GAGCCAGTCT GAATCTCTGT GAAGATGCCC CAGTGGAGGT GGCTGAAGAT   150

TAAATGGACA GTTTATAAAG TGTTCTGGP GCCGA   185

(2) INFORMATION FOR SEQ ID :168:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 163 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID :168:

GGACAACACA GCACCCATCC ACTACCCATT CAGAATTTAT ATAGAATATG   50

TACCCATGAT TATCTAGGTG AATCAATGCA ACAGTAGCTC TGATGTCCAG   100

ATTTCCTAGT CTATTATTTT GTGTACAGAT CCTCTAACCA CTTAGAAATA   150

ATTTTTAAAA ATA   163

(2) INFORMATION FOR SEQ ID :169:

101

(i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 202 base pairs
    (B) TYPE: nucleic acid
    (C) STRANDEDNESS: double
5   (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :169:

10

AGACAAATTC NNNNTNNNNN NTGCCTGATA ATTTCAGATG CCACCGTATA   50

GCAAAGGGTG AACATGTTTT CAACCCTTTA ACTTTTTACG GTGTTTGAAG   100

15

ACCAGCTACT CCTTAATATT TATCAATGGA TTAAGAAGTT TAAGATTTTG   150

CAGATTTACA ATTTGGGTTT TTGTCTGGAG TTGCTTCGGT TTGAAGCCCC   200

CT   202

20

(2) INFORMATION FOR SEQ ID :170:

(i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 168 base pairs
25   (B) TYPE: nucleic acid
    (C) STRANDEDNESS: double
    (D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :170:

TCAGGGAACC AAAAAACTGG CTTGCTTGGC ACCCAGGGAC AGTAGCTGTT   50

35   TGGCTCTCCA CCCAATTAAA AAAACAAATC CCTGCCCTTT CCCCCACCCC   100

ACTAGCTAAG CAAGAGCAGA GCTCTGATGA AGAGCCAGTG CCGGGTGCCT   150

GGTGCCCAGG GCTGTAAA   168

40

(2) INFORMATION FOR SEQ ID :171:

102

```
          (i) SEQUENCE CHARACTERISTICS:
              (A) LENGTH: 144 base pairs
              (B) TYPE: nucleic acid
              (C) STRANDEDNESS: double
5             (D) TOPOLOGY: linear




          (xi) SEQUENCE DESCRIPTION: SEQ ID :171:
10

      AGAAGTCAAC TAAAGCTTCA ATGCATCAAT TTATAANGCC TCANAGATCA         50

      GCAATTTATG ACACTTACAT TTACAGTCGA CCTTTACTAA CCAGGCAAAC        100

15    TTCCCGAAAT GATCAGGACT GATTCATCTC CTGAAATTNN CNGT             144


      (2) INFORMATION FOR SEQ ID :172:


          (i) SEQUENCE CHARACTERISTICS:
20            (A) LENGTH: 91 base pairs
              (B) TYPE: nucleic acid
              (C) STRANDEDNESS: double
              (D) TOPOLOGY: linear


25



          (xi) SEQUENCE DESCRIPTION: SEQ ID :172:

      ACCCACAGNN NNNACCTAGA GGCCCAGCGC CCAGAGAGGC ACGTAGAAAT         50
30
      GGGGACAGCA CGTTTATAGA CCACCAGAAA TTGAAGAGGA A                 91


      (2) INFORMATION FOR SEQ ID :173:


35        (i) SEQUENCE CHARACTERISTICS:
              (A) LENGTH: 204 base pairs
              (B) TYPE: nucleic acid
              (C) STRANDEDNESS: double
              (D) TOPOLOGY: linear

40
```

103

(xi) SEQUENCE DESCRIPTION: SEQ ID :173:

GATTTTTTAA TGGGTNGCCT CTTTTAGCTT GGAATATTAC GTTTACTTTA   50

ATCCAAGTCT AGGCCTTTTA AAGGGTCCTT AAAATTAAAG TTCAGAATGT   100

GAATCCCTTT GACATCTATT ACAGGTTATA GGACCTTTTT GGTGTGATTA   150

CGGTTTTCAA TACGATTGTA TAAATGAAGT TAACTTGGCA GAAGTTAAAA   200

TGGA   204

(2) INFORMATION FOR SEQ ID :174:

        (i) SEQUENCE CHARACTERISTICS:
             (A) LENGTH: 241 base pairs
             (B) TYPE: nucleic acid
             (C) STRANDEDNESS: double
             (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :174:

GTAAATTTCA CTACATCTTT TNNTNTGACT TTCATGCATT TCTCATACAT   50

TNNTNNCNGA TGCTTGACTT TATTGCTTCC TAGCAATAAT CTGCATTTAA   100

ACGAAAGGCG GTTCAATTCA TCAACTTGAA ATGACTATTT ATTTTTNAGG   150

ATTTTTTAGG GGAAGAGTAC CCATTTCGTT TATAAAAACA GATGACAAAT   200

TTCTTAAAGA AACAGAAGCA CAATACTTTC GAAATACAAC G   241

(2) INFORMATION FOR SEQ ID :175:

        (i) SEQUENCE CHARACTERISTICS:
             (A) LENGTH: 211 base pairs
             (B) TYPE: nucleic acid
             (C) STRANDEDNESS: double
             (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :175:

GGTGGGCTCN NNNANNANNG TTCTACACTG TGGTATAAAC TTGTCGTGGT   50

TCTCGTGATA GAAAACAGAC ACTGACCTTG GGTATAGTGG GCCTATAAAT   100

AACAAACCCT TGGGTACTCC TGAATAGGGG CAGGGCCCCC TGGGCCTCCC   150

TTACAGGTTT CTTCAGGGAA ATGGTCCCTG GGATAATTCT TTAGGGCCCT   200

TTGGCCCTTT T   211

(2) INFORMATION FOR SEQ ID :176:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 252 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: double
            (D) TOPOLOGY: linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID :176:

AAAATAAGAA TAAACATCCA TAATAGTNAT AGATANATCC NTTTATTTAG   50

NACATCAGCA ACGACTGCTT CACACCAAAT CCCTTCCTCT GNGAATGATN   100

TATATAACTC TAGTACTGCT TTCCATGAAG AACCTTGCAA ATTGATTGAA   150

AGTCCAGGAT NNCTCGCTAA TCCTCCACCA TAAGATTTCT GACCTATGAT   200

AACTCCAAGG TGGCAAACAG AGAAATCAAC TTCCTTATAA ANAAATCCNA   250

AT   252

(2) INFORMATION FOR SEQ ID :177:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 279 base pairs
            (B) TYPE: nucleic acid

        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID :177:

```
GCGGGCGACT TTCCATCCCT CGAACCAAGG CATGTTAGCA CTTGNCTCCA          50

GCATGTTGTC ACCATTCCAA CCAGAAATAG CACAAATGCT ACTGCGCGAG         100

TTGCAGCCAA TCTTCTCAAA GCAAACCGAC TTCCTAACAA CTNTCTACAT         150

CTGGCTCGCT GCAGGCGACT CAATGAAATC CATCTTTAAC ACCACAATCA         200

TTGTTTNACA CCCAGTGTGC AAGCCAGGAG GGCATGTTCT GAGTCTNTCC         250

ATCTGAAGAT ACCAGCTTCA AATACTAAT                                279
```

(2) INFORMATION FOR SEQ ID :178:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 157 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID :178:

```
TATGCCCTGA AATGAAACCT CTAAGTTTGA CAAAATACCC ACAAAAACAG          50

ACCTTCCTNG TTAACACTTT ATAAGAAGGT GTGACATTTG GTGGGTGGTC         100

GTTCTCAATT TATAAAANAA TAAATGACTT TAAAGGAGAA ATAAATTTAT         150

GTCAGGA                                                        157
```

(2) INFORMATION FOR SEQ ID :179:

    (i) SEQUENCE CHARACTERISTICS:

106

                              (A) LENGTH: 39 base pairs
                              (B) TYPE: nucleic acid
                              (C) STRANDEDNESS: double
                              (D) TOPOLOGY: linear

    5

              (xi) SEQUENCE DESCRIPTION: SEQ ID :179:

    10   GATAATGCAA CTTTTGACAG GAAAGCGCGA TTTTACTAT   39

         (2) INFORMATION FOR SEQ ID :180:

              (i) SEQUENCE CHARACTERISTICS:
    15   (A) LENGTH: 157 base pairs
                  (B) TYPE: nucleic acid
                  (C) STRANDEDNESS: double
                  (D) TOPOLOGY: linear

    20

              (xi) SEQUENCE DESCRIPTION: SEQ ID :180:

         GCAAACTCAA ACTACGGACG CACTCACAAT CGCTCATAAT CCTCTCTAAG   50
    25
         GACTTAAACT CTACTACACT AATACTTTTT GATGACTTCT AACAAGCCTC   100

         GCTAACCTCC CTTACCCCCC ACTATTAACA CGGGAGAACT CTCTGTCTAG   150

    30   TACCACA   157

         (2) INFORMATION FOR SEQ ID :181:

              (i) SEQUENCE CHARACTERISTICS:
    35   (A) LENGTH: 195 base pairs
                  (B) TYPE: nucleic acid
                  (C) STRANDEDNESS: double
                  (D) TOPOLOGY: linear

    40

              (xi) SEQUENCE DESCRIPTION: SEQ ID :181:

107

CCATCCAGGC CAAATAAGCN CCGGCTATGC CCNTGTATTG GATTGCCACA   50

CGNCTCACAT TGCATGCAAT TTGCTGAGCT GAAGGAAAAG ATTGATCNCC   100

ATTCTGGTAA AAACTGGAAG ATGACCCTAA ATTTTGAAGT TGATGATGTG   150

CCATGTGATA TGGTTCTGAC AAACCCATGT GCGTTGAGAG CTTTT   195

(2) INFORMATION FOR SEQ ID :182:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 146 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: double
            (D) TOPOLOGY: linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID :182:

CATGGTCTTA ACCAGTGTCA GATGGAATCA GTGGATAAAT CCCCAGGTTT   50

GTTTGTCCTT CAAATGGGAC AATTTGAGGA ATGCTTTAGG CAGAGGACTC   100

AGATGACAGA GCGCCAACCA CCCACAATAG AAACCTGCTC ATCACA   146

(2) INFORMATION FOR SEQ ID :183:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 50 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: double
            (D) TOPOLOGY: linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID :183:

TAGAGGAATA GGGNNNGNGA CGCCCCNAGT TGTAGGGACG GACGGAGGAC   50

(2) INFORMATION FOR SEQ ID :184:

108

(i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 248 base pairs
    (B) TYPE: nucleic acid
    (C) STRANDEDNESS: double
    (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :184:

```
ACGNTTACGG TCACTGATAG TTGATGTGCN NCTGAAACCC ACATCCGATC        50

AATCTCCTCA TAGAGCTTCT TCTTCACCTG AGGATTGCGC AACAGGAAGG       100

CCAGGATCCA TTTACCACAG AGGCGGGATC TCCACGCCAA CCCCAAAGAT       150

GTCCCCTATG ACGACGAGAA TGTGATTATC TGAAAGCAAC TTGATCTTGA       200

TCTGGGCCAG CATGCCTCAT CTGATTCATC TCGCTTCCAT CAATGNGT        248
```

(2) INFORMATION FOR SEQ ID :185:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 113 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :185:

```
AATGATGAGT AAAAGATTCA ACAACTCACA GCCCTGGGGG CACTCAGGCT        50

ACTGCTAAGG CCTGAGAGTT TTGCAAAAAT GCGCAGAGAA ACACCCTTTG       100

AACGTGGCTT TCT                                              113
```

(2) INFORMATION FOR SEQ ID :186:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 148 base pairs

    (B) TYPE: nucleic acid

    (C) STRANDEDNESS: double

    (D) TOPOLOGY: linear

5

    (xi) SEQUENCE DESCRIPTION: SEQ ID :186:

GGGCCCCCTG ATCAATTCTT TGGATGCTTT TCAAATTTCC CAGGATCCCG   50

10

ATGTCGTCAT ACACTCCGAA CATGACCCTT TTTTCTTCCA ACGATCAACC   100

ACTNCGNGGG ACGGGAGAGT GAGCCTTATA CCGATCAATC TGCACACC   148

15   (2) INFORMATION FOR SEQ ID :187:

    (i) SEQUENCE CHARACTERISTICS:

        (A) LENGTH: 248 base pairs

        (B) TYPE: nucleic acid

20   (C) STRANDEDNESS: double

        (D) TOPOLOGY: linear

25   (xi) SEQUENCE DESCRIPTION: SEQ ID :187:

TCCTTACTGT AAGAGCCATT TAAACGATTA AAATCCCACT NGCCATACCG   50

TAAGATGATA GGACCAACCA TACCTACCGA TCAAAAATTT ATCAATCCAA   100

30

GCCAACTACA CTCCCACTGC TAAAAAGATG AAAGGACCAA TCAAAGATTT   150

AATTAAACTA AAGGGAAAGA ATCAGAGACA GAGAATGAAG AAAGAAATTC   200

35 TAAGTTGCGA CGGACAAACC AGAACAGACA ATGAAGCCTT TCAACTGC   248

    (2) INFORMATION FOR SEQ ID :188:

    (i) SEQUENCE CHARACTERISTICS:

40   (A) LENGTH: 146 base pairs

        (B) TYPE: nucleic acid

        (C) STRANDEDNESS: double

110

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :188:

TATGAAGAAG TGCAGCACTG GCCAACACCA GGGTTTACTG AATCATTTCA   50

GTTTAATACA TAAGTGTCCA ATAATAATGT CAACCCTCCC TCGCCACAGC   100

CAATAATTTG TCCTCACTGA GTTGGCAACA AGTGACTGCT GTGACT   146

(2) INFORMATION FOR SEQ ID :189:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 81 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: double
            (D) TOPOLOGY: linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID :189:

ATTTACCACA AGGGACGATT TCCACACCAA CCCCAAAAAT GTCCCCTATG   50

ACGACGAAAT GTGTATTTGA AACAGCTCTG A   81

(2) INFORMATION FOR SEQ ID :190:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 136 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: double
            (D) TOPOLOGY: linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID :190:

AAGTACAGCA TCCTGCTGCA AAAATGATTG TAATGNCTTC TCATATGCAA   50

111

GAGCAAGAAT TGAAGATGCA CAAACTTCGT TCTGAATTTG TGAGCTTCCT   100

GGATCAACTG AAGAACTTCT GAGGATTGAC CTGTCA   136

(2) INFORMATION FOR SEQ ID :191:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 152 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: double
            (D) TOPOLOGY: linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID :191:

AGGATTTAAG ATGGGGACAG ACTGGTGAAA ATGCGGCTGA CTGGAAGGAA   50

ATGGGGCATA CGAGTAATAT GTACATATCA AACAATCAAT TGCCTCCTGA   100

AATCAAAAAA TCAAATGGTG AAATGGAGCC TCCTTGATAG TTTAGGCCAA   150

CA   152

(2) INFORMATION FOR SEQ ID :192:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 65 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: double
            (D) TOPOLOGY: linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID :192:

TAAGCGAGGN NGTCTTTGAT TGCGTAGTAA GGTAAAGACG ATTTTATAGA   50

ATNAAGGTGA TTCCT   65

(2) INFORMATION FOR SEQ ID :193:

112

(i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 2?9 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: double
            (D) TOPOLOGY: linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID :193:

AGGACCCAAA CTACCTTATT GCATTTGAAG TTTTACTTAT NCTATTATAA   50

TCTAAGAGCC CACCCAACAA GGCACTACAC ATAGATGCTC ACACTCTATA   100

GGCTGCCTGA TCCTGGACCA CCTGGGGCCC TGATTATGAT CTCCACGGGG   150

CTGTCAATGA CTAGGGAAAG CTTTTTAAGA CCCAGCGATC ATGCAATGGC   200

TCAACCATGG CGAATCAAAG TTAGCATAAT GTCCCAGCAA ACAATGTTA   249

(2) INFORMATION FOR SEQ ID :194:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 194 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: double
            (D) TOPOLOGY: linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID :194:

GGAAAGGGTG CCTCATCCCA GCAACCTATC CTTGTGGGNG ATGATCACTG   50

TGCTGCTTGC NNCTCATGGC AGAGCATTCA TGCCACGATT TAGGTGAATC   100

GCTGCATATG TGACTGTCAT GAGATCCTAC TAGATGATCC TGACTAGAAT   150

GATAATTAAA AGTATTTACT TCGAAGCACC ATTTGAATGN TCAT   194

(2) INFORMATION FOR SEQ ID :195:

113

(i) SEQUENCE CHARACTERISTICS:

    (A) LENGTH: 121 base pairs

    (B) TYPE: nucleic acid

    (C) STRANDEDNESS: double

    (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :195:

GTGATTTTAG TTTAAGGATA AGAAGCCACT ATATCAACGT CGGGGGGGTA   50

TTTAAGTCAC ACACATAGTT AACAACNCNC GTNGCGTGCA ATAAATACCA   100

CATCCTTTNA TATGNNCNGN A   121

(2) INFORMATION FOR SEQ ID :196:

    (i) SEQUENCE CHARACTERISTICS:

        (A) LENGTH: 175 base pairs

        (B) TYPE: nucleic acid

        (C) STRANDEDNESS: double

        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID :196:

GGGCTTCNNN NNNNNNCATG TGCACTTAGA ACCGTTACTA ACCGAAACAC   50

CATTTGCTTG TCAACAATGT ACCCTTGACA GCAGGGAGAA ACTTCTTTAT   100

AGTCTCTGCT TCAGACAAGA TTTACNGCTT TCTCCAAGGC CAGAGGCAAA   150

TTGTGACCAC AAGTCTTGTT TCTTG   175

(2) INFORMATION FOR SEQ ID :197:

    (i) SEQUENCE CHARACTERISTICS:

        (A) LENGTH: 273 base pairs

        (B) TYPE: nucleic acid

        (C) STRANDEDNESS: double

114

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :197:

ACTGGCAACT TCTATGTACC TGCAGAACCC AAATTGACAT TTGTCATCAG   50

AATCAGAGGT ATCAATGAAA TGAGCCCAAA GGTTCGAAAG CTCGCAACTT   100

CTTCACCTTC ATCAAATCTT CAACGACCTT CGCAACTCAA CAAGCTTCTT   150

ACAGTGAGGA TTGCAGAGCC TATATAGCTG ATACCCCAAT CTGAATCATA   200

AATGACTAAT CTACAAGCNT GTTATGCAAA ATAAATAAGA AACGACTTGC   250

TTACAGATGC NTTTTAATTG TGG   273

(2) INFORMATION FOR SEQ ID :198:

          (i) SEQUENCE CHARACTERISTICS:
              (A) LENGTH: 56 base pairs
              (B) TYPE: nucleic acid
              (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

          (xi) SEQUENCE DESCRIPTION: SEQ ID :198:

GATTCCCCAA TAAGCAGACA CCTTGAACCA GCCTGGGGTG AGCGAAAGAT   50

GNTATA   56

(2) INFORMATION FOR SEQ ID :199:

          (i) SEQUENCE CHARACTERISTICS:
              (A) LENGTH: 132 base pairs
              (B) TYPE: nucleic acid
(C) STRANDEDNESS: double
              (D) TOPOLOGY: linear

115

(xi) SEQUENCE DESCRIPTION: SEQ ID :199:

GGACGCTGNN NNNNNNATCC TGCAATGCAC AGCACAGACC CCACCACAGG   50

GGTTTTATCC AGCCCAAATG TCAACAGTGT CAAGTTTAAG CAACTCTTAC   100

CGAGTGGGAC TCAATTCCCN AGTTGTATGG AA   132

(2) INFORMATION FOR SEQ ID :200:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 284 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :200:

AAACTTTTTN GCACTTACAC AGACGAGACT TCACTGCNTG AGGATCATAC   50

GACATTTCAA TCGNACACAA ANTTAAAAAA TAAAACAAAT TTTAAAAAAC   100

CATNTTGAAT TTCCTTAAAA TTATTCCAAT ACTTTCCAAC TTAAAATTCA   150

GAACAAATCC TCCTAGAGAC TATCAATACC AATATCTTCA CATTGCTCAG   200

CTGNTACATA CGNCCCACCA GTTCACAACT AATGACACAA CACTACATGN   250

TCAAATCTTA TCTNNNATAG CACAGTAACA AAGT   284

(2) INFORMATION FOR SEQ ID :201:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 106 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

116

(xi) SEQUENCE DESCRIPTION: SEQ ID :201:

CCTGACACCA ATTTCGCCCA CATGTATGCG GGAAGAGGCC TGAGACTAGA   50

AGTCGTTGCC CTGTCCATCT CCCGGCCACA GGCTTCATTC CCAGATTTNT   100

CTTGNT   106

(2) INFORMATION FOR SEQ ID :202:

    (i) SEQUENCE CHARACTERISTICS:
       (A) LENGTH: 270 base pairs
       (B) TYPE: nucleic acid
       (C) STRANDEDNESS: double
       (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :202:

CTTTGGAAAA CAAACATTTN TTATTACTGA AATAGCAAAA ATCATTCTAC   50

ACTCCTCCTA AGCATGTTCA ATTAGCATAC ATTCCAACAA TGCATGAAAA   100

AATTNCTAGC CAGAGGCATT TAAGTGATTT CTTCCTAAGT GTTTGCTAAT   150

TCAATGCCAA GAACTATGAT GTTTATCNTT CTGATGGACA AATCAAGAAA   200

CAAAACAGAT ATAATACCAA GGGTAAAGCT GATATGACCC ACAACATTGT   250

CATTACTCTA ACTGTTAATC   270

(2) INFORMATION FOR SEQ ID :203:

    (i) SEQUENCE CHARACTERISTICS:
       (A) LENGTH: 173 base pairs
       (B) TYPE: nucleic acid
       (C) STRANDEDNESS: double
       (D) TOPOLOGY: linear

117

(xi) SEQUENCE DESCRIPTION: SEQ ID :203:

AACTAAGGCA CATTGCCCTT TTTGACCTTT CTNNNGNACT ATTGAAATCA   50

AGCTTATTGA TTAGGTGATA TTTTTATAAC AATTGAAAGG GCAATATCAA   100

ATAATGACAT ATGAGAATTT TTTATTACAT ATTAAAACTG ATTTTTACTT   150

TACAAAANNG NAATTTGCAA TTA   173

(2) INFORMATION FOR SEQ ID :204:

    (i) SEQUENCE CHARACTERISTICS:
       (A) LENGTH: 164 base pairs
       (B) TYPE: nucleic acid
       (C) STRANDEDNESS: double
       (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :204:

CTGCTTCACC ATCCTGGCGT CTACCAGCCT GGTGNGGCTG GGTACTGTGN   50

ATCGTCTTCC TCAACAAATG CGAGACCTGC CAACCTGCAC TACACCACAT   100

CCGCNCAAGA AGAAGAACCT GCTGCTTCAT ACAACACGGG GAGGCCCTGT   150

CATTAACATT ANTT   164

(2) INFORMATION FOR SEQ ID :205:

    (i) SEQUENCE CHARACTERISTICS:
       (A) LENGTH: 99 base pairs
       (B) TYPE: nucleic acid
       (C) STRANDEDNESS: double
       (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :205:

118

GACCGCCCAN NNNCATCCAA AACTTCTAGG CACAATCTAT ACTGCTGCTG   50

AAGAAATTGA AGCAGTTGGG GGAAAGGCCT TGCCATTGAN TTTTGATNT   99

5   (2) INFORMATION FOR SEQ ID :206:

            (i) SEQUENCE CHARACTERISTICS:
                (A) LENGTH: 118 base pairs
                (B) TYPE: nucleic acid
10   (C) STRANDEDNESS: double
                (D) TOPOLOGY: linear

15   (xi) SEQUENCE DESCRIPTION: SEQ ID :206:

GTACCTTGGG NNNNNNANNG GGAATGAGGT TCTACCACTC TGGAAAATTC   50

ATGCCTGTCA NTNTAANTNC AGGTGCCAGT TNNCNNTAGG TCGCCAAAGT   100
20
TGGGGTTAGN TGTTCNAA   118

        (2) INFORMATION FOR SEQ ID :207:

25   (i) SEQUENCE CHARACTERISTICS:
                (A) LENGTH: 170 base pairs
                (B) TYPE: nucleic acid
                (C) STRANDEDNESS: double
                (D) TOPOLOGY: linear
30

            (xi) SEQUENCE DESCRIPTION: SEQ ID :207:

35 CACACTANCG ACCAACACTT AAAAGNCTNC TCACACAAGN ATCTTTTAA   50

TAAAAATACC TCTTTCNTAA CTCCACTTTA ACTCCCTAAA ACCCATGTCG   100

AAGCCCCCAT CCTGGTCAAT AGTACTTGCC CAGTACTTTT AAAACTAGGC   150
40
GCTATGCATA ATACCCTCAC   170

(2) INFORMATION FOR SEQ ID :208:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 129 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID :208:

TTCAATGAAA TGCTTGTATA CAATGATATA ACAAAGAAAC CCTAAGACAA   50

CGAGAACTTC AACTAAGTGC ACTCATGCAG AATCTCTGCG GGGAGAATTT   100

TTTCTCGGGG AAGTAACCCT GCCTTTGAA   129

(2) INFORMATION FOR SEQ ID :209:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 190 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID :209:

CTTGGCGTCA TTTTCTGTAC TTCTGACAGT GCCCTCAGAG TCTGCAGGTG   50

GATCCTTTTT TGCATGGCAT TAATTATATG AGCAGCCTCC TTCTGACAAT   100

CCAAATTTTG GCTCCAGAGT CATTTCTGAA NNTCTACACT TANGGNCTTN   150

AGCNTGCTCA TTCAAGGTNA AGGGGAGTTT TNAAAAATAT   190

(2) INFORMATION FOR SEQ ID :210:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 129 base pairs

120

(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :210:

TCATTGAGTC ATCCTTTTTG CCTGCTGCTG TAAGGTTTTT TTTCTTCTAG   50

10

TAACTGTATG ATCCAGAGCG ACCCAGCAAG GACTCAATCG ATCACCAACT   100

GATGCAGAAC TGTTTCATAT CTAGAAATG   129

15   (2) INFORMATION FOR SEQ ID :211:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 152 base pairs
(B) TYPE: nucleic acid
20   (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

25   (xi) SEQUENCE DESCRIPTION: SEQ ID :211:

CTGTAAGGTT TTCTTTCTTC TAAGTAACTG TATGATCCAG AGCGACCCAG   50

CAAGGAATCA TATCGATCAC CAGCTGATGT AGAACTGGTT TCANATCTAG   100
30

AAATGGAANC NNNGNGTTTN TTCCTTAATG GACCCCCCCN GGGGCNGAAT   150

GG   152

35   (2) INFORMATION FOR SEQ ID :212:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 186 base pairs
(B) TYPE: nucleic acid
40   (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

121

(xi) SEQUENCE DESCRIPTION: SEQ ID :212:

CTTAACCCTT TGGAAGGNTT GACTGTGTGA CCCGCAGCAA ATAATTCATG　　　50

TCGAAAGATG AAAACAACTA AGTTCATAAC CCCCTGCCCG CCATTGACCT　　　100

CCCTTTNAAA ANCGAGACCA AGACTCCATC ACTGGTTTCG AATTTACATC　　　150

NAACTGCTAA GATTGATACA TTNCAAGTCT GCAAAT　　　186

(2) INFORMATION FOR SEQ ID :213:

　　　(i) SEQUENCE CHARACTERISTICS:
　　　　　(A) LENGTH: 152 base pairs
　　　　　(B) TYPE: nucleic acid
　　　　　(C) STRANDEDNESS: double
　　　　　(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :213:

CTTAAATGCC TGTTGTGATA TCTTCTTTAA ACCTGGAGAG ATTGAATCAA　　　50

CCTTTCTCTA AAATTCCTTT CCTTTGCCTC CTCCTCTAAC TTTTCCTCCT　　　100

TTCNCGCTTT TCCTCAGGCT TTGNTTTTCC TCATGCTTTG CTTCACTCTA　　　150

TT　　　152

(2) INFORMATION FOR SEQ ID :214:

　　　(i) SEQUENCE CHARACTERISTICS:
　　　　　(A) LENGTH: 290 base pairs
　　　　　(B) TYPE: nucleic acid
　　　　　(C) STRANDEDNESS: double
　　　　　(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :214:

122

TCTTCAGGAG AAGGGGCACC ACTGCTTTAA AAAACAATAC TCCNTTATAG   50

ACTTGAACAT TTGCAGACAT TATGATCTTG CTTCCAACTC CCACCGTATG   100

TCCAGCAAAC TCTCGCATGT GGCCACTAGG AGGAATGCGC AAGAATGTTC   150

ATATTACATA TTTATAACAT TAATAACTGG AAAAAGTGAA ATGCATGTCT   200

GTTACAGGAA AATAGGCGAA TAATCAGATA TATATATCTA NNNCCGGGAT   250

ATTATTCAAT AGTGGAAATG ATGACTACAG CTATACCTCA   290

(2) INFORMATION FOR SEQ ID :215:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 273 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: double
            (D) TOPOLOGY: linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID :215:

GTTTCTTCCA GTACATCCAA GTTTAAAATT ATTAGCGAAA TGGTCCATGT   50

TTTTTCAATT ACTGCTGACA CGATTCTAAG CTAAGTGAAG GGGAAGATCT   100

GAGAGCATGC TGTTTGGACT GTTGATGCAT ATTCATGATG TAACAGGTCC   150

TGGGCCTCAC TTTACCCCAT TCGTAAAATG GGGATAATGT CACCTGCCTC   200

TTACCTACCT CAGAGGGATT TGCGAAGCAA ACTGTTAATC TTCGAAAACG   250

ACCATTTACT TTTAGGATAT CAA   273

(2) INFORMATION FOR SEQ ID :216:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 118 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: double

123

(D) TOPOLOGY: linear

5   (xi) SEQUENCE DESCRIPTION: SEQ ID :216:

ATCTACGGCT AGGGAGAAAC AATGTTCCTA CATATTATGG GTAGTGAGAA   50

CATTATCTGT ATAACAGGGA ACTGTGATTA TTTAAAATTA TGCAGAACTT   100
10

ATTTCATCTG TGCTTTAG   118

(2) INFORMATION FOR SEQ ID :217:

15   (i) SEQUENCE CHARACTERISTICS:
               (A) LENGTH: 197 base pairs
               (B) TYPE: nucleic acid
               (C) STRANDEDNESS: double
               (D) TOPOLOGY: linear
20

           (xi) SEQUENCE DESCRIPTION: SEQ ID :217:

25   GAGGCTGGTG GCGAGGGAGT TGTGGAGGAT AACAAGAAGA AAACAAGTCT   50

ATCACTAATG ACTTATTTTA CTTAGTTTCC ATTCACGAAA CCCTTTTAAA   100

TACAAGGCAA CATTTTCACA GCTGAAAAAT TACAACTAAA NGNNNTGATT   150
30

TACCACCAAA AGCAATAGAT GTAGTTATGT ATAATCTATA GATAATA   197

(2) INFORMATION FOR SEQ ID :218:

35   (i) SEQUENCE CHARACTERISTICS:
               (A) LENGTH: 177 base pairs
               (B) TYPE: nucleic acid
               (C) STRANDEDNESS: double
               (D) TOPOLOGY: linear
40

124

(xi) SEQUENCE DESCRIPTION: SEQ ID :218:

CTCGCGAGCA CTCGTCCGAG AGGTCCCATA CNNNNNNNCC CAAGCCCCTC   50

AAGGGCCTTT GCCAATCTNG TCATTTTATG CCAAGTCCTC TAAAACGCAC   100

TCAGGGGTAT CTACATCGCA CTTGTACAGA ATATCAAGAT CTTATCCTCC   150

TATTTTAGGC TNCNAGGTCA AAATAAA   177

(2) INFORMATION FOR SEQ ID :219:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 118 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: double
            (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID :219:

GAAATGAAAA AGAGAGCATT ATTGGAAGAA TGAAAAATAC ATCTCAGAAA   50

GAAACCTANT AGTTCAACAA ATTAAAAGAA AGAAAGAAAA AAAGCAAAAG   100

TNGGTNTCAG GGCTGGAC   118

(2) INFORMATION FOR SEQ ID :220:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 233 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: double
            (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID :220:

GAGAGCCCAG CACGTCATCC CCTGATCTGA GTCTACTGAA CACCTGTTTT   50

ATGGACTACA CTGTCTTTTC CTTTGAATCC CCACTTCTCC TGGAACTGTA   100

CTTGGACCAC CAGGAACATC GTAAGACACA ACCCAATACA CTCACCGCAT   150

TCAGACAACT GTCCAGACAC TGCCCTGACA CCACAGGGNC CCCTTTACAN   200

NGGTTGGNGG AAATATNNTT TAATCTCAGG CCA   233

(2) INFORMATION FOR SEQ ID :221:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 235 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: double
            (D) TOPOLOGY: linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID :221:

GCACACAGAT ACCATCCCAC CTTGCTTTNT GACAGGCCAG CCACACAATA   50

ACCCTTTCCC TACTCACTAA AGCATCCCTA GGACACCAAC AATGAGGACA   100

GGCAGACTTA CCCCCGCCAT CTAGAGAGAA TGTCGTTATT ACCCATAAAA   150

CTCGACCACC CCCATATNCA CTNTTGGGTA AAAACAAACG CTTAAACCTG   200

TGAGCCTGCC ATTCCTTTTT ACGTGTTAAT CAATT   235

(2) INFORMATION FOR SEQ ID :222:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 101 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: double
            (D) TOPOLOGY: linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID :222:

126

GCCAATNNNN NGGCGCGAGG GNNAGAGAGA ATGGCAAACA GGGACCCGGG   50

CCTTAGGAAT TGANTGAGGA CTTAAATTTC CCCNGAGGGA GAGNAGTGGA   100

G   101

(2) INFORMATION FOR SEQ ID :223:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 271 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID :223:

ACGGTGACTT TCCATCCCTT GAACCAAGGC ATGTTAGCCT TGGCTCCAGC   50

ATGTCGTCAC CATTCCAACC AGAAATTGNC ACAAATGCTA CTGGTCGGGT   100

TGACCAATTT TCTTAATGAA GTGCTGACTT CCTTAACAAT TTNTTATATT   150

TNTTCGACTG TAGGGCGCTC ATGAATCCAT TTCGTTAACA CCGACAATTA   200

ATTGTTTCAC ACCCAGTGTG CAAGCCAGAA GGGCATGCTC TGGGTCTNCC   250

CATTCTTGAG ATACCAGCTT C   271

(2) INFORMATION FOR SEQ ID :224:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 101 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID :224:

127

AGTATTATTT ACTNGGTCAT CTGGGAACCT TAATGTGATT TATTTTGACA   50

ATTACTGTGG CACATGTTTA ATCTGCAGCT CCTGGCGACT ACTGTGCTTA   100

5   T   101

(2) INFORMATION FOR SEQ ID :225:

10   (i) SEQUENCE CHARACTERISTICS:
                  (A) LENGTH: 141 base pairs
                  (B) TYPE: nucleic acid
                  (C) STRANDEDNESS: double
                  (D) TOPOLOGY: linear

15

            (xi) SEQUENCE DESCRIPTION: SEQ ID :225:

        TTCATTCCCT CCAGTGCNCG NNCATGCGAC ATATACAGGN NNTGTACCGT   50
20
        AGGCGCTANT GTGTGGTACT CTGCCACGNN ANACCNCNNC TCGTCTTGAA   100

        GACCCTGTTA ANTTTGGTGA AAATAACTTT CCANATTTCA A   141

25   (2) INFORMATION FOR SEQ ID :226:

            (i) SEQUENCE CHARACTERISTICS:
                  (A) LENGTH: 218 base pairs
                  (B) TYPE: nucleic acid
30   (C) STRANDEDNESS: double
                  (D) TOPOLOGY: linear

35   (xi) SEQUENCE DESCRIPTION: SEQ ID :226:

        ATTTTCTTAT ACTCCTCCCA CAGATGAGTT CACAAATACA AAAANTGGTG   50

        TACATTTATA CTCAAGNACA AATCTCCAAC AGCCAAGTAA TTATAGTTTG   100
40
        TTCTGTTATG TGCAAAGTAG ATTATTTCAT ATTTACTTGG TATGGAAAGC   150

128

AGAGTACAGG CTCAATGGAC AATAATCATT AAACACACAT TATNTTTAAG   200

AAAANGCTGT TNNAAAAA   218

(2) INFORMATION FOR SEQ ID :227:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 209 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID :227:

GAAAACTTTA TTTGTCCACA CCAGGATTAC CGAACAGAAN NACNNGGTGG   50

TGAGAAGTTG GTATTNATAG CACCTTATTT ACATGATGGA CTTGAGGAGG   100

CAGTTAATCC TATGGTTGTG TATCACAACC TTTTATTAGC AATGCCATCT   150

TCGTCTTGCC TCCNCCCTAC TTGAATATCC CTTACGGTCA ACANCCCNCG   200

GGGTTGGGC   209

(2) INFORMATION FOR SEQ ID :228:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 179 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID :228:

TTTNNCAANC CAAATGGTTA TTTATTCTAA AACTGGAAGC TACTTTGCCT   50

ANCATTTTCG CCAGAATGGT GTAATGNNNA CAGGGGAGGA AAAAAGTTAC   100

129

AGATGTAAAC AATGACACAG TTACATTTTT TTTTTAAATG GTAAAACCCC   150

TTTTTACTGG NCNTTCCAGA ANCTTACAG   179

(2) INFORMATION FOR SEQ ID :229:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 184 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: double
            (D) TOPOLOGY: linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID :229:

AGTTTAATCT CANNNNNNNA TGTCACAAGT TATTGTAGCA GTGAAACAAT   50

GAGGGCATAC ACTATATNGA AAAAAAAACC TCCTCCCTNA TTCTCACGCC   100

AACCACAGGC TTCTGCCCTG CAAAGATCAC CAATGTCAAT AGTTTGGTAA   150

TACACCATCA TAAAGGNTCC TAAATTCATC TCTA   184

(2) INFORMATION FOR SEQ ID :230:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 140 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: double
            (D) TOPOLOGY: linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID :230:

GAGACAGATG TANNNAAAGT TCAGAATACA ACAGTTAAGA CTCAGTTTTC   50

TTTTTAGGTT TAGAATTTGA GAGCAAGTAT TGNTATGGTG AGCTGTTTTA   100

GTGCAAACAT TGTTGAGTAT GTTGTCAAAC GTCTAAAAAA   140

130

(2) INFORMATION FOR SEQ ID :231:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 178 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID :231:

CGGAGACTTG TCCAGAGAGT TGTCTCTTNT NNGTTGGGGG CCGTCCCGCT   50

CCTAAGGCAG GAAGATGGTG GCNNNTNNNG ACGAAAAAGT CGCTGGNGNN   100

NATNAANTNT AGGCTCNAAN TNNTTATGAA AANTGGGAAG TAANTNNTCG   150

GGGGTAAAAG NAANATNNGA ANATGGAT   178

(2) INFORMATION FOR SEQ ID :232:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 210 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID :232:

GAGCCAACGC CACNNNNNAG NTGAACCACA CTCACGAAAA AAACNCNTAC   50

CGTCGTCNTA ATACNNANTC TTCCCATACA AAAATCGTCC NTNTAAATNT   100

NNTAAACCAA TTCACAGCCC ACAGAACNAA TCAGTAATTT TATANCTTCN   150

NCGAAACCAC ACTTATCCCC ACCTTGGTCT ATTCATNACC CGGATNGAGG   200

GCAACCANGG   210

131

(2) INFORMATION FOR SEQ ID :233:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 247 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID :233:

```
ACTGTGCGAG TAGCTTNAAA ANNNNNNNNN NNACTCAGTT TNATTTATAC        50

AAAAAGAAAG GGGTGTGNAG TCCATGGTGT TGTACAGTNT NTAATTAGNC       100

CANNACGAGA AAANANATNN NNNTNNNAAA NNNTGAATTA TGGGGTNAGG       150

ACTNTCTNAC NTTCAAACNA NTATTNCACG TAAAAAACAT CACAGTGCGA       200

AGAAAGNNAN CNCANNTAGA GCANGAAGAC ATCAAAAGCC AGCCGGG         247
```

(2) INFORMATION FOR SEQ ID :234:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 169 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID :234:

```
AAACACCAAA NAAANNNNNC NAGCAANAAA GTGGAAGACT AACCAAGATT        50

GTGGACATTG GAATGTTTAC TGTTATTCTG TGTAAGAAAA CAACTNACAA       100

AAAAGAAAAA TGGNCAACAA AATTGTTTCC CGGCNAGGCT GNAGGAAACC       150

NGGGGGAAAN TGCCNGGGC                                        169
```

132

(2) INFORMATION FOR SEQ ID :235:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 51 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: double
            (D) TOPOLOGY: linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID :235:

        GCANCACANA AAGGAGACGN NANAGCAACG CAGAGATAGC CATCCAGATA   50

        G   51

(2) INFORMATION FOR SEQ ID :236:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 101 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: double
            (D) TOPOLOGY: linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID :236:

        CAAGTGTAAA TGCTTGCACC TCTCTNCCTC CCCGANTGAA CTCTCTGATC   50

        TCAAACTTTT TTAGGAAAGC CAGATTAAAA GCAGACGTAC CTAAATNCAA   100

        A   101

(2) INFORMATION FOR SEQ ID :237:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 156 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: double
            (D) TOPOLOGY: linear

133

(xi) SEQUENCE DESCRIPTION: SEQ ID :237:

CATTATAAAA CAGCCTAACT TCCCTTATGC CATATGATTG CCTTAAAAAG   50

ACCAGATCTC AAGGAAAAGA TCATCAAAGA GCAGAGATCT TGAAGCGGCA   100

CAGTTTTCCA GCAGTTTTCG TATTTNTTTT TATTTACGAA TGCCATACTC   150

TGTTTT   156

(2) INFORMATION FOR SEQ ID :238:

     (i) SEQUENCE CHARACTERISTICS:
         (A) LENGTH: 148 base pairs
         (B) TYPE: nucleic acid
         (C) STRANDEDNESS: double
         (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :238:

GCAGNCTAAT TGTGAATCTA AGAAACTACT CATAGACATC CCACCCTAAT   50

GATTTTACCT NNAACNTTTG TCCTTCATCA TAGAACCCTA GCAACATCCA   100

CCTCCTGTAG CACGAAACGA ATCAAACAAC CCCCTGGATA ACCTCTCA   148

(2) INFORMATION FOR SEQ ID :239:

     (i) SEQUENCE CHARACTERISTICS:
         (A) LENGTH: 258 base pairs
         (B) TYPE: nucleic acid
         (C) STRANDEDNESS: double
         (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :239:

GAGTTTTAAC TTAATCACCT CTTTAAAAGA CCTGTCTCCA AATACAGTTA   50

134

AATTTGAGGT ATTGAGGGTT AGGACTTCAA CATGTGAGTT TGGGAAGGGA   100

AGCACAAAAT CAGCCCCTAC CATGGTATAT TTATCATTGA TACATTACTA   150

TCAACTAAGC TCAAGATTTT ATTCAGATTT GACTAGTTTT TCCACTAAGG   200

CCCTTTTTCT TTTCTAGGNT CCCACAGAGG ATACATTACA TTTACTTACA   250

TCTTCTCT   258

(2) INFORMATION FOR SEQ ID :240:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 377 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID :240:

GAGCATTATT TGATGCAGAA GTTGAAAAAC AATAGACTCA AGAAAGAAAA   50

CAAACCAGTG ATTCCCCTTC CTCAGATACT GGGACTAACA GCTTCACCTG   100

GTGTTGGAGG GGCCACGGAG CAAGCCAAAG CTGAAGAACA CATTTTAAAA   150

CTATGTGCCA ATCTTGATGC ATTTACTATT AAAACTGTTA AAGAAAACCT   200

TGATCAACTG AAAAACCAAA TACAGGAGCC ATGCAAGAAG TTTGCCATTG   250

CAGNTGCAAC CAGNGGAGNT CCTTTNAAGN GNAACTTCTN GNATAATNNC   300

AAGGGTNAAC NTNTTTNNAA ANNNGCCNAA NCNNGATTTT GNACNCCCTT   350

TNNCATTGGC ATTNANTGAA AAAAGTT   377

(2) INFORMATION FOR SEQ ID :241:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 114 base pairs

135

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :241:

GGNGCACTGN TCCGAGAGCT TTTTTTNCTG AAGAATAGCA TCTTTAATGA   50

10

GTGTNCTAAT CCTTGTCATC TGAAGTTTTG AAATATATTT CCCAGGGTCA   100

GAACAATACA GAGA   114

15   (2) INFORMATION FOR SEQ ID :242:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 122 base pairs

(B) TYPE: nucleic acid

20   (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

25   (xi) SEQUENCE DESCRIPTION: SEQ ID :242:

CTCAAAATNC TGTGACAAAT TTNNNNGGTC AAGTTGTTNN CCATTAAAAA   50

GTACCTGATT TTCAAAAACC TAATAACCTT AAAACCNCCC CACGNAAAAA   100

30

AAAAAANCNA AAGNGGGCCC CC   122

(2) INFORMATION FOR SEQ ID :243:

35   (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 171 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

40

136

(xi) SEQUENCE DESCRIPTION: SEQ ID :243:

GAGAATGGGA AGCCTCATTT TGGGGACAAG AACCTGTACA AGGATTTGTG   50

ATGAACTTTT CCAATGGGGA AATTATAGAC ATCTTCAAGC CAGTGCGCAC   100

NTATGATATG CCTCATGATA TTNTTGCATC TGAAGATGGG ACTNTGTACA   150

TTGGNGATGC TCATCCAAAC C   171

(2) INFORMATION FOR SEQ ID :244:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 235 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: double
            (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :244:

AACTTTACTG TCAGATAATA AAATTAGGGC TTTCTCTTAA AGGGCTTCTT   50

TAAGAGAAAT ACAGAGTGTT TGGTATNTGA GAGAAAAAAA GTTAAAACAG   100

GACTTTCAAC TTAATCCAGA CTTCCTAACA GTGTTTACAT GTGAGGGAAA   150

CTCCTTTAAG TAATGCGTAG TGTTTTATTT TTACCATCAT TGGNGACAAA   200

AAAAACAAAA ACATAAACAT CTNANGTGAA ATATA   235

(2) INFORMATION FOR SEQ ID :245:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 211 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: double
            (D) TOPOLOGY: linear

137

(xi) SEQUENCE DESCRIPTION: SEQ ID :245:

GGCCTAGCCT GCCATACCCT TACGAGCAGG CTCAGTGATT AGACTTTGAG   50

TCTAAGTTAA AAACGCCCTG CCCCCTTCTC GCAGGCCACC TACACCGTNN   100

TTTTATCGAT TTGATAAAAC CACCAGCCTA CTCATCAAGN NGCACCCTGC   150

NTNTACNTCT AACCNTAACA TNACNGCGGC CACCTACTCA TGCCCTANTG   200

CAGCNCACCC T   211

(2) INFORMATION FOR SEQ ID :246:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 194 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: double
            (D) TOPOLOGY: linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID :246:

GGCTGAGAAT CCTTGAGCTT ACCATTTGAT ATTTCTATAT TATTTAAGAA   50

AAGTCAAAAG ATTTTGAAAA CAGCAATAGA AGTAAGATCC TTTAAGCTCT   100

ATTTGCAGCC CCTAAGAAAA GTGATGAGGA CACTGTGCAT GCCCATATGT   150

GAACATGGTG GTACCTTAGG NATTTCCCTT TNTCNATGAA TATA   194

(2) INFORMATION FOR SEQ ID :247:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 249 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: double
            (D) TOPOLOGY: linear

138

(xi) SEQUENCE DESCRIPTION: SEQ ID :247:

GCCCCCTCAA GGGCATCCTG GGCTACACTG AGCACCAGGT GGTCTCCTCT   50

GACTTCAACA GCGACACCCA CTCCTCCACC TGACGCTGGG GCTGGCATTG   100

CCCTCAACGA CCACTTTGTC AAGCTCATTT CCTGGTATGA CAACGAATTT   150

GCTACAGCAA CAGGGTGTGG ACCTCATGGC CCACATGGCC TCCAAGGTAA   200

GCCCCTGGAC CACCAGCCCC AGCAAGGCAC AAGAGGAAGG AGAGACCCT   249

(2) INFORMATION FOR SEQ ID :248:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 248 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: double
            (D) TOPOLOGY: linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID :248:

GCCCCCTCAA GGGCATCCTG GGCTACACTG AGCACCAGGT GGTCTCCTCT   50

GACTTCAACA GCGACACCCA CTCCTCCACC TGACGCTGGG GCTGGCATTG   100

CCCTCAACGA CCACTTTGTC AAGCTCATTT CCTGGTATGA CAACGAATTT   150

GCTACAGCAA CAGGGTGTGG ACCTCATGGC CCACATGGCC TCCAAGGTAA   200

GCCCCTGGAC CACCAGCCCC AGCAAGGCAC AAGAGGAAGG AGAGACCC   248

(2) INFORMATION FOR SEQ ID :249:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 82 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: double
            (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :249:

```
GGAGGGGACC GCAGCATCCA GCCCTCTAAG GCCGGGCAGC GGTCGCGTTG        50

GGGCAGAGCG CAGCGCAAGC AGGCTCAGTG TA                           82
```

(2) INFORMATION FOR SEQ ID :250:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 125 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :250:

```
GGGGCCCTCA GGACATCCAC GTGAGCGTCT GCCCAGCTGC ACTGATATTG       50

TNTTGCAAAT CCAGATTTGT TGNCATTACT GATGGGCGCG TGAAACCAGN       100

GAGAGATGCA CAAGATTTAC AGGCC                                  125
```

(2) INFORMATION FOR SEQ ID :251:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 130 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :251:

```
GGCCCAGAGG TCCTTTACTC TTACGGNACA CCTTAGCCAC ATTCACAGGG       50

AATGNTCCAG CACTCAGGCT CCTTCCCATN GGTTTTCAAA AGCGCGTTTT       100

TCTGGGGGAG CGGCCGCCTT TAGTCGACCC                            130
```

140

(2) INFORMATION FOR SEQ ID :252:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 216 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID :252:

    GAGAAGGCTG GAGAAAAACC ATCCACACAT AAACAATNGN ATTTACTCNA   50

    AAATNAAGTA CAGGTTTCAG GTATTTAAAA TAAATAAAGA AAAATCTCGT   100

    TTCCTTTGGC ATCTTTAGAA AATAAACTAA GCAATAAAAG AGGTGATTGT   150

    ATAAAGACAT GCGTAAGCAA ACATATGGGG AAAACCAGCA ACTTGGTTTT   200

    ATGNGATAAT ATCAGC   216

(2) INFORMATION FOR SEQ ID :253:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 249 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID :253:

    GGAGAAGGAG GCTGATTGCG TACATCCAGC AGTTACAATT TTTAAAAATT   50

    ACANTNNNNC NNTTNGATTN TTAATNTANG TAATTTCCTT CCAAAGAAGN   100

    TTCACATGTA ATAAGTAGAA ATTCTGTATA GGAAAAAAGC ATTAAAAATA   150

    TANATACNGC TTCATNCGTT GGGAACCATT AAAAGTAATA TAATNAGCTT   200

141

```
TTTTCAGAAG GATCTTTTGT AGCAGTGNTT ATGAATGNAC CCGCAAAAT          249
```

(2) INFORMATION FOR SEQ ID :254:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 166 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID :254:

```
GACCCCATTC TATATTATNC GTNNNGCGAT TTTTTAGCCA CCCTGAAGTT          50

ATATTTNTAT ACCNAGGCTT CGAATAATCT CATCNGACTN ACCACCCTNG          100

GAAAAAAAGA ACCGTTTGAT ACATAGGNAT GNTNAGCTTG ATATCAATNG          150

CTCCCTGGGN TTCTTG                                              166
```

(2) INFORMATION FOR SEQ ID :255:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 223 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID :255:

```
CCAGACCAAC CGCCTGCAGG AGGCTCTGAA CCCTCTTCAA GAGCATCTGG          50

AACAACAGAT GGCTGCGCAC CATCTCTGTG ATCCTGTTCC TCAACAAGCA          100

AGATTTGCTC GCTGAGAAAG TCCTTGTGGG AAATCGAAGT TGAGGACTAC          150

TTTCAGAATT TGCTCGCTAC ACTACTTTGA GGATGCTACT CCCGAGCCCC          200
```

142

CTTCTNTTGT NACAGACAGC AGA   223

(2) INFORMATION FOR SEQ ID :256:

5   (i) SEQUENCE CHARACTERISTICS:
                  (A) LENGTH: 292 base pairs
                  (B) TYPE: nucleic acid
                  (C) STRANDEDNESS: double
                  (D) TOPOLOGY: linear

10

              (xi) SEQUENCE DESCRIPTION: SEQ ID :256:

15   GGAGAAGAAG GAGCAGGAGG TGATGCTACT GACTCAAGTC AAACAGCTCT   50

      TGATAATAAA GCTTCATTGC TCCATTCAAT GCCTACTCAC TCCTCTCCGC   100

      TCTCGAGACT ATAATCCATA TAACTATTAA GATAGCATCA GTCCCTTCAA   150
20
      CAAGTCTGCC CTCAAGGAAG CCATGTTTGA TGATGATGCT GACCAGTTTC   200

      CTGACGATCT TTCCCTAGAT CATTCTGACC TGTTGTAGAG TTGTTGAAGG   250

25   AGCTGTCTGA CCATAATGAG CTGTAGAAGA AAGAAAAATT GC   292

      (2) INFORMATION FOR SEQ ID :257:

                  (i) SEQUENCE CHARACTERISTICS:
30   (A) LENGTH: 238 base pairs
                      (B) TYPE: nucleic acid
                      (C) STRANDEDNESS: double
                      (D) TOPOLOGY: linear

35

              (xi) SEQUENCE DESCRIPTION: SEQ ID :257:

      AAGGAGCAGG AGGTGATGCT ACTGACTCAA GTCAAACAGC TCTTGATAAT   50
40
      AAAGCTTCAT TGCTCCATTC AATGCCTACT CACTCCTCTC CGCTCTCGAG   100

```
      ACTATAATCC ATATAACTAT TAAGATAGCA TCAGTCCCTT CAACAAGTCT        150

      GCCCTCAAGG AAGCCATGTT TGATGATGAT GCTGACCAGT TTCCTGACGA        200

5     TCTTTCCCTA GATCATTCTG ACCTGTTGTA GAGTTGTT                     238
```

(2) INFORMATION FOR SEQ ID :258:

10
    (i) SEQUENCE CHARACTERISTICS:
       (A) LENGTH: 137 base pairs
       (B) TYPE: nucleic acid
       (C) STRANDEDNESS: double
       (D) TOPOLOGY: linear

15

    (xi) SEQUENCE DESCRIPTION: SEQ ID :258:

```
      GGAGAGAAAA GTTCCTGAGT GACAGAGAAA AAGAACAAAA AGCTGCAGAA         50
20
      GGCNTCAGCA GAGGCCACTG CTGGCCCTGA GGCTGCACCA AGTGACGAAG        100

      AACCGGCTCC AAGCATTCGT CACAGCACTA ATTTAAA                     137
```

25   (2) INFORMATION FOR SEQ ID :259:

    (i) SEQUENCE CHARACTERISTICS:
       (A) LENGTH: 241 base pairs
       (B) TYPE: nucleic acid
30
       (C) STRANDEDNESS: double
       (D) TOPOLOGY: linear

35   (xi) SEQUENCE DESCRIPTION: SEQ ID :259:

```
      GCGCGACTTT TAAGGGATTT GCNGTGATGC CTGTTGACCC AGTGCCTTCC         50

      TAGCCGGGAA GGGGCTCGGC TGGAGTGNNA AGGCTCAGAA AAATTTCGCG        100
40
      AAGAAAAAAA CCTATGAGGT AATAATAGGA TTATTCCGTA TCGAAGGCCT        150
```

144

```
TTTTGGACAG GTGGGTGCGG TGACCTTGGT ATGTATTTTT CGTGTTACAT          200

CGCGCCATCA TTGGATATGT TAGTGTGTNG GTTAGTAGGT C                   241
```

(2) INFORMATION FOR SEQ ID :260:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 248 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID :260:

```
GCGGACTTTT AAGGGATTTG CNGTGATGCC TGTTGACCCA GTGCCTTCCT           50

AGCCGGGGAA GGGGCTCGGC TGGAGTGNNA AAGGCTCAGA AAAATTTGCG          100

AAGAAAAAAA CCTATGAGGT AATAATAGGA TTATTCCGTA TCGAAGGCCT          150

TTTTGGACAG GTGGGGCGGT GACCTTGGTA TGTATTTTTC GTGTTACATC          200

GCGCCATATT GGTATATGTT AGTGTGTTGG TTAGTAGGTC TCGTATGA            248
```

(2) INFORMATION FOR SEQ ID :261:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 239 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID :261:

```
GGATCTTTCA GGTGATGAAA TAGTTCTGTA TCTTGATTTT GGCGAATCTA           50

CACANGTGAT GAAGTAACGT GATAAAATGA CATAGACCTG TATGCCTACT          100
```

145

```
ACAATACAGT ATCAAAACCA GGGATTGATT CCTGGTTCTT TTCCAAATCC        150

ACTTCCCAAA CTTATGGTAA GGTAATATTA AAAAGGCACC AAAGAGCCCT        200

GATCCCTGGA TAAACAGGAT CATTTCAAAG NNGTTTATA                    239
```

(2) INFORMATION FOR SEQ ID :262:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 143 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID :262:

```
GCCGGGTGAT GGCCAGGAAG GTGCCCTCTG TTTTTTGTAA AACAGCCATT         50

GGCCTTTGTC ATTGAGTCAC CACCTGCAGG GCTTGGGAGT GAGCGTTGGG        100

TAGGNTCAGG CCCCCAGAAC CGCCTGGGTA CTCACCGCTA GCA               143
```

(2) INFORMATION FOR SEQ ID :263:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 246 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID :263:

```
GGCGCTCAGC CTCCCCAAGG ACAAGCTCCT CCCCCTGTAA TACCTCCTCC         50

TAACAGCCGG ATATGGATGG CAAGTTACCA AACACAGTGA GCCGGGACTC        100

TAAAAAAAAA TAGCAATCCA GATAGGCTTC GATTTCCCGT GACACTCTGA        150
```

AGACATGAAA GTAGACATCG AAAATGAAAA TANTTATNNA AATGAAATGT   200

TTGGAACCTT TAGCACAGAT TTGTTTGGGA AGACACGGTC TTTTAG   246

5   (2) INFORMATION FOR SEQ ID :264:

            (i) SEQUENCE CHARACTERISTICS:
                (A) LENGTH: 199 base pairs
                (B) TYPE: nucleic acid
10   (C) STRANDEDNESS: double
                (D) TOPOLOGY: linear

15   (xi) SEQUENCE DESCRIPTION: SEQ ID :264:

        GGCTCCATTA AGGACCAAAT TNATGCTACC ACTAAACAAA AANNTATAGT   50

        CTGTGTTAAA TCGTATGCTT TTTAAAGGTA TTTAAAGATT CAACTAGCTT   100
20
        TAAAGAGGCT GAGCAGCTCA GGAAGCCTGT AATGTGACAT AACTCTTTGG   150

        ACCTGATCTT GATGTTCTGC TGTTGTNAGT CTTGAAGAGC GTATNTGAT   199

25   (2) INFORMATION FOR SEQ ID :265:

            (i) SEQUENCE CHARACTERISTICS:
                (A) LENGTH: 245 base pairs
                (B) TYPE: nucleic acid
30   (C) STRANDEDNESS: double
                (D) TOPOLOGY: linear

35   (xi) SEQUENCE DESCRIPTION: SEQ ID :265:

        GGTTTCAATC GTCCATCCAA GATACAAGAG AACGCATTGC CACTGATGCT   50

        TGCTGAGCCC CCACAGAACT TAATCGCCCA ATCTCAGTCT GGTACTGGTA   100
40
        AAACAGCTGC CTTCGTGCTG GCCATGCTTA GCCAAGTAGA ACCTGCAAAC   150

147

AATATCCCGT GTCTTCTCTN TCCCAACGTA TGAGCTGCCC TCCAAACAGG   200

AAAAGTGATT GAACAAATGG CAAATNTTAC CCTGAACTGA AGCTG   245

(2) INFORMATION FOR SEQ ID :266:

    (i) SEQUENCE CHARACTERISTICS:
       (A) LENGTH: 121 base pairs
       (B) TYPE: nucleic acid
       (C) STRANDEDNESS: double
       (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID :266:

AGGAAAAGAT GGGAATATGT TTCTTTCCTT TGAGAATTCA CAAAANGGGG   50

TCAAAAACAA AGCAATGCTG AAAGCGAACA TCCATTTNGC CTGCAATTCA   100

AGGCGAAAAT CCAAAGGCAT C   121

(2) INFORMATION FOR SEQ ID :267:

    (i) SEQUENCE CHARACTERISTICS:
       (A) LENGTH: 169 base pairs
       (B) TYPE: nucleic acid
       (C) STRANDEDNESS: double
       (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID :267:

GGGTCGCTCT CCCCCCCTCT TTCTTCGGGT TGTGTGCGTC TCCGCTTTCG   50

TGATGTGAGG AACTCTGGGG TGGGCGACGG GTCCAACTCG CGTTGTCATC   100

TCCCAGGTTG GTACACCCCC CCCCCGTTTC CCCAGCCACA CTCCACGGCC   150

AGGGTGGAGG CAGATGTCT   169

148

(2) INFORMATION FOR SEQ ID :268:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 200 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID :268:

    TCGCAGGAGA GGAATTACAT GCTCATCCTA GAAGGGGGGG CTGACTGCAG   50

    GTGTTGCTGG GAAGCCTCTC CAGGCCTGGA GCTGGAGTAC CCGTCCTCAG   100

    CACTGCCAGC AGAAAAAGTT GTGATTCAAG GAAAGCACAT TGAATGCATT   150

    ATAGCAATCC CAGACCTAAG TTCGAAGTTG CTTTGTAACA AGTGCTGCCT   200

(2) INFORMATION FOR SEQ ID :269:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 163 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID :269:

    AGGGGGGCGC AAGAGAGAAG AACTTCACAC TTCTTTATTG CTCAGCCTAG   50

    ATAGCAGCAG CTGGGAATAC GTAGGACAAA CAGGACGTCG AACAAATTAC   100

    TCCACTATAT TAATATTCAC TACACCACTT ATTCTTTCTT GAATTGTAAA   150

    CACTAAGTGT AGT   163

(2) INFORMATION FOR SEQ ID :270:

        (i) SEQUENCE CHARACTERISTICS:
              (A) LENGTH: 115 base pairs
              (B) TYPE: nucleic acid
              (C) STRANDEDNESS: double
  5   (D) TOPOLOGY: linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID :270:
 10

        TCACACTTCT TATTGCTCAG CCTAGATAGC AGCAGCTGGG GAATACGTAG   50

        GACAAACAGG ACGTCGAACA AATTACTCCA CTATATTAAA TTCACTCACA   100

 15   CCACTTATTC TTTCT   115

        (2) INFORMATION FOR SEQ ID :271:

        (i) SEQUENCE CHARACTERISTICS:
 20   (A) LENGTH: 178 base pairs
              (B) TYPE: nucleic acid
              (C) STRANDEDNESS: double
              (D) TOPOLOGY: linear

 25

        (xi) SEQUENCE DESCRIPTION: SEQ ID :271:

        CCCGAGACCT GCGANAATGG TGCTGTGACG ACGAATAGCC ACGCATTATA   50
 30
        GGGTNTTNTG TTATGGGGGA CACTCTACTA CGGGATGCGT ATGATGNGGN   100

        NCCATTATNG NAGTGGGCAT TGGGGGGAAA CAGAGCACCT GATGCTTTAC   150

 35   TGCAGAAATN CCTATGTGAC TCTTATAA   178

        (2) INFORMATION FOR SEQ ID :272:

        (i) SEQUENCE CHARACTERISTICS:
 40   (A) LENGTH: 178 base pairs
              (B) TYPE: nucleic acid
              (C) STRANDEDNESS: double

150

(D) TOPOLOGY: linear

5   (xi) SEQUENCE DESCRIPTION: SEQ ID :272:

CCCGAGACCT GCGANAATGG TGCTGTGACG ACGAATAGCC ACGCATTATA   50

GGGTNTTNTG TTATGGGGGA CACTCTACTA CGGGATGCGT ATGATGNGGN   100

10

NCCATTATNG NAGTGGGCAT TGGGGGGAAA CAGAGCACCT GATGCTTTAC   150

TGCAGAAATN CCTATGTGAC TCTTATAA   178

15   (2) INFORMATION FOR SEQ ID :273:

           (i) SEQUENCE CHARACTERISTICS:
               (A) LENGTH: 135 base pairs
               (B) TYPE: nucleic acid
20 .   (C) STRANDEDNESS: double
               (D) TOPOLOGY: linear

25   (xi) SEQUENCE DESCRIPTION: SEQ ID :273:

CTCTAGTAAA AATGTTTGAG GAAACAAAAA TGGGGAAGAA GATCAGAACA   50

AAAANATTGT TAACACTGAC CGTCCTCATG CAGGTAGGCT ACTACCAACG   100

30

CTGGTTGTTA CTCCAGGAAA ATCGAGGTGA ACATC   135

    (2) INFORMATION FOR SEQ ID :274:

35   (i) SEQUENCE CHARACTERISTICS:
               (A) LENGTH: 231 base pairs
               (B) TYPE: nucleic acid
               (C) STRANDEDNESS: double
               (D) TOPOLOGY: linear

40

151

(xi) SEQUENCE DESCRIPTION: SEQ ID :274:

TGTCGAGGAG AAGAAACCAC TTGATAACAC CCCGCGACAT CGTGGGGCTG   50

5   CTTGTCACAN GAAAGCACCA TGTTCGCAAT GGATTGCTGC AGGTGCTGCC   100

GTTGCCTCCT CAGGGTCTGC TGAAAGTCAT CTTCTAGGGT CTGAACGACA   150

TAACGCAGGA AAAGGACTCG CCCAGGCAGA GTTTGTCCCT CTTCCTTCAT   200

10   GACATAGGTG AGCAGTTTCC AGTCCCACTC C   231

(2) INFORMATION FOR SEQ ID :275:

15   (i) SEQUENCE CHARACTERISTICS:
                (A) LENGTH: 170 base pairs
                (B) TYPE: nucleic acid
                (C) STRANDEDNESS: double
                (D) TOPOLOGY: linear
20

(xi) SEQUENCE DESCRIPTION: SEQ ID :275:

25   TCGCAGGAGA AGAAACCTNG TTGCTCCACA ATGCAACCAC ACTGATTTTC   50

TCTTTTCTCT NNAGTTNTCC TTGTCTGTAA CAGGAATGTC CCTTACTATA   100

GCAGGCGGAC ACGGCCATGG GTCAAGCACC CTGCTTCTGG AACTTGNNNG   150

30   NCGTNCCCAC CATTGATTGA   170

(2) INFORMATION FOR SEQ ID :276:

35   (i) SEQUENCE CHARACTERISTICS:
                (A) LENGTH: 315 base pairs
                (B) TYPE: nucleic acid
                (C) STRANDEDNESS: double
                (D) TOPOLOGY: linear

40

152

(xi) SEQUENCE DESCRIPTION: SEQ ID :276:

ATATGAAGGA GGAAATGGCT CTCACCTTCG TGAATACCAA GACCTGCTCA   50

ATGTTAAGAT GGCCCTTGAC ATGAGATTGC CACCTACAGG AAGCTGCTGG   100

AAGGCGAGGA GAGCAGGATT TCTCTGCCTC TTCCAAACTT TTNTCTGAAC   150

CTGAGGGAAA CTAATCTGGA TTCACTCCCT CTGGTTGATA CCCACTCAAA   200

AAGGACACTT CTGATTAAGA CGGTTGAAAC TAGAGATGGA CAGGTTATCA   250

ACGAAACTTC TCAGCATTAC GATGACCTTG AATGAAAATN GTACACACTT   300

AGCGTAGCAT ATTNA   315

(2) INFORMATION FOR SEQ ID :277:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 209 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :277:

ACGTTCTGCG CCTTCCTAGG AGAGTCTTAC AGTGTTGAGA TTTCACAAGC   50

AATGCGAGTG TAAAATACCA GCTCTACAAG AAGCTAGGCT CTGTGACGGC   100

ATAGTTTTCA GTAGCTTTAT CACAATGAAA CGAGAATTAT ATGACATGGT   150

AGCAGAAATA GGCCCTTTCG TGNGCTGTTC TATTTNCTCG GATNGTAGAT   200

ATAGTAATC   209

(2) INFORMATION FOR SEQ ID :278:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 107 base pairs

        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID :278:

AAGACATCCT AAGCTATGTT GAGGAGGGAG AAGATCTGAG ACTCAAGTTC   50

TGCTGTTAAC CATGAGGTGA TTTAGTAGCT AAGTACGCCT TAGCCTTTTA   100

GAGTCTT   107

        (2) INFORMATION FOR SEQ ID :279:

            (i) SEQUENCE CHARACTERISTICS:
                (A) LENGTH: 276 base pairs
                (B) TYPE: nucleic acid
                (C) STRANDEDNESS: double
                (D) TOPOLOGY: linear

            (xi) SEQUENCE DESCRIPTION: SEQ ID :279:

ATGAAGAGAA AACCATCCTC CCATATGAAA ATATTTGCAG TAGGAGAACA   50

CAGTGCAATA GGCTCCAAAA ATGGCTTTTA AGACCTTTGG NGGGGCAGTT   100

ACTACTGCTT TAAAAGCCAG GTTAAAGTAT ACTCTAAGCA AAGATGACCG   150

TAGAGCAGCT AGCTTCCTTT TCTATAANNA TAGGGAAAGC TCTCTCCATC   200

GTCCATCAAA TCAGCTCTAG AAGGTTTTTC TTTCCCCNCT ATAAGTGCAC   250

AAAGGGGAAA CACTGATTTC AAGCTT   276

        (2) INFORMATION FOR SEQ ID :280:

            (i) SEQUENCE CHARACTERISTICS:
                (A) LENGTH: 185 base pairs

154

                (B) TYPE: nucleic acid
                (C) STRANDEDNESS: double
                (D) TOPOLOGY: linear

            (xi) SEQUENCE DESCRIPTION: SEQ ID :280:

    AGGAACAGGA TAGGTGTATG CATACTACGG CTAAGGAGAA ACAAGTCCTA   50

    CATACCAGGG TAGTGAGAAC ATTACCGCAT AACAGGGAAC TGTGATTATT   100

    TAAAAAACGC AGAACTTATT TTATCCGTGC TTTAGAAATA ACTGTATACA   150

    GTGTTATAAG TTGAAAAGAA CTCAAAACAA CCAAT   185

        (2) INFORMATION FOR SEQ ID :281:

            (i) SEQUENCE CHARACTERISTICS:
                (A) LENGTH: 186 base pairs
                (B) TYPE: nucleic acid
                (C) STRANDEDNESS: double
                (D) TOPOLOGY: linear

            (xi) SEQUENCE DESCRIPTION: SEQ ID :281:

    AGGAACAGGA TAGGTGTATG CATACTACGG CTAAGGAGAA ACAAGTCCTA   50

    CATACCAGGG TAGTGAGAAC ATTACCGCAT AACAGGGAAC TGTGATTATT   100

    TAAAAAACGC AGAACTTATT TTATCCGTGC TTTAGAAATA ACTGTATACA   150

    GTGTTATAAG TTGAAAAGAA CTCAAAACAA CCAATA   186

        (2) INFORMATION FOR SEQ ID :282:

            (i) SEQUENCE CHARACTERISTICS:
                (A) LENGTH: 198 base pairs
                (B) TYPE: nucleic acid
                (C) STRANDEDNESS: double

155

(D) TOPOLOGY: linear

5   (xi) SEQUENCE DESCRIPTION: SEQ ID :282:

TGTGGGCTCA GTAATGTCCC CGCTGATGAC AATTTCGAGA GTCCATGTTC   50

TATAGAAACC TTGAGGTCGG CCAGCCGTGT CTTGGCCAAT GAGATGTAGT   100

10

TGTGAGGAGG GGGCGTACTT GGGGACCAGG GGTGGGTGGA GATGTGCCCT   150

GTAGGCACAG GGAGACTCAA AAGCACGAGT TNTGAAAGCG TAAATGGG   198

15   (2) INFORMATION FOR SEQ ID :283:

(i) SEQUENCE CHARACTERISTICS:
      (A) LENGTH: 222 base pairs
      (B) TYPE: nucleic acid
20   (C) STRANDEDNESS: double
      (D) TOPOLOGY: linear

25   (xi) SEQUENCE DESCRIPTION: SEQ ID :283:

AGAAAAAGGT GAAGCGAAGC CCAAGGACAC CATGCTAAGG GCAAAAGTAA   50

GAGACAGTCT CAGAACTGAG AGAATCGTGT CTTCTGCTTT TTGAAGTAGA   100

30

CTGTCACACT CAGGCAGCCT GTCAATGCTG AATGTTAGGA CTTCTGTCTC   150

CGCTGGAGAC ACGCCTGGGC AAGTCAGCGT TTAGTGTTTG ACAGCTTTCT   200

35   CAGCTCCCTG ACTCCGTTTA CC   222

(2) INFORMATION FOR SEQ ID :284:

(i) SEQUENCE CHARACTERISTICS:
40   (A) LENGTH: 162 base pairs
      (B) TYPE: nucleic acid
      (C) STRANDEDNESS: double

156

(D) TOPOLOGY: linear

5   (xi) SEQUENCE DESCRIPTION: SEQ ID :284:

ATGGATCAAA CTACCTCTAT AATGAAGACT GTTCTCAAAA ACGCGAGGNA   50

ATGTGNGACG ACACTGACCT ATCAGACAAG AGGGCATGCC CCCCTGGCCA   100
10
CCTTTGNCGC TGTTTNTGCA ACGTTCGCAG TGNTACTCTG CGTGAACCGG   150

TAGACTGCTT GG   162

15   (2) INFORMATION FOR SEQ ID :285:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 67 base pairs
(B) TYPE: nucleic acid
20   (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

25   (xi) SEQUENCE DESCRIPTION: SEQ ID :285:

GGATCCANGC AAAGCCCACT CCTCCAGGGT GAAGTTTTTC TCCCGCGACA   50

GACAGCAGAC TCGAGCC   67
30
(2) INFORMATION FOR SEQ ID :286:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 153 base pairs
35   (B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID :286:

GGTCGGATCA GGTCACCCGG CAGCAGCAGC TCTCGAGAGC TGAGGCACAA   50

GGCAGGGGCC CGGCTGTACA CCTGCAGGAC CCAGGAGAGC CTGTTGCAGT   100

TCTTGTCCGA AGCGCCGAGA TAGCCACTCA GTGTCCCTGC AGCAGGAGCA   150

GAA   153

(2) INFORMATION FOR SEQ ID :287:

     (i) SEQUENCE CHARACTERISTICS:
         (A) LENGTH: 293 base pairs
         (B) TYPE: nucleic acid
         (C) STRANDEDNESS: double
         (D) TOPOLOGY: linear

     (xi) SEQUENCE DESCRIPTION: SEQ ID :287:

TACTACGGCT AAGGAGAAAC AATGTTCCTA CATATCACGG GTAGTGAGAA   50

CATATCTGCA TAACAGGGAA CTGTGATATT TAAAAACAGC AGAACTTATT   100

CCATCGTGCT TTAGAAATAA CTGTATACAG TGTTATAAGT TGAAAAGAAC   150

TCAAAATAAC TGATATAAAT ACATCTATGT ATTAGAATTT AAAAAAGCTG   200

CTTTCTGTGA AGTCAATCAG CTATATTAAA AATGACACAA ATCCAAAACC   250

GATGCATGCC ATATANAAGG GACATTGNAA GTCCGCTCGC TGC   293

(2) INFORMATION FOR SEQ ID :288:

     (i) SEQUENCE CHARACTERISTICS:
         (A) LENGTH: 114 base pairs
         (B) TYPE: nucleic acid
         (C) STRANDEDNESS: double
         (D) TOPOLOGY: linear

158

(xi) SEQUENCE DESCRIPTION: SEQ ID :288:

AGGGTAAATG TACGTTGTTG AGTCACAGGC CTGCCAGACC TCTACTACCT   50

CATTGTCCCC TCCGGTGACC AGTTCTGCCG TCACTGTCAG GAGAATGCCC   100

GTGTTGAATC ACTG   114

(2) INFORMATION FOR SEQ ID :289:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 290 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: double
            (D) TOPOLOGY: linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID :289:

ATGAACCAGT GCCCGAGGTA CCCGGGTGTG GACCAGAGAA GTTTGCTGGA   50

AAGGACGTTG CCAGGACTTA CACGTTTACA GATCCAGCAA CTGCTCTNCC   100

CAGTGCCACA ACCATGGGGC GCCAACCACA AGCAGGAGTG CCACTGCCAC   150

GCGGGCTGGG TCCCACCCNA CTGCGCGAAG CTGCTGACTG AGGNGCACGC   200

AGCGTCCGGG AGCCTCCCTG TCCTTGTGTG GGGTATGGNG CTCTGGCGTT   250

GNGCTGGTTA CCCTGTAGGA GTTANTGNCT ACCGGAAGCT   290

(2) INFORMATION FOR SEQ ID :290:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 179 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: double
            (D) TOPOLOGY: linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID :290:

     AACCGCTCTC CACACCGCTC CCACGAGCTC CAAGCTTAAA CGTCCAGATN   50

 5   NACTTTGTTG CTTTGCTGAT TTTAACAGCT TGATTCTAAG CNCTTACTAG   100

     TATCATNTGT GGCAGGACTT GNTCCATATC AGTGTTACTT TTGCTACTGT   150

     TTTGTAGAAC GATGTACATG AATGAGCCT   179
10
     (2) INFORMATION FOR SEQ ID :291:

          (i) SEQUENCE CHARACTERISTICS:
               (A) LENGTH: 199 base pairs
15   (B) TYPE: nucleic acid
               (C) STRANDEDNESS: double
               (D) TOPOLOGY: linear

20
        (xi) SEQUENCE DESCRIPTION: SEQ ID :291:

     TCTTTCATTT TGNCTGCCAA TCATTGTCAG AAATTTAGGG AAGTCAATTG   50

25   TGCCATTACC ATCGGCATCT ACTTATTAAT TATGTCCTGT AACTCTGCTT   100

     CTGTGGGATT CTGCCCAAGA GATCTCATTA CAGTTCCCAA TTCTTTGTTG   150

     TTATAGTACC ATCACCATTT CGTTAAATAG TGAAAGAGCT TTTTGAATC   199
30
     (2) INFORMATION FOR SEQ ID :292:

          (i) SEQUENCE CHARACTERISTICS:
               (A) LENGTH: 177 base pairs
35   (B) TYPE: nucleic acid
               (C) STRANDEDNESS: double
               (D) TOPOLOGY: linear

40
        (xi) SEQUENCE DESCRIPTION: SEQ ID :292:

160

GGAAGACCAT TCTGATCATC CTCACTGACG CCA⁻ ⁻GGCAA GAGGGTGGTT   50

TTCCTGAAGC AGCTGGCTGT GGCTTATACT CGTGACTGGA CCTCTGGNCT   100

CAATTGAGTT CCTCAACGAA GACCACACCA GAAATTGTCA TTGCCACCTC   150

AACCGAANNG ATATTACAAT GTAAAAA   177

(2) INFORMATION FOR SEQ ID :293:

            (i) SEQUENCE CHARACTERISTICS:
                (A) LENGTH: 295 base pairs
                (B) TYPE: nucleic acid
                (C) STRANDEDNESS: double
                (D) TOPOLOGY: linear

            (xi) SEQUENCE DESCRIPTION: SEQ ID :293:

ATTGGTTTTC CTCATCCACT GAGAATGCTG CTGGTTACTG CAAACGTTCA   50

CCAACCANAG CTTTGGTCCA TACAGCTTTC TTCTAGATTN GGAGACTCTC   100

AAGGACAGCA GGNGCTTTAA AATCCCTGGA CTGTGTTGAG AGGGCTTCTT   150

TAGGCTTTTC ATGATGTGAA TAGCCAGTCA TGAACTTTGN GTCTGTTTCT   200

TTTAGGCTCT TTTTGCAGCA GCAGAGCCAT GCTATNGAAG GAGTGAGAAC   250

CTATGCGAGN GACCCNGTGN TTGNACTTGC CAGGGAGCTT GGCGT   295

(2) INFORMATION FOR SEQ ID :294:

            (i) SEQUENCE CHARACTERISTICS:
                (A) LENGTH: 78 base pairs
                (B) TYPE: nucleic acid
                (C) STRANDEDNESS: double
                (D) TOPOLOGY: linear

161

(xi) SEQUENCE DESCRIPTION: SEQ ID :294:

AATGATCCTT TTTTCGCTCT TACCTATAGT ACAAGTCCAT GATACTACTG   50

CATATTTTAC CATTTTGNAA ACTGTGAG   78

(2) INFORMATION FOR SEQ ID :295:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 163 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: double
            (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :295:

ATTCTGTACC TGTTCTGAAC CTCGCCATAA GGGACTTGCA GCTTCGATTT   50

GCTAACCTGA AATTCTGCTG CTGCCATGGA ACAAGCCTGG GCTAGCTTGG   100

GGGAGGAGGA GAGACCATGT GGAGTAGAGC CAAGCTCTGG ACATTTGAGA   150

GAGCCCGGTA ATA   163

(2) INFORMATION FOR SEQ ID :296:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 189 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: double
            (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :296:

AGCTTAGAGC GGAACGGGTT CCACGTGCGG TACTCCTGCT TCACGCCGCC   50

CTCGGTCACC GTGACGCGCC TCTCGCCGTA CACAGACTGG CCCGGCACCA   100

162

TGTTAGCGTG ACCAGCGCGT CCTCCGCCCC GCGTNAGATG AAGAGGCCCT   150

CGTGCCGGTG CGCTCCACCG ACACCACCAT GGCCCCTTC   189

5   (2) INFORMATION FOR SEQ ID :297:

          (i) SEQUENCE CHARACTERISTICS:
              (A) LENGTH: 199 base pairs
              (B) TYPE: nucleic acid
10   (C) STRANDEDNESS: double
              (D) TOPOLOGY: linear

15   (xi) SEQUENCE DESCRIPTION: SEQ ID :297:

GGAAACCAGC CCCTCACATC CTCCCTGAAC TTCCTGTCCC CACTCACACA   50

AGTGGTCCGG TGTCACCCTG CAGTTGGGTA TAGTCATAGG TACCATTGAT   100
20
GACGCCTTCT ACCTCGGCCA TGTAGGCCTT CCAGTCAACC TCTGTGTCTG   150

GAAGAAGACA AGATGATCTG GTTACTTTTG AGTCTAGAAC TTGTCTGCC   199

25   (2) INFORMATION FOR SEQ ID :298:

          (i) SEQUENCE CHARACTERISTICS:
              (A) LENGTH: 181 base pairs
              (B) TYPE: nucleic acid
30   (C) STRANDEDNESS: double
              (D) TOPOLOGY: linear

35   (xi) SEQUENCE DESCRIPTION: SEQ ID :298:

AAAAGATGAT AAATCCACCC TCNTGCTCTT AAAATCCCAT AAACGNTAGG   50

CTCTGGAGAA ACAAGTTGTT CTGTCGAGCC CTTGCCATCA ACACACTAAG   100
40
CAATCATAGT CCCCCAGAGC ACNAGATACT GCTAATGACC ATTANATNTT   150

GTATCATCAT GCTGCCTCCT GCATTTGAAT T   181

(2) INFORMATION FOR SEQ ID :299:

(i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 314 base pairs
    (B) TYPE: nucleic acid
    (C) STRANDEDNESS: double
    (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :299:

AACATTGTTT ATTCATCCAG CAGTGTTGCT CAGCTCCTAC CTCTGTGCCA   50

GGGCAGCATT TTCATATCCA AGATCAATTC CCTTTTTAGC ACAGCCTGGG   100

GAGGGGGTCA TTGTTCTCCT CGTCCATCAG GGATCTCAGA GGCTCAGAGA   150

CTGCAAGCTG CTTGCCCAAG TCACACAGCT AGTGAAGACC AGAGCAGTTT   200

CATCTGGTTG TGACTCTAGC TCAGTGCTCT TCCACTACTT ATATNCGCCT   250

TGGTGCCACC AAAAGTGCTC CCCAAAAGGA AGGAGAATGG GATTTTTTCC   300

GAGGCATGTA CATT   314

(2) INFORMATION FOR SEQ ID :300:

(i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 168 base pairs
    (B) TYPE: nucleic acid
    (C) STRANDEDNESS: double
    (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :300:

AAGAGTCCTG AAGGCATATC CAAGCCTGTT GTTCCTGCAG ACCTCATTAC   50

164

CACGCCAACA GAGAAGGCTG GACTGCTGCC CACATGCTGC TTCCAAAGGT   100

TTTAAGAACT GCCTAGAAAT CTCGTGTAGG CACGAAGGGC TTGAGCCAGA   150

5   AAGGAGAGAC AAGTGCAA   168

        (2) INFORMATION FOR SEQ ID :301:

            (i) SEQUENCE CHARACTERISTICS:
10   (A) LENGTH: 142 base pairs
                (B) TYPE: nucleic acid
                (C) STRANDEDNESS: double
                (D) TOPOLOGY: linear

15

            (xi) SEQUENCE DESCRIPTION: SEQ ID :301:

        ACCCCACATG CCCAGATGTC CACGNGCTTG CNATACGCCT CTTTGCAAAG   50
20
        GACCTCAGGG GACAGGTACC TGGTGTGCCA GCGAAACCAA ACCATGCCTG   100

        CTGGTTCCCC TGACCTCGAT AGCTAGGCCA AGTTTGCCAG CT   142

25   (2) INFORMATION FOR SEQ ID :302:

            (i) SEQUENCE CHARACTERISTICS:
                (A) LENGTH: 197 base pairs
                (B) TYPE: nucleic acid
30   (C) STRANDEDNESS: double
                (D) TOPOLOGY: linear

35   (xi) SEQUENCE DESCRIPTION: SEQ ID :302:

        AGAATTCGTA ACTCATCCTA GAGTGGGCAC ATTTTAGACA TAGCAGGCGT   50

        GATGACCAAC AAAGACTGAA GTTCCCTATC TACGGAAAGG CATGACTGGG   100
40
        AGGCCCACAA GGACTCTCAT TGAGTTCTTA CTTCGTTTCA GTCAAGACAA   150

165

TGCTTAGTTC AGATACTCAA AAATGTCTTC ACTCTGTCTT AAATTGG   197

(2) INFORMATION FOR SEQ ID :303:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 236 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID :303:

AGAATTGCAA CTCATCCTAA GTGGGCACAT TTAGACATAG CAGGCATGAT   50

GACCAACAAA GATGAAGTTC CCTATCTACG AAAAGGCATG ACTGGGAGGC   100

CCACAAGACT TTCATCGAGT TCTTACTTCT TTCAATCAAG ACAATGCTTA   150

TTCAGATACT CAAAAACGTT TCACTCTGTC TTAAATGAAC AATTGAATTT   200

AAAAGTTTTT GAATAAATGA TGAAAATTTT TTAACT   236

(2) INFORMATION FOR SEQ ID :304:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 220 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID :304:

ATGTCATTCT CCTCATCCTC CGCATCTCCA CTGTCGTGCA CAAGGACCAC   50

CATGTTTCCT TTAGTTCCCA GCACACGGGG CTCTGCAGTA GTGAATGAAG   100

TCTAGCACAG CCACCGCCCC CATGCCCAGG CTCAGGAGCA CACTGAGGTC   150

166

GTCCACCAAC ACACCGGGTA CGTCCACCGA GCCTCTCCAC TGCTCTGGCT   200

TTAGGCCTCC CGTACAAACT   220

(2) INFORMATION FOR SEQ ID :305:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 145 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: double
            (D) TOPOLOGY: linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID :305:

AGAAGAAAGG ACACCATTAC CATCCATATT GACATCGCAT TTCCATAGAA   50

ATGCCAAAGA AAGAAGGTCC TGGGGTTTTT TATAGAAGCT CAAAAAGNTC   100

AACCTTCGAT GCTATCCCCC AGCCCAATAC AAAATCAGAA AAAGC   145

(2) INFORMATION FOR SEQ ID :306:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 120 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: double
            (D) TOPOLOGY: linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID :306:

AGTCAAGGCA TTATGGTTTT TAATCTGAAA CTTAGAGAAC CCTTTAATAT   50

TNGCTTTTAC TGGCGTACAT ATGAGTGGAA TATAAACTGT ACACACNNNG   100

NGNTGATATA AACAGATNNA   120

(2) INFORMATION FOR SEQ ID :307:

167

(i) SEQUENCE CHARACTERISTICS:

    (A) LENGTH: 120 base pairs

    (B) TYPE: nucleic acid

    (C) STRANDEDNESS: double

    (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :307:

AGTCAAGGCA TTATGGTTTT TAATCTGAAA CTTAGAGAAC CCTTTAATAT   50

TNGCTTTTAC TGGCGTACAT ATGAGTGGAA TATAAACTGT ACACACNNNG   100

NGNTGATATA AACAGATNNA   120

(2) INFORMATION FOR SEQ ID :308:

    (i) SEQUENCE CHARACTERISTICS:

        (A) LENGTH: 247 base pairs

        (B) TYPE: nucleic acid

        (C) STRANDEDNESS: double

        (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :308:

ACTGCACCCA CCCCAAGGCC ATGGCAGGGT ATGGAGATGT CATTTATCAT   50

AAGATGGACA GATAAGCTGG ACCAATAATT AAGATTCCAG CAGAGGGTGA   100

GGACACCCAG ATGCGCCAGG ACTGTAGGAA ATCACAATGA TGGCAACGTC   150

TTGCCTTCCT GGGGACAGGG AGCCCTATTC AAANANAGTC ACATCTGAGG   200

AGCCGGGGGT TATAACATCA AGTCTGTCCT TGACCTCACA AAGCCAG   247

(2) INFORMATION FOR SEQ ID :309:

    (i) SEQUENCE CHARACTERISTICS:

        (A) LENGTH: 107 base pairs

168

```
            (B)  TYPE: nucleic acid
            (C)  STRANDEDNESS: double
            (D)  TOPOLOGY: linear


5


         (xi) SEQUENCE DESCRIPTION: SEQ ID :309:


    AGGTAAGGTT GTCACGTGGA ACAACTGATA AAGGTCAGCT ATATATGTAG          50

    AGCTATATAT GTGAGTCACA AGGTGTGTGA CATACGTGTA TACGTATAAT         100

    ATGCGTT                                                        107


         (2) INFORMATION FOR SEQ ID :310:


            (i) SEQUENCE CHARACTERISTICS:
                (A)  LENGTH: 114 base pairs
                (B)  TYPE: nucleic acid
                (C)  STRANDEDNESS: double
                (D)  TOPOLOGY: linear


         (xi) SEQUENCE DESCRIPTION: SEQ ID :310:

    GGAAGACCTC GCTGGACATC CTGCAGGGCC ACATGGTGGC TCTGCTTGTG          50

    ATTCTGGGGT CCACCCTCTC CAGTCAAGAG AACCCCCGTC GGGTTTAATG         100

    TATCAGGAAA GAGA                                                114

         (2) INFORMATION FOR SEQ ID :311:

            (i) SEQUENCE CHARACTERISTICS:
                (A)  LENGTH: 237 base pairs
                (B)  TYPE: nucleic acid
                (C)  STRANDEDNESS: double
                (D)  TOPOLOGY: linear
```

(xi) SEQUENCE DESCRIPTION: SEQ ID :311:

ATGGCAAATA GGAAGAAGCT CAGTATCCTC CTCCCACCAT AACCCCACTC   50

5   TCCACTGCCT CCTGGACCAT AGTTTCCTCC ACTATACGGT CCCCCCATGT   100

TCCTGCTACC ACCAAAGTTT CCACTCTTTA TCGAACCGTA TTAGAAGGTC   150

GCTGGTTATA ATTTCCAAAA TATGTAATTT CCACTTCCAA ATCCTTTATA   200

10   GTTGTCATAA CCACCTCCGT AGCCCCCACC CTGTTGC   237

(2) INFORMATION FOR SEQ ID :312:

15   (i) SEQUENCE CHARACTERISTICS:
                 (A) LENGTH: 147 base pairs
                 (B) TYPE: nucleic acid
                 (C) STRANDEDNESS: double
                 (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :312:

25   TNNTCCACAA CAGNGGGACT ACTGAAGACT AGAGAACGCC TCTGTGNGAG   50

TGGTGCAGAC AAAGACCTCA CTAAAGTGNG CTTAACAGAG TACTAGAGGA   100

GAGAACTTGG CAATAGCAAG TACAGACAAC TATGTGAGAA ATACTGC   147

30   (2) INFORMATION FOR SEQ ID :313:

           (i) SEQUENCE CHARACTERISTICS:
                 (A) LENGTH: 151 base pairs
35   (B) TYPE: nucleic acid
                 (C) STRANDEDNESS: double
                 (D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID :313:

170

CACAACAGNG GGACTACTGA AGACTAGAGA ACGCCTCTGT GNGAGTGGTG   50

CAGACAAAGA CCTCACTAAA GTGNGCTTAA CAGAGTACTA GAGGAGAGAA   100

CTTGGCAATA GCAAGTACAG ACAACTATGT GAGAAATACT GCTCCCAAAG   150

G   151

(2) INFORMATION FOR SEQ ID :314:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 287 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: double
            (D) TOPOLOGY: linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID :314:

GAAGGTTGTA CGTGGACACT ATAAAGGTCA GCAAATTGGC AAAGTAGTCC   50

AGGTTTACAG GAAGAAATAT GTTATCTACA TCGAACGGGT GCAGCGGGAA   100

AAGGCTAATG GCACAACTGT CCACGTAGGC ATTCACCCCA GCAAGGTGGT   150

TATCACTAGG CTAAAACTGG ACAAAGACCG CAAAAAGATC CTCGAACGGA   200

AAGCCAAATC TCGCCAAGTA GGAAAGGAAA AGGGCAAATA CAAGGAAGAA   250

ACCATTGAGA AGATGAGGAA TAAGTAATTN ATATANA   287

(2) INFORMATION FOR SEQ ID :315:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 183 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: double
            (D) TOPOLOGY: linear

171

(xi) SEQUENCE DESCRIPTION: SEQ ID :315:

GGAATCAAAC GNCTCTATAA TGAAGATAAT GTTCAGAAAA CGTGGGTTCT   50

GTGGTGACAC TGATTTATCA AGACAAGAGG GACATGCTTC CCCTTGTCCA   100

CCTTTGCAGC CTGTTTCTGT CATGTAGTTT CAACAAGTGC TACCTTGAGT   150

GTAAACTAAG GTAGACTACT CTGNGAATAA GAA   183

(2) INFORMATION FOR SEQ ID :316:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 135 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :316:

GGAATGAATC AAACGNCTCT ATAATGAAGA TAATGTTCAG AAAACGTGGG   50

TTCTGTGCGT GCACTGATTT ATCAAGACAA GAGGGACATG CTTCCCCTTG   100

CCACCTTTGC AGCCTGTTTC TGTCATGTAG TTTCA   135

(2) INFORMATION FOR SEQ ID :317:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 187 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :317:

CGTTTGAAAT TCATCCCAAC TGTAGGCTGA GTGACCTGAA GTTGACAGAC   50

172

TGCCGAAGTC CAAAAGCTTC AGCATTTCCT TAGTGTCAGG ATCTACTTCA   100

ATAATNNTGA TCCAAGGCTG AGACCTCAGA AACATAATGC TCTCCTTTCC   150

CTATNTTTTC TGCGGCTTGA TGGAGATACC TTTACTG   187

(2) INFORMATION FOR SEQ ID :318:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 268 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: double
            (D) TOPOLOGY: linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID :318:

TCCCAGGAGA AGGAACTTTG AAATTCATCC CAACGTAGGC TGAGTGACCT   50

GAAGATTGAC AGACTGCCGA AGTCCAAAAG CTTCAGCATT TCCTTAGTGT   100

CAGGATCTAC TTCAATAATN NTGATCCAAG GCTGAGACCT CAGAAACATA   150

ATGCTCTCCT CCCTTNCTTT TCTGCGCTTG ATGGAGATAC CTTTCACTGT   200

GCCTCTCTGA ATCGTTTCAT CAGATGCTGA CGTAACCTGC TATTTGTTGN   250

AGCTTTCNGT TGNNNTAA   268

(2) INFORMATION FOR SEQ ID :319:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 138 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: double
            (D) TOPOLOGY: linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID :319:

173

ACTGCACCCA CCCCAAGGCC ATGCAGGGTA TGGAGATGTC ATTTATTATA   50

AGATGAACAG ATAAGCTGGA CCAATAATTT ACAGATTCCA CAGAGGGTGA   100

GGACACCCAG ATGCGCCAGG ACTGTAGGAA ATCACAAT   138

(2) INFORMATION FOR SEQ ID :320:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 118 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: double
            (D) TOPOLOGY: linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID :320:

AAATGATGAT AAATTCATCC TCTTCTGCTC TTAAAATTTC ATAAACCTCA   50

GGCTCTGGAG AAACAAGTTG TTCTGTTGGG CCCTTGCCAT CAACACACTT   100

GTAATCATAC TTCCCCCA   118

(2) INFORMATION FOR SEQ ID :321:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 160 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: double
            (D) TOPOLOGY: linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID :321:

AGAACAGTTG AAGGTCTGAG GTGTTGAGAG GCAAATGGGG TCTCTGGGTG   50

GATCCTGGTC CTGTCAGCAG GCCTGGACTT GTTCAGGATG GACTGGTGGC   100

GTTATAAAGG GCAGATCAGG GTGCCTGTCC CTTGGCATGT CCCTTAAGAT   150

174

TTCCTTTTCC   160

(2) INFORMATION FOR SEQ ID :322:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 281 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: double
            (D) TOPOLOGY: linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID :322:

AGGAGGGAGT TAATCCAAAC CACACAATGA AGTCTTCAAA CCACCNCCCG   50

AACAGGGCTG CTGATTGTTC CTTTCACTTT TGNGGTGACC TTGAGCTCCC   100

TTAAAAAAAA AACTTGGAGA ATCACAACTG GCAATGCACC GCAGTTCTCG   150

AACTACACAA GCATAGTCTG ACTAAGTCAC ATGTGTTTCC ATATCAACTT   200

GTTTGACAGG GCGACCTACT GCAAAGCAGG CTCAGTTACC CCACCAGTCA   250

ACCCCCTGGG AGTATAATNN TCTCCATANA A   281

(2) INFORMATION FOR SEQ ID :323:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 99 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: double
            (D) TOPOLOGY: linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID :323:

GGAATTTTCT CAAAGAAAAC GCAATAGCCA ATTGGAACCT ACTNTANCGC   50

ANTTTATNNN GTCTTCTTTA ANNTAGAGTG ACTTACTGAT TTATTATTG   99

175

(2) INFORMATION FOR SEQ ID :324:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 167 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID :324:

GGAATTTTCT CAAAGAAAAC GCAATAGCCA ATTGGAACCT ACTNTANCGC   50

ANTTTATNNN GTCTTCTTTA ANNTAGAGTG ACTTACTGAT TTATTATTGA   100

CACNNGTCCN NNGCNCNAGN TTACCATCCT TATGTGAATA CTNCAAGGGA   150

TTGCCCGCGT TTTTAGG   167

(2) INFORMATION FOR SEQ ID :325:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 160 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID :325:

TGATCCAACT CTTCCTGTGT GAAAAGAAGA ATGATGGCAG GAAGAACATA   50

AAGACTTTAA AACTCCTAGC CGGGGTTTGT CGGACTCTTT GNCAGTAGTG   100

ATTTAGCCAA CCAGGCAACA GAGATACGAT CTAATCTCCT CGCCCCTCTT   150

TCGGGTCGCG   160

(2) INFORMATION FOR SEQ ID :326:

176

(i) SEQUENCE CHARACTERISTICS:

    (A) LENGTH: 124 base pairs

    (B) TYPE: nucleic acid

    (C) STRANDEDNESS: double

    (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :326:

GGAAGGGGTG TTGTTTGATA GACATTATCT GTGGCTGGGT CTTTCTGGCT   50

GATGAGAGAC ATGTAGATTA TGTGAAGCAA GTGGCTAGAA GATGAGAGAG   100

AACATGAGAG AGCAGAGTGC TCTC   124

(2) INFORMATION FOR SEQ ID :327:

(i) SEQUENCE CHARACTERISTICS:

    (A) LENGTH: 253 base pairs

    (B) TYPE: nucleic acid

    (C) STRANDEDNESS: double

    (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :327:

AGCCTAGTTT GAACATCCTC ATCCCNGTGT TAGACCGGAT CCGATATACA   50

GAGTCTTAAG GAAATCGCAT CAACGTGCCT GAGCAGTCGG CTGTGACTCT   100

CGACAATGTA ACTCTGCAAA TCGATGGAGT CCTTTACCTG CCATCATGGA   150

CCCTTACAAG GCAAGCTACG ACGCGAGGAC CCTGATATGC CGTCACCCAG   200

CTAGCTCAAA CAACCACGAG ATCAGAGCTC AGCAAACTCT CTCTGGACAA   250

AGT   253

(2) INFORMATION FOR SEQ ID :328:

      (i) SEQUENCE CHARACTERISTICS:

          (A) LENGTH: 200 base pairs

          (B) TYPE: nucleic acid

          (C) STRANDEDNESS: double

          (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID :328:

```
GAACCTCTGG GCTCTCATCC TCTCCTATTG ACAGTGAAGC CCATGGCAAA        50

TAGAAGAAGC TCAGTATCGG CTCCTCCCAC CATAACCGCG TTNAAATCGC        100

CTCCTGGACC ATAGTTTCCT CCACCATAAG TCCCCCCATG CTCCTGCTAC        150

CACCGAAGTT CCCACTCCTG NGCGAACCGT AGTTAGAAGA TCGCTGTTAT        200
```

(2) INFORMATION FOR SEQ ID :329:

      (i) SEQUENCE CHARACTERISTICS:

          (A) LENGTH: 280 base pairs

          (B) TYPE: nucleic acid

          (C) STRANDEDNESS: double

          (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID :329:

```
TGACCTGATC ATCCTGAAAA ACTTTATGGG GGAGAAAGGT CAGCAGCTTC        50

TCTTTCTTTT NTCGAAAATN ATAAAACTGC GTATTCTACT TTATATTTAA        100

TGTAAGGAAG AAAATATACA AGCCCATATT TACATCGTAT TTCTATTAAG        150

AGCAACAATA GTTCATATGT TCATGTTTGC TACTATCACA ATNCAACATA        200

TGAACACAGA TCAGCTCTAT ACCATGAATA CTGCTGGAAG TGATGGTTTA        250

GGATTACCAA CTCACTGCTG CCATGACCGA                              280
```

(2) INFORMATION FOR SEQ ID :330:

        (i) SEQUENCE CHARACTERISTICS:
                (A) LENGTH: 268 base pairs
                (B) TYPE: nucleic acid
                (C) STRANDEDNESS: double
                (D) TOPOLOGY: linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID :330:

CCTGAAAAAC TTTATGGGGG AGAAAGGTCA GCAGCTTCTC TTTCTTTTNT   50

CGAAAATNAT AAAACTGCGT ATTCTACTTT ATATTTAATG TAAGGAAGAA   100

AATATACAAG CCCATATTTA CATCGTATTT CTATTAAGAG CAACAATAGT   150

TCATATGTTC ATGTTTGCTA CTATCACAAT NCAACATATG AACACAGATC   200

AGCTCTATAC CATGAATACT GCTGGAAGTG ATGGTTTAGG ATTACCAACT   250

CACTGCTGCC ATGACCGA   268

(2) INFORMATION FOR SEQ ID :331:

        (i) SEQUENCE CHARACTERISTICS:
                (A) LENGTH: 170 base pairs
                (B) TYPE: nucleic acid
                (C) STRANDEDNESS: double
                (D) TOPOLOGY: linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID :331:

TCGCAGGAGA AGGAACCTAT ACACCCTTTA TAGAGCTTTA AATCGACTGT   50

AGAGTTTTGT GGTCTTCCAG TCCCAAATGT TTAATTTTCC ATTTGCATTN   100

TGAAATCACA TAACTCATGT CTGAAAAGTC CACCTGACAA GCATACCTGC   150

TACCATATGC CCTTAAAAAT   170

(2) INFORMATION FOR SEQ ID :332:

      (i) SEQUENCE CHARACTERISTICS:
           (A) LENGTH: 223 base pairs
           (B) TYPE: nucleic acid
           (C) STRANDEDNESS: double
           (D) TOPOLOGY: linear

      (xi) SEQUENCE DESCRIPTION: SEQ ID :332:

TCGCAGGAGA AGGAACCTAT ACACCCTTTA TAGAGCTTTA AATCGACTGT   50

AGAGTTTTGT GGTCTTCCAG TCCCAAATGT TTAATTTTCC ATTTGCATTN   100

TGAAATCACA TAACTCATGT CTGAAAAGTC CACCTGACAA GCATACCTGC   150

TACCATATGC CCTTAAAAAT NNGGNNNNNG NNNNGGNTGA ANGGTTCTGT   200

GTTCCAAAAA TNTAAGATTT GTT   223

(2) INFORMATION FOR SEQ ID :333:

      (i) SEQUENCE CHARACTERISTICS:
           (A) LENGTH: 132 base pairs
           (B) TYPE: nucleic acid
           (C) STRANDEDNESS: double
           (D) TOPOLOGY: linear

      (xi) SEQUENCE DESCRIPTION: SEQ ID :333:

AGACAATTGG CGGCATCCTC GTAGGCTTCA CTAACTCCCA CAAGTTCTTC   50

TGGTTTCATT TCGGTTATTT TTTGCAGCCA ATTCTCTCCA TGTTTGGCAG   100

TCACAAGGCT CATGTGCTTC ACCAAGGCAC TC   132

180

(2) INFORMATION FOR SEQ ID :334:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 235 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID :334:

```
AAGTTGTTCA TGGNAGGCAT TTATCCTNTC AATAATNCAA ACGAGGCTTC        50

TGGAATAACC AGTGCCCCAT TCCATCAGAG TCTTTGCGCG ACTAAAGCCT       100

CCATNTTTGC CAATTTCAAT TGTTTGGGAT TCTAGCACTC CTTACCNGCA       150

GTAATGCCCT TGCTGCAGAC AACAACACCT GGACTGNGAG ATGGACCAAT       200

TCTCAATGGC AATCCAGGGA AAGAGTGATC CTTCT                       235
```

(2) INFORMATION FOR SEQ ID :335:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 169 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID :335:

```
ATGCCCGCAC CATCCGCTAC CCCGATCCCC TCATCAAGGT GAATGATACC        50

ATTCAGATTG ATTTAGAGAC TGGCAAGATT ACTGATTTCA TCAAGTTCGA       100

CACTGGTAAC CTGTGTATGG TGACTGAGGT GCTAACCTAG GAAGAATTGG       150

GNGATCACCA ACAGGAGAG                                        169
```

(2) INFORMATION FOR SEQ ID :336:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 193 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID :336:

ATGCCCGCAC CATCCGCTAC CCCGATCCCC TCATCAAGGT GAATGATACC   50

ATTCAGATTG ATTTAGAGAC TGGCAAGATT ACTGATTTCA TCAAGTTCGA   100

CACTGGTAAC CTGTGTATGG TGACTGAGGT GCTAACCTAG GAAGAATTGG   150

GNGATCACCA ACAGGAGAGG CACNCTGNAN TCTTTTGGCN NNG   193

(2) INFORMATION FOR SEQ ID :337:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 307 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID :337:

CAAAAGTCAT CCACAAGTTC TTTGTCTAGG ACTTCTAGCT GCTCAGACCC   50

TCAGGGTCTT TGGATTGTTA CCAAAGTCTG TCAAACAGAC CAGTAGTTTA   100

ATACCTGTAC AGAAAAATGT TTCTATTATG CTTCTAGTAT CTAGAAATTG   150

CTTGCTACAG CATGGAGGTG GTTCTGCCTT TCCCTGGCTC CTCACACTCT   200

CATCTGCAGG ATTCCCAGCT TTGCTCAGTC TTCATGCCCA CCAGAGGCAA   250

182

AAAGGCAAAC TAAAACTGTC ATGCAGTGGT AGGTTTGAAA TNAGCTGCTG   300

CATCATG   307

5   (2) INFORMATION FOR SEQ ID :338:

             (i) SEQUENCE CHARACTERISTICS:
                  (A) LENGTH: 305 base pairs
                  (B) TYPE: nucleic acid
10   (C) STRANDEDNESS: double
                  (D) TOPOLOGY: linear

15   (xi) SEQUENCE DESCRIPTION: SEQ ID :338:

         AAAAGTCATC CACAAGTTCT TTGTCTAGGA CTTCTAGCTG CTCAGACCCT   50

         CAGGGTCTTT GGATTGTTAC CAAAGTCTGT CAAACAGACC AGTAGTTTAA   100
20
         TACCTGTACA GAAAAATGTT TCTATTATGC TTCTAGTATC TAGAAATTGC   150

         TTGCTACAGC ATGGAGGTGG TTCTGCCTTT CCCTGGCTCC TCACACTCTC   200

25   ATCTGCAGGA TTCCCAGCTT TGCTCAGTCT TCATGCCCAC CAGAGGCAAA   250

         AAGGCAAACT AAAACTGTCA TGCAGTGGTA GGTTTGAAAT NAGCTGCTGC   300

         ATCAT   305
30
         (2) INFORMATION FOR SEQ ID :339:

             (i) SEQUENCE CHARACTERISTICS:
                  (A) LENGTH: 101 base pairs
35   (B) TYPE: nucleic acid
                  (C) STRANDEDNESS: double
                  (D) TOPOLOGY: linear

40
             (xi) SEQUENCE DESCRIPTION: SEQ ID :339:

183

AATATAAAGA GGAAATGGCT CNTCACCTTC ATAATACCAA GACCTGCTCA   50

ATTTAAGATG GCCCTTGACA TTGAAATCGT ACCTACAGAA AGCTTGNAAG   100

G   101

(2) INFORMATION FOR SEQ ID :340:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 113 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID :340:

GTCGCAGGAG AAAAAAGTCG TCACGTCATG CGAGTGCGCA GGGGGCGTGG   50

AGAGTAGCAG TAGAGCAACA AAGTACATAT AGGACAGTGC AGCGAGGACA   100

AGGACTTCCC GCA   113

(2) INFORMATION FOR SEQ ID :341:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 209 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID :341:

ACACAAATAA CTACATNTAC GCAATATAAT NTTTAAAAAT CCAAAGCAAT   50

ATAAAAGAGC AGAGCTAGGA CTGAACAGAA CATTTTGGTG TATAACCGGC   100

AGCTCAAAAT CGCCAGCTGA TTGGAGTAAA ACTGATTCTA AGCGTATTAA   150

184

```
ATACGATTGA TTGTTTCCAT CACTAAGGGT GCCTATGAGT TTCTGAACCA        200

TTTCTAGGG                                                    209
```

(2) INFORMATION FOR SEQ ID :342:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 252 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID :342:

```
GATCAANCAA AGCACAGGGA AAAGAGGCAA AATGATCACA GAAATCCGTT         50

TTTTAGACAG GTGTGACTTA CACTAACGAA AAAGAAAAAC ACATGAATAA        100

GCTTTTAATC TTCATTTTTN NNTTTTGTNA TGGTAGGCTG AGATGCTTTT        150

AAATGTGATG TTATAAGCCT AAGGCAGCTT GACTGCAGCA ACAAGTTTTT        200

TACCCTCCTT GGCAAAGCAG GTCTCCTTAT GTAGCCTTGC AGCACTTCTC        250

TA                                                          252
```

(2) INFORMATION FOR SEQ ID :343:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 258 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID :343:

```
GATCAANCAA AGCACAGGGA AAAGAGGCAA AATGATCACA GAAATCCGTT         50
```

185

TTTTAGACAG GTGTGACTTA CACTAACGAA AAAGAAAAAC ACATGAATAA   100

GCTTTTAATC TTCATTTTTN NNTTTTGTNA TGGTAGGCTG AGATGCTTTT   150

5   AAATGTGATG TTATAAGCCT AAGGCAGCTT GACTGCAGCA ACAAGTTTTT   200

TACCCTCCTT GGCAAAGCAG GTCTCCTTAT GTAGCCTTGC AGCACTTCTC   250

TACAAAAC   258

10

(2) INFORMATION FOR SEQ ID :344:

         (i) SEQUENCE CHARACTERISTICS:
                  (A) LENGTH: 227 base pairs
15   (B) TYPE: nucleic acid
                  (C) STRANDEDNESS: double
                  (D) TOPOLOGY: linear

20

         (xi) SEQUENCE DESCRIPTION: SEQ ID :344:

GAAGGAACCA GTGACCAGTC ATCCCCAGAG ATAGATGAAG ACCGGATCCC   50

25   CAACCCACAT TCAAGTCCAC TTTGCAATGT CTCCACGGCA ACGGAAGAAG   100

ATGACAAGGA TCACACCCAC AATGAAAGAG CTCCAGATGA TGGTTGAACA   150

TCACCTGGGG CAACAGCAGC AAGGAGAGGA ACCTGAGGGG CCGCTGAGAG   200

30   CACAGGACCC AGGAGTCCGC CCACCTG   227

(2) INFORMATION FOR SEQ ID :345:

35   (i) SEQUENCE CHARACTERISTICS:
                  (A) LENGTH: 188 base pairs
                  (B) TYPE: nucleic acid
                  (C) STRANDEDNESS: double
                  (D) TOPOLOGY: linear

40

186

(xi) SEQUENCE DESCRIPTION: SEQ ID :345:

AAATAAAAAA TAAGGTCCAA GCCAATGCCT AACAGATAAT AAGAGCTCAG   50

TAAATGTTGA TTGAATACTA ACAAAGTAGT GAAAGCAGAC GACACAGTAC   100

CTGGCACACT ACTAAACTGT AAATGTTTTC AAATCTGAAT CTGTAGAATT   150

CTGTAAGGTT TTATGTAATA TGANGTCATT AGCTATCA   188

(2) INFORMATION FOR SEQ ID :346:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 262 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :346:

AAATAAAAAA TAAGGTCCAA GCCAATGCCT AACAGATAAT AAGAGCTCAG   50

TAAATGTTGA TTGAATACTA ACAAAGTAGT GAAAGCAGAC GACACAGTAC   100

CTGGCACACT ACTAAACTGT AAATGTTTTC AAATCTGAAT CTGTAGAATT   150

CTGTAAGGTT TTATGTAATA TGANGTCATT AGCTATCATG NCTCTGGATT   200

NNCTNNNAGG TTTTAAGATG GAGCATCTGN GNATGTCAGC CCGTCCTATC   250

TAGAAGTGNA AA   262

(2) INFORMATION FOR SEQ ID :347:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 159 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :347:

```
CTCTGTTTTC CAAACGCCCA TGTGTGCTAT ACTACAACTC TTCTCGAGTC        50

TGATCAATTT GCAGTAGACC ATTTTAGTTC TTACGACGTT AATAACAAAC        100

ACTTCAACAT CANTGCTCCA ATCTGAAGTT CTTGTTGCAT TGTTAAAAGA        150

AATNTCTAA                                                    159
```

(2) INFORMATION FOR SEQ ID :348:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 283 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :348:

```
TCGCAGGAGA AGGAAGCTGC ATGCACTTGA AAGGCATGGC CTGTCTCCTC        50

ACTGAGTGCA AGGTCCATCG ACCAAAGCCC TGTTCTGATC AATAACATCT        100

ACAATCGCAC CAATTTTCCG GCATGAGGTC CAAAGGAGAC ATAGGCCACC        150

CGGCCAACCT CCACGAAGCG CCTGAACACC ATGCGCTTCC CGGGACCCTC        200

TGGGAGCCGT TCGCNCCTCA GCTTCCCAGC GAGGTGGAGG TCGAGCGGCA        250

TGGNCGACGC CCCGGAGCCC ACAACAGTAA GAC                         283
```

(2) INFORMATION FOR SEQ ID :349:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 169 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

          (xi) SEQUENCE DESCRIPTION: SEQ ID :349:

 5   CAGAAAGGAG GCATTGAGCA AAAACTAGGA AAATCTGAAT AAACNGTGGA   50

      CCTCGCTTGG TTAATATATT TANACTGGTG ACTCATTTTA AAACTTTCCC   100

      GGGCGCGATG GCTCATGTCT GCAATCCCAG CACTTGNGAG GCTGAGCGGG   150
10
      TGGATCACCC AGGTCAGGA   169

      (2) INFORMATION FOR SEQ ID :350:

15   (i) SEQUENCE CHARACTERISTICS:
              (A) LENGTH: 175 base pairs
              (B) TYPE: nucleic acid
              (C) STRANDEDNESS: double
              (D) TOPOLOGY: linear
20

          (xi) SEQUENCE DESCRIPTION: SEQ ID :350:

25   GAAGNAACCA GTACCAGTCA TCCCCAGAGA TAGATGAAGA CCGGATCCCC   50

      AACCCACANT TAAGTCCACT TTGCAATGTC TCCACGGCAA CGAAGAAGAT   100

      GACAAGGATC ACACCCACAA TGAAAGAGCT CCAGATGATG GNGAACATCA   150
30
      CTTGGCAACA NCACAGGAAG GGACC   175

      (2) INFORMATION FOR SEQ ID :351:

35   (i) SEQUENCE CHARACTERISTICS:
              (A) LENGTH: 206 base pairs
              (B) TYPE: nucleic acid
              (C) STRANDEDNESS: double
              (D) TOPOLOGY: linear

40

         (xi) SEQUENCE DESCRIPTION: SEQ ID :351:

   AAATAAAAAA TAAGNACCCA ACCAATGCTA CAGATAATAA GAGCTCAGTA   50

5 AATGTTGATT GAATCACTAA CAAAGATAAA AGCAGACGAC ACAGTACCTG   100

   GCACACTACT AACTGTAAAT GTTTTAAAAT TGAATCTGTA AAATTTGTAA   150

   GGTTTTATGA ATATAATATT ATTAACTATT ATGTCTCTGA ATTTTTNNNN   200

10 NAGGCT   206

         (2) INFORMATION FOR SEQ ID :352:

15   (i) SEQUENCE CHARACTERISTICS:
                (A) LENGTH: 76 base pairs
                (B) TYPE: nucleic acid
                (C) STRANDEDNESS: double
                (D) TOPOLOGY: linear
20

         (xi) SEQUENCE DESCRIPTION: SEQ ID :352:

25 AGACATACTG TAGTGTCTAA ATAATATTTG TCNGAAGATA ACAATTATGG   50

   GACTTTAAAG CCGACAGTGA AATTAT   76

         (2) INFORMATION FOR SEQ ID :353:
30
            (i) SEQUENCE CHARACTERISTICS:
                (A) LENGTH: 245 base pairs
                (B) TYPE: nucleic acid
                (C) STRANDEDNESS: double
35   (D) TOPOLOGY: linear

         (xi) SEQUENCE DESCRIPTION: SEQ ID :353:

40
   ACATTTGGCC CTCAGACTGT AATTTCCATA CTACTNTGAC TGATACTAGA   50

190

```
TGACCTGGCT GCCTAGGGGC TGTGCTGGTC TGATTTTTTG TGAGACAAAA        100

ACCACTCTAA ACCTCCTGGT GCACTGAGGC TGTACACACC GNCAGAACAG        150

GGCACTGCGT TTAAAAGTTT CTGACCAAGT GGTGACAACA GAGGNCAAAC        200

GTAAGGCTGT CTGGATAAGT TGAACCTNGC TGANCGGTAG CACCA             245
```

(2) INFORMATION FOR SEQ ID :354:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 179 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: double
            (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID :354:

```
GGAATCTGTG CCACACAGCT GCACACGACT ACTGGCCAAA GGACAGCCTC         50

AGAACATCAT GAGCTGGCGT GACCTCATGA TGNNCCTCAN TGCTGTGGGG        100

CTTCTGCTNG AGGCCAGCAG AGGCTCGTAT GACTACCTGT NAGACCTGCT        150

CTTTGGGTTG AGACTTTTCA GNGACAACT                               179
```

(2) INFORMATION FOR SEQ ID :355:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 139 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: double
            (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID :355:

```
AAGGAACGNA TGACTTTCCA TCCCTTGAAC CAAGGCATGT TAGCACTTGC         50
```

TCCAGCATGT TGTCACCATT TCAACAGAAA TCGCACAAAT GCTACTGTGC   100

AAGGTGCAGC CAATTTTNTT GTAAGTGTGA TTTCTTACG   139

5   (2) INFORMATION FOR SEQ ID :356:

             (i) SEQUENCE CHARACTERISTICS:
                 (A) LENGTH: 100 base pairs
                 (B) TYPE: nucleic acid
10   (C) STRANDEDNESS: double
                 (D) TOPOLOGY: linear

15   (xi) SEQUENCE DESCRIPTION: SEQ ID :356:

         TCCAGGAGAA GGAAAACTTC CACTTATAAC TGTNTCAGCC TGACTATAAT   50

         GAAGAGACTA GCAACACCTC CTGAACACAA GCCTANTGAG CCCAGTCTTT   100

20   (2) INFORMATION FOR SEQ ID :357:

             (i) SEQUENCE CHARACTERISTICS:
                 (A) LENGTH: 137 base pairs
25   (B) TYPE: nucleic acid
                 (C) STRANDEDNESS: double
                 (D) TOPOLOGY: linear

30   (xi) SEQUENCE DESCRIPTION: SEQ ID :357:

         AGAAGGAAAC ACCAAAGAAA CATCCAAGCA ATAAAGTGGA AGACTAACCA   50

35   AGATTTGGAC ATTGGAATGT TTACTGTTAT TCTTTAAGAA ACAACTACAA   100

         AAAGAAAATG TCAACAAATT TTTCCTAGCT AACTGAG   137

         (2) INFORMATION FOR SEQ ID :358:

40   (i) SEQUENCE CHARACTERISTICS:
                 (A) LENGTH: 228 base pairs

192

```
                    (B) TYPE: nucleic acid
                    (C) STRANDEDNESS: double
                    (D) TOPOLOGY: linear
```

```
          (xi) SEQUENCE DESCRIPTION: SEQ ID :358:


     AAGGAACAAG TGGGTCATTC TCACTAAGGC TGCCTGTCAC TGCAGTCTTG      50

     ATCAGCTTGT CAATTTGATA CTTCAGCTTT TGGTCCAAGG GACGAAGCTT     100

     TTCCAAAACC GTTCGAATCT CTACCAGTCT CAAAACTGCA TCATGTCCCT     150

     GAAGAGATCC TCCTGAGGCT TTGTCCAGAA TGAGGTGGGT CAAATNNANG     200

     GGNACATGAG CAGCAGCTGN TCTTTAAC                             228


     (2) INFORMATION FOR SEQ ID :359:

               (i) SEQUENCE CHARACTERISTICS:
                    (A) LENGTH: 248 base pairs
                    (B) TYPE: nucleic acid
                    (C) STRANDEDNESS: double
                    (D) TOPOLOGY: linear




          (xi) SEQUENCE DESCRIPTION: SEQ ID :359:

     CAGGAGCAAG GAGGCCATTT TGCTGAGCTC TCACAGCTGC TAGAGATGCT      50

     CAATGACTCC CAATACAACC CAAAGAGACA AACGCTTGTT TTTTCTGCCA     100

     CACTCACCCT GGTGCATCAG CTCCTGCTCG AATCCTTCAT AAGAAGCACA     150

     CCAAGAAAAT GAATAAAACA GCCAAACTCG ACCTTCTTAT GCAGAAAATT     200

     GGCATGAGGG GCAAGCCCAA GGTCATTGAC CTCACAAGGA ATGAGGCC      248


     (2) INFORMATION FOR SEQ ID :360:
```

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 253 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID :360:

AGGCACCTGT GGAGCCATCC TCCTTGTTTT AATCGTCCTG CTGCTGCTGC   50

CGTTCCGTGT CGCGTCGCCC ACATGACCCT GAGGTCGCAA TGATGAGTCC   100

TCTCTGGTCA GACACCGCTG GAAATGAATA CCAGGCCTGA CCTCAAGCAA   150

CCATGAACTA GCTATTAAGA AATACANNGG NAGGGCGGCA GCCGGATCGT   200

GNNGGCGTTT NTCTGNGCCG CCCGTCTCAA TCTNTGTTCT GCTTCCAGAT   250

GCC   253

(2) INFORMATION FOR SEQ ID :361:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 154 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: double
            (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID :361:

GAGAACCACG GGCTCCATCC TGGCCTCCTG TNCACCTTCG AACAGATGCG   50

GATTAGCAAG CAGGAGCACA CGAATCAAGC CCCTCCAGCC ACCAAATTTT   100

CTAAACNGGC TNGGCNATGT CGTAGTTNGT TGTCAGTNGA TCGGTAGAGA   150

TAAT   154

194

(2) INFORMATION FOR SEQ ID :362:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 168 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID :362:

GAGAACCACG GGCTCCATCC TGGCCTCCTG TNCACCTTCG AACAGATGCG   50

GATTAGCAAG CAGGAGCACA CGAATCAAGC CCCTCCAGCC ACCAAATTTT   100

CTAAACNGGC TNGGCNATGT CGTAGTTNGT TGTCAGTNGA TCGGTAGAGA   150

TAATCCTGNC CACGCCCT   168

(2) INFORMATION FOR SEQ ID :363:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 198 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID :363:

AAGGGATAAA AGGAAGCTTT GNCACCACTC TACCATCAAA NNGGAATTGA   50

ACATTCCCAT TAAGGCAGTA AAACAAAAGC CAATAGCAAA CATGNATTTC   100

ATTCAACCAT TGATAGATCT CTGCCGTTAT TCTTCAGTTT CTCTTCTCGT   150

CTCTCTATTT NTTTCTCTGG TTGTCGACCA GCTGACTNTG NCATCGTT   198

(2) INFORMATION FOR SEQ ID :364:

195

(i) SEQUENCE CHARACTERISTICS:
   (A) LENGTH: 121 base pairs
   (B) TYPE: nucleic acid
   (C) STRANDEDNESS: double
5 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :364:

10

TTATACAAGT CAAACTTGGA AGGTCATAGT AAGCATACCT ATGCTGAGAG   50

AAAAGCATCA AATCCTCCGC GACACATCTA GTTCATCGTA ACAAAGCAAC   100

15 TCGTACACTT TCAAGTTTAA A   121

(2) INFORMATION FOR SEQ ID :365:

   (i) SEQUENCE CHARACTERISTICS:
20   (A) LENGTH: 211 base pairs
      (B) TYPE: nucleic acid
      (C) STRANDEDNESS: double
      (D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :365:

GGTAAGTTGT ATTTGGGCCA GAATTTTAAA GAGCACTATT TCGACATTAA   50
30
AATGTATTCT TCTCGTATTA ATGCCTACAT CTTCAGAGTT TTCAATGCTT   100

TCTAAAAGTT TCCTCTTTGG AAAGAAGAAA TCTGAAAGAC CTATCATGCC   150

35 GTTCTTCCTG GCGTCTATAT TTCCTTTAGA GAGGCAAGGT AGGATTCCGT   200

CTCCAAGGGA G   211

(2) INFORMATION FOR SEQ ID :366:

40
   (i) SEQUENCE CHARACTERISTICS:
      (A) LENGTH: 285 base pairs

196

```
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: double
            (D) TOPOLOGY: linear


        (xi) SEQUENCE DESCRIPTION: SEQ ID :366:


    CGGCTACAGC ATCACATCCA CTAAATGCAC AGTTGTTGAA GTCACGCCCT        50

    GCCAGACCTC TACTACCACA TTGTTCCCTC CGGTGACCAG TTTGTCCGTC        100

    ACTGTCAGGA GAATGNCCCG TGTCGAATCA TCGATCTCCA TCCGAGCCAA        150

    AAGTTTTCCA TATGCTGAAA TTACTGAATT GCCCTCGTTT ATAGTATATG        200

    ATACAGTGGC CTTCGTTGGA GGCAGATATC AAGCATGGGG ATAAGCAGTT        250

    TTCTGGTCCT TAAGGGCTCT CAGCAAATCT CCGTG                        285

    (2) INFORMATION FOR SEQ ID :367:


        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 149 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: double
            (D) TOPOLOGY: linear



        (xi) SEQUENCE DESCRIPTION: SEQ ID :367:

    GACACTGAGG CAGCTACTGA GAAGGGCAGA ACATGTCTCA ATCCATAGAG        50

    GTCTTGGCAG GCGAACCCAG AGAGACTTGC AGTACGTGAG AAGATGGAGA        100

    ACCAAATAAA AGGACTGGAG TCCAGTTCAA ACAAGGAGGG AGTGGTAGT         149

    (2) INFORMATION FOR SEQ ID :368:


        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 137 base pairs
```

197

```
                    (B)  TYPE: nucleic acid
                    (C)  STRANDEDNESS: double
                    (D)  TOPOLOGY: linear


  5


           (xi)  SEQUENCE DESCRIPTION: SEQ ID :368:


       GGTTCCCGCT CTCACAGCCA TTGCAGTACA TGAGCTCCAT AGAGACAGCG        50
 10
       CCGGGGCAAG TGAGAGCCGG ACGAGCACTG GCGACTTGTG CCTCGCTGAG       100

       GCAATACTAT AATANGCAAG GAACTTTTGA GGCCGAG                     137


 15   (2)  INFORMATION FOR SEQ ID :369:


               (i)  SEQUENCE CHARACTERISTICS:
                    (A)  LENGTH: 192 base pairs
                    (B)  TYPE: nucleic acid
 20                 (C)  STRANDEDNESS: double
                    (D)  TOPOLOGY: linear




 25        (xi)  SEQUENCE DESCRIPTION: SEQ ID :369:


       GCCATCATAA GTTCAAAAGA AAAGAGAAAG TGTTATTTTT CTGTTAGTGA        50

       CATGTAGTCC CTTTGTTCTA GTAGGAAAAA AGGTGCCTAG AGGTAGTATA       100
 30
       TAGAGTAAAT ATTGTTCCTT TGCCTACTCG TGCTTCCAAT GATTAAGGAA       150

       ATGTTAAACA NNNGTNAAAG TCTGTTTTGT CAATGCGGGA GT               192


 35   (2)  INFORMATION FOR SEQ ID :370:


               (i)  SEQUENCE CHARACTERISTICS:
                    (A)  LENGTH: 197 base pairs
                    (B)  TYPE: nucleic acid
 40                 (C)  STRANDEDNESS: double
                    (D)  TOPOLOGY: linear
```

198

(xi) SEQUENCE DESCRIPTION: SEQ ID :370:

GAGACTTAAG TAAAACGGCT GCAGGCCAGA TTCGCCCACC AGCTCAGAGA   50

CCACCTTTAT CCATGCTTTG AAGTAGGACT CCTTCCGTCT TCAAAATNTT   100

GAAGACCCTA ACANGCTTTT ATGATGGGGG TCATATCTAT GGTCACGNAT   150

ATAGTAGAAA CCAAAAGAAT GTAAGTATTT GTNNATGATT TAAAAAT   197

(2) INFORMATION FOR SEQ ID :371:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 114 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: double
            (D) TOPOLOGY: linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID :371:

GCATCTGNCA GCTGCTGCAG GCTGACAGCC TCCAGACCTG GACAGAATTC   50

ATACACTCCC GGAGCTGAAA AAACCGAACA TAAGGGAGTG CACAAGAGCC   100

GGGCTTTGGA GAGG   114

(2) INFORMATION FOR SEQ ID :372:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 127 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: double
            (D) TOPOLOGY: linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID :372:

CTTTCTCTAC TCCATCCATT ATCTCCGGGA TTCCTCCACA TTCCCTTCAG   50

199

CTCCTAGTTG TTCCACCTTG GCTAACAATT TACCAATCTT TTTTTCTATG   100

AACACGTTCT GCCTTTGCTG CTACTTC   127

(2) INFORMATION FOR SEQ ID :373:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 257 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID :373:

AAGCGCTCAA TTCGCATCCA CAATGCAACC ACGAACTGAT TTTCTCTTTC   50

TTTTTCAGTT CTCCTTGGTC TGTAACAGGA ATGCCCCTTA CTCAGTAGCA   100

GGCGGACACG GCCATGGGTC AAGACACCCT GCTTCATGGG GAAACCTTGT   150

TTGTCGTTCC CACCACTGAT TCGGACCACA TAACCTTATN NNATCCCGAG   200

CGTTAGCAGC AACTTTTGTG GCCATACGCT TCTCATAGAA AGTACGAAGT   250

TTGGCAT   257

(2) INFORMATION FOR SEQ ID :374:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 180 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID :374:

GCATCATCAT TGACATCCCT ATCAATGTCT ACGCTGCTGG CAGAGGACTG   50

200

NCCATTTGGA GCTGAGATGT GTAAGCTGGT GCCTTTAATA CAGAAAGCCT   100

CCGTGGGAAT CACTGTCTGA GTCTTGTGTC TAGTATTGAC AGATATAGCT   150

TTGTTCTTGG AGTAGAATTA AGGAATTGCG   180

(2) INFORMATION FOR SEQ ID :375:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 323 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID :375:

GGACCATTCT GATCATCCTC ACTGGACGCC ACAGGGGCAA GAGGGTGGTT   50

TTCCTGAAGC AGCTGGCTAG TGGCTTATTA CTGTGACTGG ACCTCTGGNC   100

TCAATCGAGT TCCTCTACGA AGAACACACC AGAAATTTGT CATTGCCACT   150

TCAACCAAAA TNGATATCAG CAATGTAAAA ATCCCAAAAC ATCTTACTGA   200

TGCTTACTTC AAGAAGAAGA AGCTGCGGAA GCCCAGACAC CAGGAAGGTG   250

AGATCTTCGA CACAGAAAAA GAGAAATATG AGATTACGGA GCAGCCAAGA   300

TTGATCAGAA AGCTGTGGAC TTA   323

(2) INFORMATION FOR SEQ ID :376:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 223 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :376:

GGGGAATCCC ACCTCACCCA TTGNGGTGAA ATGCTTTTTT CTAAGAGGTG   50

AAATCACTCG CTGGTGTTTA TTTCGGCACA ACCAGAAAAT AGTGNGGGAT   100

ATTGAATTAT GGGAGGCTCT GACTGTCTCG NGTGCAGCTT ACATTCACAG   150

ATGGGGGGTA GTTTTTATAT TCTATAAGCG AGCATATTAA ANGCAATATG   200

AGTCAGTCCT GCATTTATGT CTT   223

(2) INFORMATION FOR SEQ ID :377:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 122 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: double
            (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :377:

GGCTCAGGAT CCGGCATCCT TTATGCCTCC ACAGCACCTT GCTCTTTCCC   50

CAGCCAATCA CTTTAGATGC TGAATCGATT TTAAACANAT GTTTTGTCAT   100

ATGGCTAATC AAGAGCCAGG TA   122

(2) INFORMATION FOR SEQ ID :378:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 195 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: double
            (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :378:

202

GGCAGTGCGT GCTTCATCCC TTTATGAAGA ACAGAAAATT ATGACTACTC   50

TACAAGGTGG ATAATACTTC GGTACCTTGC TTGCCACAGC CCTGTTCCTC   100

AAAGCTGAAT TGATAAATTT CTCTTTGACT TCCAAGACCT AGCAGTTATA   150

AGGCGCCTTG AATAAAGTTT GTGCCTGAAA ATGTGGAGCA ATGCT   195

(2) INFORMATION FOR SEQ ID :379:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 210 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: double
            (D) TOPOLOGY: linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID :379:

GTAGCCCTGA GGTCATCCTG CAAAGNGCGT ATCAAAAAAN ACGAAGTTAG   50

GGTGACAAAG TTTGACAGTG ATGTTTACAA GTCAAACTTG GAAGGTTATA   100

GTAAGCATAC CTANGCTGAG AGAAAAGCAT CAAANCTNNG GNACATANTN   150

GGTTTNTNGN AACAAAGCAA CTTGTAATTT AAGNTTAAAC NGAGCATCAT   200

ATANNNNGG   210

(2) INFORMATION FOR SEQ ID :380:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 238 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: double
            (D) TOPOLOGY: linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID :380:

CTGGCTCACC TGGACAACCT CAAGGGCACC TTTGCCACAC TGAGTGAGCT   50

GCACTGTGAC AAGCTGCACG TGGATCCTGA GAACTTCAGG CTCCTGGGCA   100

ACGTGCTGGT CTGTGTGCTG GCCCATCACT TTGGCAAAGA ATTCACCCCA   150

CCGTGCAGGC TGCCTATCAG AAAGTGGTGG CTGGTGTGGC TAATGCCCTG   200

GCCCACAAGT ATCACTAAGC TCGCTTTCTT GCTGTTCA   238

(2) INFORMATION FOR SEQ ID :381:

       (i) SEQUENCE CHARACTERISTICS:
           (A) LENGTH: 275 base pairs
           (B) TYPE: nucleic acid
           (C) STRANDEDNESS: double
           (D) TOPOLOGY: linear

       (xi) SEQUENCE DESCRIPTION: SEQ ID :381:

GTCCTATGGC ATGAATGTTT GCAACCAACC CAGGAAAAGC CTTAAAGGAA   50

ATAGCTGTTC ACATAGGAGA CCGTGACAAT GCTGTACGCA ATGCTGCACT   100

CAACACCAAG CAACGATGCA CAATGTACAT GAGGATCAGG TGTTCAAACT   150

GATTGGAAAT CTTTTTGAAA AGGATATGAG CATGCTCGAG GAGAGGATTA   200

AGCGTCAGCA AAGAGACCCT CTCTGCACCA ATAAAACAGG TGGAAGAAAA   250

CCTAGCNCGC ACAGAACATA AGCTC   275

(2) INFORMATION FOR SEQ ID :382:

       (i) SEQUENCE CHARACTERISTICS:
           (A) LENGTH: 96 base pairs
           (B) TYPE: nucleic acid
           (C) STRANDEDNESS: double
           (D) TOPOLOGY: linear

204

(xi) SEQUENCE DESCRIPTION: SEQ ID :382:

AAGCAGAGTA CGCACGTCAG GCCCTTCCAC GCCCACCCCA ACACTTTAAA   50

CNTACTGGGC GATGGGGCCG TTTNGCTGGC AGTTCAAGAT AAAACA   96

(2) INFORMATION FOR SEQ ID :383:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 196 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :383:

GGACTTGATG GCTTCTTTCA AAGTCATAGA CTTGTGGTAA ACTTCTTGCA   50

AGGAGCTCTG GGCACCCTCT GAAGCAGAGC CAATTGCTCG AGCATCACAC   100

TGTACAAAGG TCCAGATGGG TTCATATGAA ACAGCTGGAG TCCTTTTCAT   150

CAATNCNAAT NGANNGGTTA CTCCAAAGGG ACGAGACATG CACCTG   196

(2) INFORMATION FOR SEQ ID :384:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 206 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :384:

AAGGAGGCCT TTGAGTCCCA TCCTCTGCCA CGCAGAGAGG CAGGCCTGGC   50

ATTTCAGCCT CACTTTGTGT AGGTCACTTT TCGGTCTGTG TTGTAGCTCA   100

205

CCAACCAACA GTCAAACCCC AGCGTGGTAG CACGAGGTCC AGAACCTCTG   150

CTTAGTGGGC CCGTATAATA AACGCAACCT GACCCAATTN NGGTTTCTTT   200

5   CCCCAT   206

(2) INFORMATION FOR SEQ ID :385:

        (i) SEQUENCE CHARACTERISTICS:
10   (A) LENGTH: 134 base pairs
                (B) TYPE: nucleic acid
                (C) STRANDEDNESS: double
                (D) TOPOLOGY: linear

15

        (xi) SEQUENCE DESCRIPTION: SEQ ID :385:

        GAATGCTTGG GATCATCCAG GTGNCTCTAT TTATAGGCAC CTGTGTTCAC   50
20
        CAGCAGTCTC TCTATTAGAA TGCTTGGTGT GCCAATGTTT CTTGAATTAG   100

        AAGCCTGGGG NCACCTAGGT GTTTCTATTA TAAA   134

25   (2) INFORMATION FOR SEQ ID :386:

        . (i) SEQUENCE CHARACTERISTICS:
                (A) LENGTH: 161 base pairs
                (B) TYPE: nucleic acid
30   (C) STRANDEDNESS: double
                (D) TOPOLOGY: linear

35   (xi) SEQUENCE DESCRIPTION: SEQ ID :386:

        CAAGGCCTTC CTGCACTGGT ACACGGCGAG GGCATGGACG AGAGGAGTTC   50

        ACCGAGGCCG AGAGCAACAT GAACGACCTG GTGTCCGAGT ACCAGCAGTA   100
40
        CCAGGACGCC ACGCCGACGA ACAAGGGGAG TTCNGAGGAG GAGGAGGCGA   150

```
GGACGAGGCG T                                                     161
```

(2) INFORMATION FOR SEQ ID :387:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 170 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: double
            (D) TOPOLOGY: linear

        (xi) SEQUENCE DESC   ON: SEQ ID :387:

```
GGTGAGCCTC CGCCATCCAG C    CAAAC TGTGC  GAC CGCAGCTGTG          50

CCGTGGCACG ATGGCGAGGA AGCCAGCCCC AAGGA  CAC TGAAAACACA          100

ACCAGTCAAT GCCGTGTGGT TTTGTTTGAA TATAAATNGC TGAAAGTGTT          150

GTTTTTTNAG GCAGTAATNT                                          170
```

(2) INFORMATION FOR SEQ ID :388:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 250 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: double
            (D) TOPOLOGY: linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID :388:

```
TCCATCTGAC ATCGCATTTC CATAGAAATG GCCAAAGAAA GAAGGTCCTG          50

GGGTTTTTCA TAGAAAGCTC AAAAAGTTCA ACCTTTGATG CTATCCCCCA          100

GCCCAATACA AAATACACAG AAAAAGCAAT TATTAAAAAC GGCTTCGGTT          150

TCTTTTTTCT CTTTAATNNC CTACAATNGC TTTACATATT CGTGTGCAGC          200
```

ACCTACTTCT TTATGCCGTG AACTGAAATC TAAGATTTCA AACTGAAATC   250

(2) INFORMATION FOR SEQ ID :389:

5   (i) SEQUENCE CHARACTERISTICS:
                   (A) LENGTH: 268 base pairs
                   (B) TYPE: nucleic acid
                   (C) STRANDEDNESS: double
                   (D) TOPOLOGY: linear
10

               (xi) SEQUENCE DESCRIPTION: SEQ ID :389:

15   GCCATCTCCC CGCCACCCNC TCGTCCCCTT CTTNTCNNGC CACCCTTCCT   50

        CNCTCNTCCG TTTTNGCTCC ACTCCACTCC TCCNTTTTNA GTACCCTCCT   100

        CNTTTATNTA GAGTTACTGA GAGCCGACCT GACGTCTCCA ACATNCCGTN   150
20
        TCTTATATCT CATCNCGGTT NTNGANGAAT GNAGTNAGGG TTTCCGGGAG   200

        AGACCNAACT TGCTCTAGCC CTTTCCAGCC GCTGTTGTTA AACTGACCTC   · 250

25   GTAGGGCNTG AGGGAGGT   268

        (2) INFORMATION FOR SEQ ID :390:

               (i) SEQUENCE CHARACTERISTICS:
30   (A) LENGTH: 177 base pairs
                   (B) TYPE: nucleic acid
                   (C) STRANDEDNESS: double
                   (D) TOPOLOGY: linear

35

               (xi) SEQUENCE DESCRIPTION: SEQ ID :390:

        GTCAGAGGCA GCCCATCCAG CACGTGCTAG GTGTTCCCAT ACGCACAGGA   50
40
        GAGGCGAGCT AGCCAGCCAA GGCGGGCAGG CGGGGAGGCC CTCTAGCTGT   100

TTGCCTCACC TGTGGGGCCC CAGCAGGGAG GAGTCACCAG CCTAGAGGGG   150

CCAGGTATAC ACCTTANAGA GGATGAC   177

(2) INFORMATION FOR SEQ ID :391:

        (i) SEQUENCE CHARACTERISTICS:
             (A) LENGTH: 139 base pairs
             (B) TYPE: nucleic acid
             (C) STRANDEDNESS: double
             (D) TOPOLOGY: linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID :391:

GCTCCACTTC CCACATAANA CNAGACCTCT CACAAAAGAG TTCACTGATA   50

TGTGAATGCA GCTTTCTCCC CATGGTAGCC AGGACAGGGT GCACATTAAG   100

GCAACCCCAA AAACACCTCT TNCTGNCTGC CTCTGCAAA   139

(2) INFORMATION FOR SEQ ID :392:

        (i) SEQUENCE CHARACTERISTICS:
             (A) LENGTH: 259 base pairs
             (B) TYPE: nucleic acid
             (C) STRANDEDNESS: double
             (D) TOPOLOGY: linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID :392:

GAGGAGCTGC CCTCAAGGTC GTGCGTCTGA AGCCTACAAG AAAGTTTGCC   50

TATCTGGGGC GCCTGGCTCA CGAGGTTGGC TGGAAGTACC AGGCAGTGAC   100

AGCCACCCTG GAGGAGAAGA GGAAAGAGAA AGCCAAGATC CACTACCGGA   150

AGAAGAAGCA GCTCATGAGG CTACGGAAAC AGGCCGAGAA GAACGCGGAG   200

209

AAGAAAATTG ACAAATAATA GAGGTCCTCA AGCCCACGGA CTCCTGGTCT   250

GAGCCCAAT   259

5   (2) INFORMATION FOR SEQ ID :393:

            (i) SEQUENCE CHARACTERISTICS:
                (A) LENGTH: 189 base pairs
                (B) TYPE: nucleic acid
10   (C) STRANDEDNESS: double
                (D) TOPOLOGY: linear

15   (xi) SEQUENCE DESCRIPTION: SEQ ID :393:

AAAGATCATC AGTTTGGAAG GTACTGGTCC AATTTATCTA GGAAGTATCT   50

CTTGGAGTTT CAGAAATGCT AGCTTGGACA ACTGAAAAGT CACATCACAG   100
20
CTGGCATTCT GGGGGCTACC AAAACACCCC TCNNGGAGTA GAAGCTGCTG   150

GAAGGCAGGC CTGAGCCATT CACCACGGAC AGGAAGAGC   189

25   (2) INFORMATION FOR SEQ ID :394:

            (i) SEQUENCE CHARACTERISTICS:
                (A) LENGTH: 97 base pairs
                (B) TYPE: nucleic acid
30   (C) STRANDEDNESS: double
                (D) TOPOLOGY: linear

35   (xi) SEQUENCE DESCRIPTION: SEQ ID :394:

AGAAGGGGAG GTCGAAGAAA TGTGGCTGAT CATAAGAAAG GAGCAAAGAA   50

AGCTAGAATT GAAGAANNNN GAAAGAAACA GAGGACAAAA AAACAGA   97
40
        (2) INFORMATION FOR SEQ ID :395:

210

(i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 244 base pairs
    (B) TYPE: nucleic acid
    (C) STRANDEDNESS: double
    (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :395:

AAGAGGGGCT AAGACCCAAG TCATCCTCCA CTTTCGTTTT GTTATATTTC   50

GCTTAGAATT GCCTCTTCTT CTCCACTTCA GAACTGCCTC AAAATTGACC   100

CCCTTGACTG ATTTATTGTC GTCAAAAGCA TGTTCCTCTA TCTTTTNNNN   150

TCAGACGATC CGCTGCCTTT CTACATCTGA GAATCTTGTC AAGCATGGAT   200

AAACTTGNTT TTATGTTGCA TATTTTNACG GCTTCAACTT GAGT   244

(2) INFORMATION FOR SEQ ID :396:

(i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 185 base pairs
    (B) TYPE: nucleic acid
    (C) STRANDEDNESS: double
    (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :396:

TAATATCGCC ATGTAATGGT ATACATTGTA AGGCTTATGT CACTAAAGAT   50

TTTTATTCTG ATCTTTCCAT AATAAAGGTC ATATGATACT GTATAGACAA   100

GCTTTGCAGT GAAGTATAGT AGCAATAATT TTCGTACCTG ATCAAGTTTA   150

TTGCAGCCTT TCTTTTCCGT TTCTTTTNTG AAGGG   185

(2) INFORMATION FOR SEQ ID :397:

211

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 218 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: double
            (D) TOPOLOGY: linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID :397:

        GGACACATCC ACCCAGTGAA CTGGACTGTG GCCATGACCC AGGGTATCAG   50

        CTCCAAACTC TGCCAGGGCT GAGAGACACA TGAAGGAAGA TGATGGGAGG   100

        AAAAGCCCAG GAGAAGTCCA CCAGGGACCA GCCCAGCCTG TATACTTGCC   150

        ACTTACCACC AGGACTCCTT GNTCTGCTCT GGCAAGAGAC TCTTGTCTGA   200

        ACACTGCTTA TCTGACCC   218

        (2) INFORMATION FOR SEQ ID :398:

            (i) SEQUENCE CHARACTERISTICS:
                (A) LENGTH: 250 base pairs
                (B) TYPE: nucleic acid
                (C) STRANDEDNESS: double
                (D) TOPOLOGY: linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID :398:

        GGAAGCAAAA AAACAAAACT AAGCTCGAAT TTGCTTCCAA ACCTGTAGAT   50

        TGCATCTAAC CANGTGTCCC TATGCACCTC AGAGTACTGG AATACGAACC   100

        CAGCGAGACC TTGTCCCCTC CCATTTTGCT GNACTTTTGT TGGTGAAAAT   150

        GAGAATGAGT TNATCCCTAC NTACTTAGTT TAATGCATTT GACCCCAGAA   200

        AACCCCAGTA CCTTTNNACA ATGACCCAAC CANTACCTAC CATCGGCCAG   250

212

(2) INFORMATION FOR SEQ ID :399:

   (i) SEQUENCE CHARACTERISTICS:
       (A) LENGTH: 278 base pairs
5   (B) TYPE: nucleic acid
       (C) STRANDEDNESS: double
       (D) TOPOLOGY: linear

10
        (xi) SEQUENCE DESCRIPTION: SEQ ID :399:

    TCACTTGATT CATCCGTCGC GGGATTTGGG AGCACTAGCA ACATAATCAA   50

15 CACACTCCTA CAATCTTAGG CTTCACATGT GCTGATGATG ATGAAACCAA   100

    CTCTGCCCCA ATCATCTCCC CTTCTNTTAG GGTCTTACTA CATATCGCAA   150

    CAGAAGATAA TATTGAGGTG AAGAGGGTAA CATGAAGTTT GGCACTACCC   200
20
    TGAAGAACTG TAGGCATCTC TTGGAATGTG CTAAGGAACT TGATGTCCAA   250

    ATAATGAGAT TAAATTTATG TTTCGAGT   278

25 (2) INFORMATION FOR SEQ ID :400:

       (i) SEQUENCE CHARACTERISTICS:
           (A) LENGTH: 207 base pairs
           (B) TYPE: nucleic acid
30   (C) STRANDEDNESS: double
           (D) TOPOLOGY: linear

35   (xi) SEQUENCE DESCRIPTION: SEQ ID :400:

    GGCCAAACTC ACAGGAGCCT AGGCACAGAG CACTGAACAC TGGCTCTGCA   50

    GCGGGAAGGA ATTAGAGCCT TCTGCTTTTG CACCTGCTTT GAGTTAGGAA   100
40
    GCAAGCTCTC TTCCTTGCCA GACTTCCCTT TGGGGCAGGA CACTTTTTA   150

213

TACNCTGAGG CAAGGCAAAC AGTCATAGAA CAGTTATTAA ACAATANAAA   200

ATGTGTT   207

5   (2) INFORMATION FOR SEQ ID :401:

          (i) SEQUENCE CHARACTERISTICS:
               (A) LENGTH: 217 base pairs
               (B) TYPE: nucleic acid
10   (C) STRANDEDNESS: double
               (D) TOPOLOGY: linear

15   (xi) SEQUENCE DESCRIPTION: SEQ ID :401:

     GAGGCATGGC CACATTCCAA GAAATGGAAT AAGGAGTGGG ACAGCAGGCA   50

     GGGGGCCAGC CTGGGGCCTG GGCCTTTTAA TCTAAGGACT GGGGAGAACC   100
20
     AAGGGACCTT AGAGGTCCTC CAGTCCTCCC CATATNNAAA GAGGGAGAAC   150

     AAGCCTGGAG AGGAGGCTAC CTTAAGACCC TAAGAAGAAT TTAGCAATCG   200

25   NTTCTCCAAA GATAGCC   217

     (2) INFORMATION FOR SEQ ID :402:

          (i) SEQUENCE CHARACTERISTICS:
30   (A) LENGTH: 225 base pairs
               (B) TYPE: nucleic acid
               (C) STRANDEDNESS: double
               (D) TOPOLOGY: linear

35

          (xi) SEQUENCE DESCRIPTION: SEQ ID :402:

     TTTACAATAG ATTTCACCTT CANTTTAGTC AGAGTTGTTG ATTCAAGACT   50
40
     CTTCCCACAC TCGCACATCG AAACATTTTT GTGCCAGGGC TTTCCAGCTC   100

214

CAATTATCTT CTCGACAGCA TATACAGAAT CCCCACATCT GGAACACTTC   150

TCAGCACCTC CATANNTTGA GCAAATTTAG AAGTGTTTGG ATTTGTTGTA   200

GGCCTGTGAG GCTGAACACT CTCTG   225

(2) INFORMATION FOR SEQ ID :403:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 95 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: double
            (D) TOPOLOGY: linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID :403:

AGAAGGGGCA TACTCGCTGG AGACCTGGTG CCTCTATCCA CTGNACGCTG   50

ACTGNGGCTT CCACTGCGCC CGTGTACNTT ATCGAAGCTA CAGAT   95

(2) INFORMATION FOR SEQ ID :404:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 239 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: double
            (D) TOPOLOGY: linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID :404:

AGGAAAAATT GACATTACTT GTTAGAAGAG CAACTCTGAA AGAAAACAAG   50

CAAATTCCAA AACAGAAAG ATTCACAATN NAAAGGTGCA TACATTAAAG   100

GGCCACACTG TGTAATACTG TGCCAACTTA TGCGAGTCTC ATTGTTCAGG   150

ATGAAATGTG AGATTGTAGT TTGAATGCTA TAAGCAGGTT CCAAGATACC   200

215

CCAAATGACT GTAAGCCAGA CTNGAAGCAT GTCAAAAAG   239

(2) INFORMATION FOR SEQ ID :405:

5   (i) SEQUENCE CHARACTERISTICS:
                 (A) LENGTH: 189 base pairs
                 (B) TYPE: nucleic acid
                 (C) STRANDEDNESS: double
                 (D) TOPOLOGY: linear
10

          (xi) SEQUENCE DESCRIPTION: SEQ ID :405:

15   GGCTATTATT CTAAGTGAAG TAACTCAGGA ATGGAAAACC AAACGTTGTA   50

      TGTTCTCACT GATCATTGAG AGCTAAGCTA TGAGGACTCA AAGGCATAAG   100

      AATGATACAA TAGACTTTGG GACTTGGGAG GAAGAGCGGG AGTGGGGCGA   150
20
      GGGATAAAAG ACTACAAATA TGTGCAGTGT TTACTGCTC   189

      (2) INFORMATION FOR SEQ ID :406:

25   (i) SEQUENCE CHARACTERISTICS:
                 (A) LENGTH: 75 base pairs
                 (B) TYPE: nucleic acid
                 (C) STRANDEDNESS: double
                 (D) TOPOLOGY: linear
30

          (xi) SEQUENCE DESCRIPTION: SEQ ID :406:

35   CACCATCCTC CAAGTAAATC CCCCCTTAGG AAAGTAAGGG AAAAGACCCC   50

      TTATAGCCCT GAGCTCCCCC TTGGA   75

      (2) INFORMATION FOR SEQ ID :407:

40   (i) SEQUENCE CHARACTERISTICS:
                 (A) LENGTH: 190 base pairs

216

```
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear
```

```
    (xi) SEQUENCE DESCRIPTION: SEQ ID :407:

TATTCATCCA GCAGTGTTGC TCAGCTCCTA CCTCTGTGCC AGGGCAGCAT        50

TTTCATATCT AAGATCAATT CCCTCTTTTA GCACAGCCTG GGGAGGGNGT       100

CATTGTTCTC CTCGTCCATC AGATCTCAGA GGCTCAGAGA CTGCAAGCTG       150

CTTGCCCAAG TCACACAGCT AGTGAAGCCA GAGCAGTTTC                  190
```

```
(2) INFORMATION FOR SEQ ID :408:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 194 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear
```

```
    (xi) SEQUENCE DESCRIPTION: SEQ ID :408:

GAAGACATGG CGCCCTAACA CTTCGAGACC TGCTGNTAAA TTAAAAGCTA        50

TTTTTCATTA AACCACCATT TCCTCCACCT ATTGGAGTCA AATATGAAAG       100

CTGTCGATGA AGCCTGNCTG GCTGCACAAG TTNGACTGNG TCTGAATAAG       150

CACTTTCATC ATGGACTAAG AATCCTTGGT GTGGNCNTGA TCTT            194
```

```
(2) INFORMATION FOR SEQ ID :409:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 97 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
```

217

(D) TOPOLOGY: linear

5   (xi) SEQUENCE DESCRIPTION: SEQ ID :409:

GCAGCACAAG AGTCATCCAT GGATACAGTT CCAATCATTA TAACCACTTC   50

TAAAACAAGA TCATCTTCTG CAGCACCTGG TTTTAGTTTA TCCTTGA   97

10
(2) INFORMATION FOR SEQ ID :410:

          (i) SEQUENCE CHARACTERISTICS:
              (A) LENGTH: 155 base pairs
15   (B) TYPE: nucleic acid
              (C) STRANDEDNESS: double
              (D) TOPOLOGY: linear

20
          (xi) SEQUENCE DESCRIPTION: SEQ ID :410:

TTTGAGCTCC TGGACCCTTC TTTGCCTACA CTGGCCTTCC TCTCGGAGGG   50

25   ACAAGGAAGC TGGCCTCCCT TTACTCTACC NTTNNTTNTG GTCCAGGGCC   100

AGCTCTTCCG AGGCTCCAGC CTGCTTTTCG CCGGTGTCAT CAGATCATGC   150

TTTGC   155
30
(2) INFORMATION FOR SEQ ID :411:

          (i) SEQUENCE CHARACTERISTICS:
              (A) LENGTH: 249 base pairs
35   (B) TYPE: nucleic acid
              (C) STRANDEDNESS: double
              (D) TOPOLOGY: linear

40
          (xi) SEQUENCE DESCRIPTION: SEQ ID :411:

218

AACGAAGNGT TCCTGAATAC CACAGCCTGC TGGGAAATGA CTAGGCGGTA   50

AGGTTCTGCC ATGCCTGTGA CCCACCATGG ACATACTGGA CCTTAATTCC   100

TCTGCTTCTG TGCTCCCTCC TGAGAACCCT TTATGAGCCT GATTCCTCAG   150

TCTCACCAGA ATTCTGGATC ACCCAAGAGG AAAAGACTGC CAGTTCTAGA   200

TTCCTCTATA GGGAGACCTG GATTGTTGAC CAGGTGAGAA GCCAATGGT   249

(2) INFORMATION FOR SEQ ID :412:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 143 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID :412:

AGAAGGAGAC AAAACACCTC CTCTGTAATA GTACCTCGAA TGGATTCAGC   50

TTTACTCCTC TATAACTCAT CTTCACACCN GCATATTTAA ACAAACTAAC   100

AAAATGAAAT ACTAATAGTA AAAAGGCTGA CCCATGTGGC TTT   143

(2) INFORMATION FOR SEQ ID :413:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 256 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID :413:

GGGTCCCCCC ATTCACGTAC TCCATCACAA AGTACAGGCG GTCCATGGTC   50

219

TGGAAGCAGG AGTGGAGCTG TCAGGAAGGG CGGCTTCCCG GGCAGGCCAA   100

CACCCACTTC TCCACCATAG TGCACTCCAC GTCATCATCT GATCACAACG   150

TCCTTCTTCA GGATCTTCAC AGCATAGAGC TCATCTGTGC CTTTCGTTCT   200

GAAAGCATGA CCTTGCCAAA GCTGCCTTTC CCCAGCACCA TTAGGAAGTT   250

AAAATC   256

(2) INFORMATION FOR SEQ ID :414:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 87 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID :414:

TCGCAAAAGA AGNGTACCAT AACTCCTATT TCNAATGGCT GATTGTAGTA   50

GCACTGGAAG TTTATCAAAA CCCAGGTGTA AATATGC   87

(2) INFORMATION FOR SEQ ID :415:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 247 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID :415:

AGAGGGGGAC CAATCTAACC ATCGCTCTTC CAGTCCTACC AGCACACTCT   50

TGCAGCGCCA TNCCACTCCC TGAGCTCAGG ATCCTAGCCC GCCCGCCCGC   100

220

```
GGATGCTAGT NNNCTCCACC CTNCCCACCT GTCATACCTG TGTANTACAC          150

ACCCACCCGT ATCACGCAGG ACATGAACCA GCACCACTAA GGCCCCGGNG          200

CAGTGTTCTG NNNTTCTTCT CTANCTGTCT GCCCTGAGTC CCGGACC            247
```

(2) INFORMATION FOR SEQ ID :416:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 162 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: double
            (D) TOPOLOGY: linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID :416:

```
TCTAGCACAC AGCTGCGCTC ACAAAAACTG CGCGACTTGT TAGAACTAAT          50

TGAGTGGAGC CTGCAGGTGA GGGGAGGGAG GGGCTGCAGG TCAGGTAAGA          100

TCTGGAAGAC AACGCACACT TGAAGGGCAG GGGACTCTAA GCAGGGATTT          150

ACATTGAAAG GA                                                   162
```

(2) INFORMATION FOR SEQ ID :417:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 109 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: double
            (D) TOPOLOGY: linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID :417:

```
CAGAAGAAGG AGAACTCATG ATTCCAGAGA GCTTTGGGGC TTATTTTTAA          50

GTACTTAGCA AAATATTTGT TTTNCGTGAT TTAGCTTGTC ATTAAACNAA          100
```

221

GAGCTACTG 109

(2) INFORMATION FOR SEQ ID :418:

(i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 202 base pairs
    (B) TYPE: nucleic acid
    (C) STRANDEDNESS: double
    (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :418:

GGATGTAAAT TATATGTTGT TTAAATTTTT CCAGCATCTG AAAACCTTAT 50

CTGCTAGACA ATGCAAGATT CACACAGAGT TATCTGGGAT TCTGATTTTT 100

TAAATAGTAC ATATCATTAA ACCATTCNTT CTAAANGTAA GAAGAGCAGA 150

AAAAATCTTA TAAGATTATC AGATTTTCCT AATGACACAG AAATGNAAGA 200

AA 202

(2) INFORMATION FOR SEQ ID :419:

(i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 152 base pairs
    (B) TYPE: nucleic acid
    (C) STRANDEDNESS: double
    (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :419:

TAGCAAATGT GGATTACAAG CAAATACAAC AAGTCGTGCC CCTCCAACCC 50

ACCACAAACT TCTAAACGCC ACTCAGCAGA TGCATAGGAT TCGTTACACG 100

CAACGATTGA AATAAAAATA AAAGCTNCAA ATGCAATACC CANACTAGCC 150

222

TA   152

(2) INFORMATION FOR SEQ ID :420:

5   (i) SEQUENCE CHARACTERISTICS:
                (A) LENGTH: 218 base pairs
                (B) TYPE: nucleic acid
                (C) STRANDEDNESS: double
                (D) TOPOLOGY: linear
10

            (xi) SEQUENCE DESCRIPTION: SEQ ID :420:

15   CAGCCCTACA CTCGCCCGCG CCATGGCCTC TGTCTCCGAG CTCGCCTGCA   50

        TCTACTCGGC CCTCATTCTG CACACGATGA GGTGACAGTC ACGAAGGATA   100

        AGATCAATGC CCTCATTAAA GCAGCCGGTG TAAATGTTGA GCCTTTTTGG   150
20
        CCTGGCTTGT TTGCAAAGGC CCTGGCCAAC GTCAACATTG GGAGCCTCAT   200

        CTGCAATGTA GGGGCCGG   218

25   (2) INFORMATION FOR SEQ ID :421:

            (i) SEQUENCE CHARACTERISTICS:
                (A) LENGTH: 237 base pairs
                (B) TYPE: nucleic acid
30   (C) STRANDEDNESS: double
                (D) TOPOLOGY: linear

35   (xi) SEQUENCE DESCRIPTION: SEQ ID :421:

        GATGCCAATG TTTCATCCAC CGGCTGCACA GGCACAAACT CCCCCACCCA   50

        GGACGACTGT GATGAGGTGG CCCTCCCTGT CAACCCTGGT CCCTGGAGTC   100
40
        CCCAGCACCT GGGGCCCTGA CGGTCTCGAT GTCACAGGCG CTTACTGTGC   150

TGCTGGCTGT CCTATGCCAG CCTCACCCAT GTGGGGACCA CGNAAGGCAC   200

ACTCCCTCAC CCCGGTGCCG GGCCGTGCGA TCCCCCA   237

(2) INFORMATION FOR SEQ ID :422:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 202 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID :422:

AGGNGTAATA AATACTGCAT CCTTTCCACA ACATAGCAGG AATCTTATAG   50

GGAAATCCAT ATAGTTTCTG AACATGTATT NATATACTAA GTCTATATTG   100

TTTCTTTACG AAGTGTAAAT AAGTGCTGCA CCATACTGTA AACAAAACTC   150

GAATATTGAC TAAATAAAAT CAAAAGTTCA TCTTGTAGTC ATGTCTTTCT   200

CC   202

(2) INFORMATION FOR SEQ ID :423:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 216 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID :423:

GGGACACCAT TACCATCCAT TGACATCGCA TTTCCATAGA AATGCCAAAG   50

AAAGAAGTCC TGGGGTTTTT CATAGAAAGC TCAAAAAGTT CAACCTTTGA   100

224

TGCTATCCCC CAGCCCAATA CAAAATACAC AAAAAAGCAA TTATCAAAAT   150

ACTGACTTCG GTTTCTTTTT CTCTTCAAAT NCCTATAATN GCTTTACATA   200

TTCGTATCAG CACCTA   216

(2) INFORMATION FOR SEQ ID :424:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 168 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID :424:

CGACGAAGGG AGTACTCGCG CTTTGTCTCC CTATCCACAC TTGAGCAAAT   50

GCTCGCTGGT CTACTGCCAA AACCCATTTC ACCAACCATA TGTCCCTCGC   100

CCATACCCCC TCTCCCTCTC AAACCCTGGG GACAAATTCA AGGACCCAGG   150

GGTGCCCTTT TAAAAAAA   168

(2) INFORMATION FOR SEQ ID :425:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 258 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID :425:

TCGCAGGAGA AGGAGTCGCT TACTATGCAT CCAAAGGCTA CCGTGGTTAC   50

TCCTATATGA CATTCCAGAT TTTGATGACT AGCACCCACC CCACAGCTGA   100

225

GAGGAGTCAC AGTGGAACTT CCCAGCTTTA AGATATCTAG CAGAAACTAT   150

AGCTGAGGAC TAAGGAATTC TGCAGCTTGC AGATGTTTAA GAAAATAATG   200

GCCAGATTTT TTGGTCCTTC CCAAAGATGT TAAGTGAACC TACAGTTAGC   250

TAATTAGG   258

(2) INFORMATION FOR SEQ ID :426:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 275 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID :426:

TCCACATCAT CTCCAAAGCC CATAGGCCGA GAAATGGCAT CTGAGATCTG   50

CTGGGCCACC TCCTGTTGTT CCGTATGTCA GTCATCAGTT CATCTACCTN   100

GTCAATGTCC ATGTCCTGGT AGGCCTTCTT CATGCTTTGN CAGCAAGCTC   150

CATGCACGAA GGACTTCTGC ATTGGTAGTG GCATTCTCAA TAGCCTCACG   200

CTGAAACTCC AGGGTGGATA ATGCCCCGTC AATTTGTGCC AGCTGCTGTT   250

CGAATNNTTT TCTTTCTCGT AAAGC   275

(2) INFORMATION FOR SEQ ID :427:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 162 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

226

(xi) SEQUENCE DESCRIPTION: SEQ ID :427:

CTCTGTGCCT CGCTGAGGAA AAATAACTAA AATGGCAAAG AAGATCCTAA   50

GAAGCCGAGA GGCAAAATGT CATCATATGC ATTTTNTGGC AAACTGTCGG   100

GAGGAGCATA AGAAGAAGCA CCAGATGCTT AAGTCAACTN TAAGAGTTTT   150

CTAAGAGTGC TC   162

(2) INFORMATION FOR SEQ ID :428:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 220 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID :428:

ATGCAGAAAA GGAGTCGTGA GCGTAACACC CTCGCTGCTG GTCATAAAAC   50

CCATAGTTCC TGAACTCATC AAAGAACTTA ACTTCCTGAC GCCAGATATC   100

TGCCATGCGC GAAGGGNTGA TACCACTCAG GATTATGAAT TTTGTTTAAA   150

GTCGNGTTTA CAATGATTTG NCCTGGACTG AAATTCANGC TGCCTTAAGG   200

TGCTGATGAT ATTGAGAAGT   220

(2) INFORMATION FOR SEQ ID :429:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 185 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

227

(xi) SEQUENCE DESCRIPTION: SEQ ID :429:

GACTCATCTT GCCCAAGAAG AGCCAGGATA TGAGAAGATG GGAGAGGGAA   50

GGGGAGGTGT GAAACGTGCT GGTGCTTCCT GTCCTCATGG TGTGATGGCT   100

GCCCAGGCTG CTCCTTCGAG GCAGGACAGG ATTCCCATGG GAGATATGAG   150

GACCATGGTG ATTTCCAGGA CCAGTTATGT CCAGA   185

(2) INFORMATION FOR SEQ ID :430:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 277 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :430:

GGGATGCCCT GACCTGATGG CCCTTGACCA ACATGGTGCT GGAGGAGCAC   50

TACCTGGTCG TGGGAGTAGT GGTCATCGTG GACCCAGGGG TGATCCCTAT   100

CAACTCTTGG GGTGAGAAGC AGCGCATGCA CCTGCGGGAC GCTTCCTGGC   150

TGACCAGCTG GACCCCATCT AGTCGCCTAC AACAGCGAGC CAGCACACCG   200

GCCCAGGTGC CGGAGATGAA TGAGCCCCAG CAGTCCAAGG TGTGATGTGG   250

GAAGACACCG CAGAGCTCAC TTACCAA   277

(2) INFORMATION FOR SEQ ID :431:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 125 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

228

(xi) SEQUENCE DESCRIPTION: SEQ ID :431:

AAAGTGCGCT TGGGCATCCT GCCAGCCTGC CATGTCTTCA TGCGCTGGTC   50

GAAGGCAGCC NGGACTATGG CCAGGAGGCG AATGTAGTCA CTCAGGAGCT   100

CAGCAAGGAG GAAGAAGTCA TTGTT   125

(2) INFORMATION FOR SEQ ID :432:

    (i) SEQUENCE CHARACTERISTICS:
       (A) LENGTH: 222 base pairs
       (B) TYPE: nucleic acid
       (C) STRANDEDNESS: double
       (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :432:

GCCTAACTGT CAAAGCACAG AAAAGTTAAC AAAGGGTGGG ACTCGCCATT   50

TCGAAATAGC ACATTTTTAG CAATAGGCTC TCTACACTAG AGAGCCAGTA   100

GACTGATATT CTTTAATGCC AGTTTCCTAG TTAATCGTAA AGATAGACAC   150

AATTCCCCCC TTTATAAAAG CTTCTGTCGT TTCACATAAT GACTTTAACT   200

ANAANGGAAA TGGGGCAGGA CA   222

(2) INFORMATION FOR SEQ ID :433:

    (i) SEQUENCE CHARACTERISTICS:
       (A) LENGTH: 213 base pairs
       (B) TYPE: nucleic acid
       (C) STRANDEDNESS: double
       (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :433:

229

CCATGNCGGC CCCCAGGTCC TCGATCTTTT CGAGCTGACT TCTCATGGCT   50

CGATTTCCTG GTGCTTGGTT TGGTAGCTTC AAGCTGGGAT TCGAGGGTCC   100

CCGACTNTTC CACCATACAG GACCCATCGA GGAGGCATGT TCTGGTCTNT   150

TGGATCCACT GGTGGAAGGG TTGCGCGCTG GNCAAACTGT TGGTNTAACT   200

NGNCGTTTCC TCT   213

(2) INFORMATION FOR SEQ ID :434:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 221 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID :434:

CCATGNCGGC CCCCAGGTCC TCGATCTTTT CGAGCTGACT TCTCATGGCT   50

CGATTTCCTG GTGCTTGGTT TGGTAGCTTC AAGCTGGGAT TCGAGGGTCC   100

CCGACTNTTC CACCATACAG GACCCATCGA GGAGGCATGT TCTGGTCTNT   150

TGGATCCACT GGTGGAAGGG TTGCGCGCTG GNCAAACTGT TGGTNTAACT   200

NGNCGTTTCC TCTGCCGGTG T   221

(2) INFORMATION FOR SEQ ID :435:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 70 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

230

(xi) SEQUENCE DESCRIPTION: SEQ ID :435:

ACACTTGATA CTATGCATCA AAGGACGTGG AGAACTAGAG CGGGCTACAT   50

TAGTATATTT TCGTTGTCAG   70

(2) INFORMATION FOR SEQ ID :436:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 163 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :436:

AGTACGCAAT GCTTTCTTAC AGTAAGCAAG AGCTCCTCTG TAATCCTTCT   50

CGTTGAAGGA AATGCAAGCT TTACCAAGAA GGGCTGGAAT ATTATTCGGA   100

GACTGATTGA GTACAAAATG AAACTGTGCG TCAGCTTGAT CCATTTTGTC   150

ACCCTCAAGT AGG   163

(2) INFORMATION FOR SEQ ID :437:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 170 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :437:

TGTGGCTGAT CATAAGAAAG GAGCAAAGAA AGCTAGAATT GAAGAAGATA   50

AGAAGAAACA GAGGACAAAA AAACAGACGT TAAGGAAGAA GATAAATCCA   100

231

AGGACAACAG TGGCGAAAAA ACAGATACCA AAGGAACCAA ATCAGAACAG   150

CTCAGCAACC CCTGAATTTG   170

5   (2) INFORMATION FOR SEQ ID :438:

            (i) SEQUENCE CHARACTERISTICS:
                (A) LENGTH: 187 base pairs
                (B) TYPE: nucleic acid
10   (C) STRANDEDNESS: double
                (D) TOPOLOGY: linear

15   (xi) SEQUENCE DESCRIPTION: SEQ ID :438:

        AGAACTACAG AAACCTGGCC TCCCTGAGTT TATCCTATGG GGGGCACAGG   50

        AAAGAGCCCT GGACCATAGA AACCAAGTAC GAGTAGCAAG AAAACCAAAA   100
20
        GGGTGGGAAT GGATCAAAGG TGTGAAAACA GATCTGTCTC GTAACTGTGT   150

        AATCAAGGAA CTAGCACCAC AACAGGAAGA TAACCCA   187

25   (2) INFORMATION FOR SEQ ID :439:

            (i) SEQUENCE CHARACTERISTICS:
                (A) LENGTH: 234 base pairs
                (B) TYPE: nucleic acid
30   (C) STRANDEDNESS: double
                (D) TOPOLOGY: linear

35   (xi) SEQUENCE DESCRIPTION: SEQ ID :439:

        AAAAGCAACC AGGTTCGAGA AACAATAGTG TATGTGTTCC TATAGGTATG   50

        AGTTATTCAN TGTAGATTCG TTTTTCTGCA ATCCTCTGCC GAAATGATNT   100
40
        ACACTTACAA TGNNGAATGC CATAGGACAC TACAATCTGA ATCAAAACAG   150

232

TCGCGTCTGA AATGNTNGTG TGGTAGACCA CCCCCATTCA AGCCTTCATA   200

CTTCGTAAAA ATGCAAATGT TGAAGATCGN NTCT   234

5   (2) INFORMATION FOR SEQ ID :440:

            (i) SEQUENCE CHARACTERISTICS:
                (A) LENGTH: 203 base pairs
                (B) TYPE: nucleic acid
10   (C) STRANDEDNESS: double
                (D) TOPOLOGY: linear

15   (xi) SEQUENCE DESCRIPTION: SEQ ID :440:

GGACCAGGAA CCTAACTGAG ATAAGTTCAG CTTTCCAGTT GACACCAAGT   50

CATCTAGTCT TCCCGGAGTA GATATAGTTG AGGTACTCCA TTTCCCAAAA   100
20
CAGAGAGCTG ATCCCGGGCT GCAACACCTC CAATAGTCGA AGCTCCCTTA   150

ATNAAGGATA TCAATGTATT TCTTAAACGC TTGATGTCGT TCAAAGTCTG   200

25 TTC   203

        (2) INFORMATION FOR SEQ ID :441:

            (i) SEQUENCE CHARACTERISTICS:
30   (A) LENGTH: 254 base pairs
                (B) TYPE: nucleic acid
                (C) STRANDEDNESS: double
                (D) TOPOLOGY: linear

35

        (xi) SEQUENCE DESCRIPTION: SEQ ID :441:

GTGATGCACC TGACATCCCC TCACAGGCTC TTGGAGAACT GTAGTGCAAC   50
40
TCACTTAACC GCAATGCTGA GAGCAGAATT CTGGAGTATG ATCCAGGGGA   100

233

ACGTTTCCCC ACACCACCCG AGCTACTTTA CCAGCGATCA TGATTGTGAT   150

GGAATAGGCT TATTAAGTTA CACATTTAAA AAGTCATTAG AACATCTCGT   200

TCTTGCACAC TAGTGTAGAA AGGTCTTCCA AAGATAAAAG GTGTAGGCCT   250

GGTT   254

(2) INFORMATION FOR SEQ ID :442:

     (i) SEQUENCE CHARACTERISTICS:
         (A) LENGTH: 147 base pairs
         (B) TYPE: nucleic acid
         (C) STRANDEDNESS: double
         (D) TOPOLOGY: linear

     (xi) SEQUENCE DESCRIPTION: SEQ ID :442:

GGGGNGCTAG CAGTTGGGNG GTGTAGGAGG CATTGCTGAT GATCTTGAGG   50

CTGTTGTCAT ACTNTTCANG NNNCACACTC ATGACGAACA TGGGGCATAG   100

CAAGGGGCGG ANGANGACCG TTTNGNTTCC TTGAAANGAG CCCCAGC   147

(2) INFORMATION FOR SEQ ID :443:

     (i) SEQUENCE CHARACTERISTICS:
         (A) LENGTH: 198 base pairs
         (B) TYPE: nucleic acid
         (C) STRANDEDNESS: double
         (D) TOPOLOGY: linear

     (xi) SEQUENCE DESCRIPTION: SEQ ID :443:

GGGGNGCTAG CAGTTGGGNG GTGTAGGAGG CATTGCTGAT GATCTTGAGG   50

CTGTTGTCAT ACTNTTCANG NNNCACACTC ATGACGAACA TGGGGCATAG   100

234

CAAGGGGCGG ANGANGACCG TTTNGNTTCC TTGAAANGAG CCCCAGCTNC   150

TCCGNGNGAG ACGCAGTGGA CTNCGATGNT TAGCNCTAGT NNCCCGCT   198

(2) INFORMATION FOR SEQ ID :444:

  (i) SEQUENCE CHARACTERISTICS:
   (A) LENGTH: 208 base pairs
   (B) TYPE: nucleic acid
   (C) STRANDEDNESS: double
   (D) TOPOLOGY: linear

  (xi) SEQUENCE DESCRIPTION: SEQ ID :444:

ATACTACGCT AGGAGAACAA TGTTCCTACA TATTATGGGT AGTGAGACAT   50

TATCTGTATA CAGGGACTGT GATTATTTAA AATATGCAGA ACTTATTTCA   100

TCTGTGCTTT AGAAATAACT GTATACAGTG TTATAAGTGA AAGAACTCAA   150

AATAACTAAT ACCAAATATA CACCTATGTA TTAGAATTCA AAAAGCTGCT   200

TTCTGTGA   208

(2) INFORMATION FOR SEQ ID :445:

  (i) SEQUENCE CHARACTERISTICS:
   (A) LENGTH: 168 base pairs
   (B) TYPE: nucleic acid
   (C) STRANDEDNESS: double
   (D) TOPOLOGY: linear

  (xi) SEQUENCE DESCRIPTION: SEQ ID :445:

AGCACATTTC ACTACGGGNT ATGTGCATTC TGGGCTTAGT AATGTCAAAT   50

CACTCTTCTC TCCAGCTTGG CCATTCCTCA TTCCTTGCGG GCCTGCCCTG   100

235

TAGACCACAG GCTAATGGAA TGTCCCGGTC TGNGTCATCA NATTCTGTAA   150

CCTGNAGCCC CCGCTGAG   168

(2) INFORMATION FOR SEQ ID :446:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 243 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: double
            (D) TOPOLOGY: linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID :446:

AGGCAGAAGG GACGCTACTG ACTTAAGCCA AACCCTGATT GGTGGATAAA   50

GTATTCAGTT GTTCCATTCA TGCCTATCCT TTNTACAGCT CTCGCGACTA   100

TAACAAACAA CTGATAAAAT AGCATCAGTC CCTCCACCAG GTTGCCCTCA   150

AGGAAGCCAT GTTTGTGACG ATCCGACCAG TCCCTGACGA TCTCTCTAGA   200

CCACCCTGAC CTCGCCGAGA GTGCTGAAGG AGCTATCTAA CCA   243

(2) INFORMATION FOR SEQ ID :447:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 251 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: double
            (D) TOPOLOGY: linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID :447:

CAGTCAGGGT CACAGAACAG TATTCAAAAT GATTGCCCAC CTGTTTTAGA   50

AATCTAAAAT NNTAAGTAAC TAAGAGCAAA GTGCTATGTG GGTTTTAGAC   100

236

```
CATGACTGTT TGTTTGCTCT CCTGCCCTAC CACCAAGCAA AGCAGCAGGG        150

CTCCTGGGGG AGAGGGATTT CAACCCCCCT GATGGCAGGG GGTGCTCTGG        200

GGAGGAGAGA GGAGAGAACA GGCTGTTTTG GAAAATATCC AGCACTTTGA        250

C                                                             251
```

(2) INFORMATION FOR SEQ ID :448:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 253 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID :448:

```
ACACTCCAGA NCATCCCACT AGAAAAACAA TTNNGCAGGA ACGTGATGGC        50

AACAATCAGC AGCCAATATT CTCAAGAGTT CCTAATCACC AAAAACATAT       100

ACAATNTAGT CTAGAAAAAT AAGTCAATTT CATAAAATAA GTTTTTAGAT       150

CGAAAAGCAC CCCCTTCACA GGTACAGAGA TACTGAAAAA TAGTCCCTAA       200

AAATCTACTC ATAGTTTACG GAGAGAAAGG CATGCCATGT GAGTTACGGA       250

GTG                                                          253
```

(2) INFORMATION FOR SEQ ID :449:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 113 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :449:

ATATAAAAAA GATCCGCATA ATAAACCAAA TCAGAAAATA ATACCTTGTA   50

ATACCTCTGT AAGAAGCAGA ATACACCATA TGTTATTCAC ATGTATAGGA   100

GTGATAAGAA AAT   113

(2) INFORMATION FOR SEQ ID :450:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 211 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: double
            (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :450:

TAGCATCCAG GGGAAGTTAA TCAATACGCG AAAAATACTG AAATTAAAGA   50

GACAAGTAGA AGAAAATGAA ATAATCAAGA GATTGAGAAA AGTTGCCAGA   100

AAGCTTGGAG AAAAACCAAG ATATGTAATT TTCGCAGAAG TCAAAGGTAG   150

AAACTATTTG AGATCAAAGT CCTATAAACA AAGTTAAATG ATTCCAAGAG   200

GTAAATAGGA G   211

(2) INFORMATION FOR SEQ ID :451:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 194 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: double
            (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :451:

238

CTCCATTAGC TTTATGGGAC ATACGACGCA TAAAGATACT NTCCCGTGCG   50

NATTTCACAC NTGNCAGAGC TATAAACCGG TGNATGATGT GATTTTNCTG   100

TAGAATGATA TGGCCTGATA TGGAGGCCTC TTAATNGGCT TTTTCAAGCA   150

GCAAAATGGT CTTGNGTGAG TCGTGCCGAG GCTNNNGATC AAAG   194

(2) INFORMATION FOR SEQ ID :452:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 168 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: double
            (D) TOPOLOGY: linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID :452:

ACTTCAAGCT CAACCTATTC TCGTTCTCTT TGTTAGAGGT GTATTGAGGA   50

TAGCATATTG AGAATATATT CTCTGGTTCA AACCAAAGAT TTTGTGACAT   100

TAAAACTACT TGAATTTCTA CTTCATAATA GGAGTCAGTC ACTTCTGGGA   150

CTATAGTGAT GCTTGCAA   168

(2) INFORMATION FOR SEQ ID :453:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 220 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: double
            (D) TOPOLOGY: linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID :453:

CGATTCTTGC CCTAGTCAGA GACTATAGCA GCCCCCAGAC GTGAACCAAT   50

```
TGGCCATCTC CAGAAAGTTT AACAAAACCC GACCAGGTTG CCCCCTTCAC        100

TTTCTTACAA CCTCTTCCCC TTCCCCAGGG GCTCTGCTCC TCACTCCAGA        150

TCATCCTTTA GTTTAGAGCT GCGCAGTGAA GTGGATATCA CTGAAGGAGA        200

TAGGACGCCA GACTACACTG                                         220
```

(2) INFORMATION FOR SEQ ID :454:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 275 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID :454:

```
GCCATCCTTG ATGGAAAAGA AACTGAAGAG AAAAGACAGC CTGTGGAAGA        50

AGCTCAAAGG TTCTTTGAAG AAGAAGAGAG AAAATATGAC ATGATATCTT        100

TGCTTTTGAG TTCCTCACGC TCTCTGAATN TTATTGGTTG GACATTCCAT        150

ATGTAGCATT CTGCTTCAAT ATTATCTATT ATGTGTCTCT CTCTCTTCAA        200

ATANNTGCCT GTAGGTAAAA GCAAGCTCTG CATATCTGTA CCTCTNGAGA        250

TAGTTTTGCT TTGTCTTTAG CGGTT                                   275
```

(2) INFORMATION FOR SEQ ID :455:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 270 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

240

(xi) SEQUENCE DESCRIPTION: SEQ ID :455:

TCGCAGAAGG AGGAACGGGG ACTTTCCATC CCCTGAACCA AGGCATGTTA   50

5   ACACTTGGCT CCAGCATGTT GTCATCATTC AACCAGAAAT CGCACAAATG   100

CTACTGTGCC GGGGTGNAGC CAATTTTCTT AAGTAAGTGC TGACTTCCTT   150

AACANNTATC TNTNTTNTGG CTGTAGGGTG GCTCAGTGGA ATCCATTTTG   200

10

TTAACACCGA CAATTAGTTG TTTCACACCC AGTGGTAAGC CAGAAGGGCA   250

TGCTCTNGGG TCTGCCCATT   270

15   (2) INFORMATION FOR SEQ ID :456:

         (i) SEQUENCE CHARACTERISTICS:
             (A) LENGTH: 254 base pairs
             (B) TYPE: nucleic acid
20   (C) STRANDEDNESS: double
             (D) TOPOLOGY: linear

25   (xi) SEQUENCE DESCRIPTION: SEQ ID :456:

TCGCAGGAGA AGGAACCTTG ATGATACCAT TATCCTCACT TAGATGATGC   50

ACGACCCCTG CGCTGGATAC GGCGACGGTT TCTCATTTCG CCTTTGCCAG   100

30

CTCTCATTCG CTGAGGGGCA TAGACCTTTT GATATCATCC AGGCTTTAGT   150

TTCTTAAGGA GCAAAACAGC TTCCTTGNNC TTCTTGTAGC CTTCAACTTA   200

35   TTTAAACTAC CAAGGAAGTT CAGGAACTTC CTCAANACGA TGACCTTTAG   250

ACAT   254

(2) INFORMATION FOR SEQ ID :457:

40

         (i) SEQUENCE CHARACTERISTICS:
             (A) LENGTH: 236 base pairs

241

(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :457:

ACACTAACTG TTCCATCCGT TATATTTGCT GTGAGGAAAA TTAAGATTCC   50

TGTTGTATGG GCTGCACTGT TTCTGGAAGA CTACAGAAAA TCTAACATGG   100

TTGACACTTC CTGGTAGCCC TTCTGTACAT ACACACACAC AACCAAGAGA   150

GAAGACAGAG AGAAAATCCT GGTCCAAAAG ATCACATGAC CTTACTAGTG   200

TTTCCCCAAT GACTGTAATT TATAAACTAA AAATTG   236

(2) INFORMATION FOR SEQ ID :458:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 108 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: double
            (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :458:

GAGANNNNTT NNGGNAAATG NTTNCGCACT GNAGCTAAGA ANAGNNATGG   50

NNNTAGGGNG NNAGANGNCN TGAACAGAGA AAGCNTGAGG GCTCTGGGAC   100

GCTGGTAT   108

(2) INFORMATION FOR SEQ ID :459:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 155 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: double

242

```
                    (D) TOPOLOGY: linear



5           (xi) SEQUENCE DESCRIPTION: SEQ ID :459:


   ACCCATGGCA AATAGGAAGA AGCTCAGTAT CGGCTCCTCC CACCATAACC          50


   CCCACTTCTC CCGCCTCCTG GACCATAGTT TCCTCCACCA TACGGTCCCC         100
10

   CCATGTTCCT GCTACCACCA AAGTTTCCAC TCTCCATTGG ACCGTAGTTA         150


   GAGGT                                                         155


15      (2) INFORMATION FOR SEQ ID :460:


           (i) SEQUENCE CHARACTERISTICS:
                (A) LENGTH: 169 base pairs
                (B) TYPE: nucleic acid
20              (C) STRANDEDNESS: double
                (D) TOPOLOGY: linear




25          (xi) SEQUENCE DESCRIPTION: SEQ ID :460:


   TGCTATTTCC CTTTCATAAA GGCACACATT TGATCTTATC TTCTCTTACC          50


   CAACACGCAG TGGCAGTGTG TATTTTCCTT CTCTTTTTTT GTTAAATATT         100
30

   CTGGTTTGTG GAGGTTCACA GACATGTGTT AGTATATCCT TGCCTGCATG         150


   TAGTTGTTCA TTACTAGAC                                          169


35      (2) INFORMATION FOR SEQ ID :461:


           (i) SEQUENCE CHARACTERISTICS:
                (A) LENGTH: 184 base pairs
                (B) TYPE: nucleic acid
40              (C) STRANDEDNESS: double
                (D) TOPOLOGY: linear
```

(xi) SEQUENCE DESCRIPTION: SEQ ID :461:

ACCNTGTTTA ATTANTGCGC GGGCTCGCCG TTTGCATACA ATGGCTTACT   50

CAGTGCTNNC AGGCTGTGAG TNAATAGAGN GTGTATGACT TAATAAGCAT   100

TTTATCAGCG TACCTTTTTC GCCATGCGCT ACCTGCTATT GATGAAGGCG   150

GCTTAGGGCA TCGAAAAACC TAAAAGTCGA GCTT   184

(2) INFORMATION FOR SEQ ID :462:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 275 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: double
            (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :462:

AGGAACCNTG TTTAATTANT GCGCGGGCTC GCCGTTTGCA TACAATGGCT   50

TACTCAGTGC TNNCAGGCTG TGAGTNAATA GAGNGTGTAT GACTTAATAA   100

GCATTTTATC AGCGTACCTT TTTCGCCATG CGCTACCTGC TATTGATGAA   150

GGCGGCTTAG GGCATCGAAA AACCTAAAAG TCGAGCTTNG NNGTGCCGGN   200

AACGGCTCTA NANTACTTCT CATTGTAACT AGAGTACCAT ATTCGGCCGT   250

NNACTGNGTT GTTGGCGACA GATGT   275

(2) INFORMATION FOR SEQ ID :463:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 149 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: double
            (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :463:

5   AATTCACTAT GCGTGGCCGC CACAGCTATN CTTGTCCTCC TGGATCCTGA   50

       ACCTTGNAAG CTGCACTAAT GAGTTCAACG GGAGTGCTCT GGGCCCAGGT   100

       GTCAGCTGTA GCAATGCCCC NGCTGCAACT GAAGGNGCCA GCAATGCTA   149
10
       (2) INFORMATION FOR SEQ ID :464;

           (i) SEQUENCE CHARACTERISTICS:
               (A) LENGTH: 179 base pairs
15   (B) TYPE: nucleic acid
               (C) STRANDEDNESS: double
               (D) TOPOLOGY: linear

20
       (xi) SEQUENCE DESCRIPTION: SEQ ID :464:

       ATCATCAGCA GTGTTGCTCA GCTCCTACCT CTGTGCCAGG GCAGCATTTT   50

25   CATATCCAAG ATCAATTCCC TCTCTCAGCA CAGCCTGGGA GGGGGTCATT   100

       GTTCTCCTCG TCCATCAGAT CTCAGAGGCT CAGAGACTGC AAGCTGCTTG   150

       CCCAAGTCAC ACAGCTAGTG AAGACCAGA   179
30
       (2) INFORMATION FOR SEQ ID :465:

           (i) SEQUENCE CHARACTERISTICS:
               (A) LENGTH: 156 base pairs
35   (B) TYPE: nucleic acid
               (C) STRANDEDNESS: double
               (D) TOPOLOGY: linear

40
       (xi) SEQUENCE DESCRIPTION: SEQ ID :465:

245

CTACCTCTGT GCCAGGGCAG CATTTTCATA TCCAAGATCA ATTCCCTCTC   50

TCAGCACAGC CTGGGAGGGG GTCATTGTTC TCCTCGTCCA TCAGATCTCA   100

GAGGCTCAGA GACTGCAAGC TGCTTGCCCA AGTCACACAG CTAGTGAAGA   150

CCAGAG   156

(2) INFORMATION FOR SEQ ID :466:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 186 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: double
            (D) TOPOLOGY: linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID :466:

ACATCCCTGG AAGGAGGGCC TGAGGGCCAG GGAGGGAACA AGGCAGGAGA   50

CTGCTGGTTC TGGTTTTGGC CACCTCACCC TTGGCCACGT CCCCTCCGGC   100

TAAGCCACAG CACAAAGCAG AGCCAGGCTC TGGAGGCCCA GGGCCTCACC   150

ACTCCCCTNT GTCCCCCCAG CAGGGGGACA AAACAG   186

(2) INFORMATION FOR SEQ ID :467:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 87 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: double
            (D) TOPOLOGY: linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID :467:

TNNNGATGAN TATANAAGCA TCATNGACGG TATTTCCCNG TCTTGNANTT   50

TNATCGAGAN TTTANTCTAG TAANTATATT AATNTNT   87

(2) INFORMATION FOR SEQ ID :468:

   (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 187 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

   (xi) SEQUENCE DESCRIPTION: SEQ ID :468:

ACTAGAAGTA CAGCATCCTG CTGCAAAAAT GATTGTAATG GCTTCTCATA   50

TGCAAGAGCA AGAAGCCGAG ATGACACAAA CTTTGCCTGG TATTTGTTGG   100

AGCTCTCCTG GAATCACTGA AGAACTTCTG AGGATCGGCC TGTCAGTTTT   150

AGAGGTCATA GAAGGTCATG AAATAGCCTG CAGAAAA   187

(2) INFORMATION FOR SEQ ID :469:

   (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 256 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

   (xi) SEQUENCE DESCRIPTION: SEQ ID :469:

AGGGCACCAT TACCATCCAT CTGACATCGC ATTTCCATAG AAATGCCAAA   50

GAAAGAAGGT CCTGGGGTTT TTCATAGAAA GCTCAAAAAG TTCAACCTTT   100

GATGCTATCC CCCAGCCCAA TACAAAATAC ACAGAAAAAG CAATTATTAA   150

ACATCGGCTT CGTTTCTTTT TCNCCTTTGA ATNTTAATGT TTACATACTA   200

247

GTGTGCAGCA CCTACTTCTT NATCGCCGTG AACTGAAATC TAGATTTTAA   250

ACTGAA   256

5   (2) INFORMATION FOR SEQ ID :470:

           (i) SEQUENCE CHARACTERISTICS:
               (A) LENGTH: 109 base pairs
               (B) TYPE: nucleic acid
10   (C) STRANDEDNESS: double
               (D) TOPOLOGY: linear

15   (xi) SEQUENCE DESCRIPTION: SEQ ID :470:

       CTCAAAACGA CAATTCTGTG CCTGGGGGAT CTGACCTGGT GAGGTAGCCT   50

       GAAGTCTGAA TGGAGCCCAT AGTCGAAAAC AACCTAAGAA TCTCTCAGAA   100
20
       GAGGGTTTG   109

       (2) INFORMATION FOR SEQ ID :471:

25   (i) SEQUENCE CHARACTERISTICS:
               (A) LENGTH: 139 base pairs
               (B) TYPE: nucleic acid
               (C) STRANDEDNESS: double
               (D) TOPOLOGY: linear
30

           (xi) SEQUENCE DESCRIPTION: SEQ ID :471:

35   GCGGCAGTAT ACAGAAGCCA TATCAGTTGG GAAAAACTTT ATCAATCATA   50

       GAGCCTTTTG AAGAAAAATT TGCCAAGCGT GGTTTTTTGC TTGNAGACCT   100

       ATATATATTA CCTACAGGCT GAGAAAGCTT TGNATTTCT   139
40
       (2) INFORMATION FOR SEQ ID :472:

248

(i) SEQUENCE CHARACTERISTICS:

    (A) LENGTH: 262 base pairs

    (B) TYPE: nucleic acid

    (C) STRANDEDNESS: double

    (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :472:

```
TCGCAGGAGA AGGAATGTTC CCAATAGGAA CGCCTGTAGA CTGTTCAGAA        50

GAAATGCCCA AATGAGCCAG ATGAGAAGGC TGAGGGCAGG GCTGCTTTTG       100

GCTCTGAGGA CTATAGATTT ATCCTCTAGG TGATGAGGGA CTATTAACGG       150

CTGGTGAGTC TGGAGAACTG AACAGTGGAA GCTCTATTTT AGATTCACGT       200

GGCAGTAGAG GATAGAGGTG TTTGGAAGCG GTGGGCAGTT GCAAGCTATA       250

TGGGAGACAT TT                                               262
```

(2) INFORMATION FOR SEQ ID :473:

    (i) SEQUENCE CHARACTERISTICS:

        (A) LENGTH: 189 base pairs

        (B) TYPE: nucleic acid

        (C) STRANDEDNESS: double

        (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :473:

```
ACAGAAGGAC TTTGTCTCTT TAGCTTGTTT AGCTCAATGA ACATTATCTC        50

GGCAAATGAC TCTGCTTTCT CGAAGGTCCT TCTCCGCTCC AGGTTTACTT       100

GCATCTCTCA TACTTNNTAC AGCCAACATG AACACTCTAT GTATTTTCTA       150

AGCTTTCNTC TGTTCAAGAA CTTTGAATTT AAAACGTCT                   189
```

(2) INFORMATION FOR SEQ ID :474:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 166 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID :474:

TNCGTGCCTA GCAAACTTAA ACTCGAACGC ACGTAATAGT GCTCATAATT   50

CTNTNAAGGA CTTTAAACTT TACTCNGTAT GCTNTNTTGA TGACTCTAGC   100

AGCCTCGCTA ACCTAGTTTA CCCCACTGTC CCCACCGGCG AACTNTTTGT   150

GTTAGTACGC GNGTTA   166

(2) INFORMATION FOR SEQ ID :475:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 109 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID :475:

TTTTTTTTTA GTAACACTAA AGAGCTGTAA AGAACATTGA AGGTGGTCAT   50

TCCTTCAAAA CTGTGTTTTG ACCACACAAG GTGGGCATTA ACAAACAAAT   100

TCAACTTAA   109

(2) INFORMATION FOR SEQ ID :476:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 131 base pairs

250

```
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear


    (xi) SEQUENCE DESCRIPTION: SEQ ID :476:


    TCTGGGCGGA AGGTGGTGCG GTGAAAGGTG CAGGGACAGA CTGGGTTAGA      50

    GGCCACTCTT GGTCTTATCC TCCATGGCCA CAACAGAGGT GACAAATACA      100

    CGGGTCACTC AGTTACGTTT AGCCACAGCC T                          131

    (2) INFORMATION FOR SEQ ID :477:


        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 265 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: double
            (D) TOPOLOGY: linear




    (xi) SEQUENCE DESCRIPTION: SEQ ID :477:


    ACATGGATAG GTGTATGCAT ACTACGGCTA AGGAGAAACA ATGTTCCTAC      50

    ATATATGGGT AGTGAGAACA TTATCTGTAT AACAGGGAAC TGTGATTATT      100

    TAAAAATATG CAGAACTTAT TTCATCTGTG CTTTAGAAAT AACTGTATAC      150

    AGTGTTATAA GTTGAAAAGA ACTCAAAATA ACTAATACAA ATATACACTA      200

    CGTATTAGAA TTCAAAAAAG CTGCTTTCTG TGAAGTCAAT CAGCTATATT      250

    AAAAAAGACA CAAAT                                            265

    (2) INFORMATION FOR SEQ ID :478:


        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 182 base pairs
```

251

```
                          (B) TYPE: nucleic acid
                          (C) STRANDEDNESS: double
                          (D) TOPOLOGY: linear


5


              (xi) SEQUENCE DESCRIPTION: SEQ ID :478:


       AATCTACCAA CCTTAAAGCT CCCGNGATAA AGCTGTATTT CCAAAAGACC        50

10
       TGTNTTTATT NGNNGGNGTT NGCTTTCTTT GTCATCTAGA GCCTTGTTGT        100

       ACATGCAATG GGTGGGAGAT AGTGGTACCT ACTGTTGNTT CTNTCTGTGT        150

15     NTTCATCATG GTGTTGTCTA GGTCTCCTGA GG                          182


       (2) INFORMATION FOR SEQ ID :479:


             (i) SEQUENCE CHARACTERISTICS:
20                 (A) LENGTH: 169 base pairs
                   (B) TYPE: nucleic acid
                   (C) STRANDEDNESS: double
                   (D) TOPOLOGY: linear


25


              (xi) SEQUENCE DESCRIPTION: SEQ ID :479:


       AAGCCGTCGG GAGCCGCCGC CGCCATCTGA GGGAGGTACC CTGGAAACCA        50

30
       CCTTTCACGG TGGGGAAGTG CAGTCGCGGT GGGCAGCTCT GGGGCCACGA        100

       AACGGGAGCC TCTAAATCTT GGTCGGGACT GCTCGCCTGG AGCCGCACTC        150

35     TTGAGTCCGA GGCCATCTT                                         169


       (2) INFORMATION FOR SEQ ID :480:


             (i) SEQUENCE CHARACTERISTICS:
40                 (A) LENGTH: 238 base pairs
                   (B) TYPE: nucleic acid
                   (C) STRANDEDNESS: double
```

252

(D) TOPOLOGY: linear

5   (xi) SEQUENCE DESCRIPTION: SEQ ID :480:

AGATAACGCT CCCATCCCAG GCTAGAGACT CCATCTCTAA TTTNCNCAGT   50

CCGTCAATGA GAGGCAGGGA CTGAAATCCC AAGTTCTGTC TCACCGGATA   100
10

TTTTCCAGGA ATGCCTCTCT TCCAAACATC AGCGACATTT AACAGACCCT   150

GAGCAGCAAA CTTCTGCCCC AGAGGAAAGC AGAAAACCAA TTTATGTAAA   200

15   ATTAGAAGCG ATTTGCTTGA TCCATCACTN GCTTCCAC   238

(2) INFORMATION FOR SEQ ID :481:

(i) SEQUENCE CHARACTERISTICS:
20   (A) LENGTH: 201 base pairs
               (B) TYPE: nucleic acid
               (C) STRANDEDNESS: double
               (D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :481:

TCGCAGGAGA AGAAATCAAC CCCTGCTTCT CAAATCCAGA CAGGCCACAC   50
30

TGGCTAGAAC TTCCACCCAG CAGTCCTGCT CCTGCCCGAA GTCTGCAAGC   100

AAGTGAACCA CATGTCGCTA TGAAAGCACA CAGACAACAG ATTAGGGCAG   150

35   ACCTGGCAAA GATATGCCTG TCTGCCATCT TGGCCCCTGT CTGAGGGAGG   200

C   201

(2) INFORMATION FOR SEQ ID :482:
40

(i) SEQUENCE CHARACTERISTICS:
     (A) LENGTH: 162 base pairs

253

```
              (B) TYPE: nucleic acid
              (C) STRANDEDNESS: double
              (D) TOPOLOGY: linear


        (xi) SEQUENCE DESCRIPTION: SEQ ID :482:


     CGGCTCAGNC TGTTGGCGCG AAGAGAGTCT AACCCAAAAT TGCAAAACTC        50

     CCGTTGATTT CCAGGCCCTA CCACACGGCG ATGTCAACTT GTCCTCCAGA        100

     CATGGACGAC TACCAAAGAT CCCAGCTACG AAGCATGGCC TTGCTTAGAA        150

     ACNTTTTTAG AT                                                 162


     (2) INFORMATION FOR SEQ ID :483:


         (i) SEQUENCE CHARACTERISTICS:
              (A) LENGTH: 250 base pairs
              (B) TYPE: nucleic acid
              (C) STRANDEDNESS: double
              (D) TOPOLOGY: linear



         (xi) SEQUENCE DESCRIPTION: SEQ ID :483:


     ATATGAAGGA GGAAATGCTC GTCACCTTCG TGAATACCAA GACCTGCTCA        50

     ATGTTAAGAT GACCCTTGAC ATGAGATTGC CACCTACAGA AGCTGCTGGA        100

     AGGCGAGGAG AGCAGGATTT CTCTGCCTCT TCAAACTCNT NCCTGAACCT        150

     GAGGGAAACT TTGGATTCTC CCTCTGGTCG ATACCCACTC AAAAAGGACA        200

     CTTTTGATTA GGACGGTTGA AACTAGAGAT GAACGGTTAT CAACGAAACT        250

     (2) INFORMATION FOR SEQ ID :484:


         (i) SEQUENCE CHARACTERISTICS:
              (A) LENGTH: 132 base pairs
```

254

```
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: double
            (D) TOPOLOGY: linear


5


        (xi) SEQUENCE DESCRIPTION: SEQ ID :484:


    AACATTATCT TGACAAACTG AAGAACACTT CAGTTAACAC TACCTCGAAG          50

10
    AACCATCAAT GACTTGCTTT GAACAGACTA TAAAAGGCAT TCTCAAGGAG         100


    ATTAGAATGT TAATGCCACT TTGATTAGAT CT                            132


15      (2) INFORMATION FOR SEQ ID :485:


            (i) SEQUENCE CHARACTERISTICS:
                (A) LENGTH: 129 base pairs
                (B) TYPE: nucleic acid
20              (C) STRANDEDNESS: double
                (D) TOPOLOGY: linear




25          (xi) SEQUENCE DESCRIPTION: SEQ ID :485:


    TGTGCGTGGA GACGGTGGAG AGTGGAGCCA TGACCAAGGA CCTGGCGGGC          50

    CGCATTCACG GCCTCAGCAA TGTGAAGCTG AACGAGCACT TCTTGAACCC         100
30
    ACGGACTTCT CGACACCATC AAGAGCGAC                               129


        (2) INFORMATION FOR SEQ ID :486:


35          (i) SEQUENCE CHARACTERISTICS:
                (A) LENGTH: 172 base pairs
                (B) TYPE: nucleic acid
                (C) STRANDEDNESS: double
                (D) TOPOLOGY: linear
40
```

(xi) SEQUENCE DESCRIPTION: SEQ ID :486:

TCGCAAGAGG AGACATTCTG ATCATCCTCA CTGGACGCCA CAGGGGCAAG   50

AGGGTGGTTT TCCTGAAGCA GCTGGCTAGT GGCTTATTAC TTGTGACTGG   100

ACCTCTGGTC TCAATCGAGT TCCTCTACGA AGAACACACC AGAAATTTGT   150

CATTGCACTT CAACCATATC GA   172

(2) INFORMATION FOR SEQ ID :487:

    (i) SEQUENCE CHARACTERISTICS:
       (A) LENGTH: 210 base pairs
       (B) TYPE: nucleic acid
       (C) STRANDEDNESS: double
       (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :487:

ATGCTGCACA CTATGTCTCA CAAACTAAAT GGATCCATTA AAAGTTATGA   50

TTTAAAAGGC GACCACCCCC AAAAGAAGTC ATAACACTCA AGGGTGTCAA   100

TATATACAAC TGTGTAAACA CAACCAATCT ACAACTATAT CAACACAACC   150

AGCACTCCTC TATGGGCACA GACACACACA CAAAATTGTC CTTGCTTTTC   200

TCAGATATAT   210

(2) INFORMATION FOR SEQ ID :488:

    (i) SEQUENCE CHARACTERISTICS:
       (A) LENGTH: 90 base pairs
       (B) TYPE: nucleic acid
       (C) STRANDEDNESS: double
       (D) TOPOLOGY: linear

256

(xi) SEQUENCE DESCRIPTION: SEQ ID :488:

ACATGGATAG GCGTATGCAT ACTACACTAA GGAGAAACAA TGGTCTACAC   50

ANACGTAGTG AGAACATTAT CTGTATACGG GAACTGTGAT   90

(2) INFORMATION FOR SEQ ID :489:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 99 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :489:

ACCATGAGAC CTACATCCGA ATCTGACCCA GGCAAACATA CCGGGAGCCA   50

TACCGCACTA NCGGCTCTTC TCAAATCTCC TGGCCACNCA CCGAGNGCC   99

(2) INFORMATION FOR SEQ ID :490:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 186 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :490:

GGAAACCTGG AGGTGCGCAT CCTCGAGTGC GAAGAGAAGG TCTTCCCCAG   50

CCCCCTCTGG ACTCCATGCA CCAAGGTCAT GGCCAGGAGC TCTTGGCAGC   100

TCAGCCCTGC CGCCCCAGAG CATGTGGCGG CTGCTCTCTA CCAGCCGAGA   150

GCTTCGGAGA TGCAGCATCT GCGGCGAATG CCCCGA   186

257

(2) INFORMATION FOR SEQ ID :491:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 263 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID :491:

    AGCCAACTAA GTTCTCTCTT CGTGAAACAC AGGTCCATGA GTCGACACAA   50

    ACACTAATGC AAGAACCATC ACGGAAAACC ACCGCAGCAG CTGAAACTTT   100

    TATAGCCCAT AAAAGGACCA AACAAGTAAG CTGAATGACT GTGAAAATAT   150

    GACCTTCCAG AGCGGCACAT AACAGGATAT CAAATCAGGC TGATGCTTAG   200

    CAGGCTTCAA ATATNATGGT CAAATGACTG GATTACTTAN ATGAGGCAAC   250

    TTCATATCGG AAA   263

(2) INFORMATION FOR SEQ ID :492:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 159 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID :492:

    AGAGTGGGGT TAGCTCTGCC TAGCGCTACA CAAGAAAACC TCCCTCCAGT   50

    AAATNGGTGT GGGNGGTCCG CTTTTGGCCA TCATCGCACC CCCCCGGTCA   100

    CTGGGCGTTG TTGCCGGGCA CTTGTTTNNC NGGCTGGGTG TGTACCGTAA   150

258

CCGTGGGTC   159

(2) INFORMATION FOR SEQ ID :493:

5   (i) SEQUENCE CHARACTERISTICS:
                    (A) LENGTH: 197 base pairs
                    (B) TYPE: nucleic acid
                    (C) STRANDEDNESS: double
                    (D) TOPOLOGY: linear

10

               (xi) SEQUENCE DESCRIPTION: SEQ ID :493:

15   GGGCAGAGNA AGAACTGTTC CACCAGGTGA ACAGTCCTAC CTGCTTGGTA   50

      CCATAGTCCC TCAATAAGAT TCAGAGGAAG AAGCTTATGA AACTGAAAAT   100

      CAAATCAAGG TATCGGGAAG AATAATTTCC CCTCGATTCC ACAGGAGGGA   150

20   AGACCACACA ATATGTNGTG CTGGGGCTCC CCAAGGCCCT GCCACCT   197

      (2) INFORMATION FOR SEQ ID :494:

25   (i) SEQUENCE CHARACTERISTICS:
                    (A) LENGTH: 188 base pairs
                    (B) TYPE: nucleic acid
                    (C) STRANDEDNESS: double
                    (D) TOPOLOGY: linear

30

               (xi) SEQUENCE DESCRIPTION: SEQ ID :494:

35   GATGGGGAAG GGCATCCCAA CACAGCCTGT GGATCCTGGG GCATCTGGAA   50

      GGGCGCACCA TCAGCAGCCT CACCAGCTGT GAGCCTGCTA TCGGGCCTGC   100

      CCCTCCAATA AAAGTGTGAG AACTCCACTG TGTGCCCTGT CTTTGGGCAG   150

40   GGAGGGCTGC TGTGAGTGGA GTCTTGAGTN GGTGAGTG   188

(2) INFORMATION FOR SEQ ID :495:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 169 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID :495:

ACATGACCAT CCGCATCCGC CTTTATTGAC AATGAGAAGA TGGAGTCCCG   50

GACGCATCTA TCCCTCTTTG GCCCTTACAG GTTTGCCACG AGAGTGAGAC   100

GCCTTCCTGG ACCAGGGGAG GGNGNGTTGG TNCTNTGNGC GTGNGGGTNT   150

GTGGGNGCTG CTGGGGAGG   169

(2) INFORMATION FOR SEQ ID :496:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 172 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID :496:

CAGAGAGAAC GTTTCTATGG CTGCTGCTTC TAGGAGTCTC TCGCTCATAG   50

AAAAGGCACA CACTGAAAGA GGAAGCAGAT CCCATTGCTG TGGAAGTCCC   100

ATTGTTAGGA AGCTCTGCTT TTCTGGAGTT CAAATTCGCA TTCATGATGC   150

TTTAAACCGT CAAGCTGGGT GG   172

(2) INFORMATION FOR SEQ ID :497:

260

(i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 246 base pairs
    (B) TYPE: nucleic acid
    (C) STRANDEDNESS: double
    (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :497:

GAGAGTGGGG TTAGCTCTGC CTAGCGCTAC ACAAGAAAAC CTCCCTCCAG   50

TAAATNGGTG TGGGNGGTCC GCTTTTGGCC ATCATCGCAC CCCCCCGGTC   100

ACTGGGCGTT GTTGCCGGGC ACTTGTTTNN CNGGCTGGGT GTGTACCGTA   150

ACCGTGGGTC CTCTGACAAG TGCCTAACTC GGCCCACCCC TTAGGGTGTG   200

TNTCATCGAA GTGTAGNGAA TGGTGGAACG TTTGTTTGTN GTGTGC   246

(2) INFORMATION FOR SEQ ID :498:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 215 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID :498:

GCCCCTTTAC CAGCAAGTCC TCTACTCAGA AAGAACTGAC CCACGCAAGT   50

CTGGGAGAGT GACTAGTTCA AATGTGCAGG GCTGAAGCTT CCAAACACAG   100

CCACTATTTT TGTTGTATAT CTTCATCTCA ATGGCGACAT GGCCACTGCC   150

CAAGGAACTT GTGGCAGGGA TCCCAAGGTG AGGCAGCAAC AGATGTCTGT   200

GAACATCGTG CGTTA   215

261

(2) INFORMATION FOR SEQ ID :499:

    (i) SEQUENCE CHARACTERISTICS:
       (A) LENGTH: 195 base pairs
       (B) TYPE: nucleic acid
       (C) STRANDEDNESS: double
       (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID :499:

GATNGCCACA TCTCAACACT ATACNACTCG CTNTTCGAAT TCGCCGTNTT   50

AGAACCGCAA GAGACCTTGA TTTAGTCACG CGAGTTCGTC TTCCTGTTCC   100

ACANGAAAAT AAAGCTAGGG AGGTGATTTA TCTATCCGAG AAAAAAGCCG   150

GGGACTGGTG GAANNNGAAC AATGNTCTCT NTGTCGTACT ACAAT   195

(2) INFORMATION FOR SEQ ID :500:

    (i) SEQUENCE CHARACTERISTICS:
       (A) LENGTH: 260 base pairs
       (B) TYPE: nucleic acid
       (C) STRANDEDNESS: double
       (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID :500:

GCGGCCTTGG GGGCACCGGC GTGTCCTGCC CAGTGGGATT AAAAAATAAT   50

GCTCCCCACA TGGCGGGCCT TTGAGGTTCC AGTAAAAATG CTTTCAACAA   100

ATGGGCAATG CTTGTGTGAT TCACAATCGT GGCATTTAAA GTGCACAAAG   150

TACAAAGGAA TTTATACAGA TTGGTTTACC GAAGTATAAT CTATAGGAGG   200

CGCGATGGCA AGTTGATAAA ATGTGACTTA TCTCCTAATA AGTATGGGGG   250

262

GTGGAGCTGT   260

(2) INFORMATION FOR SEQ ID :501:

5   (i) SEQUENCE CHARACTERISTICS:
                (A) LENGTH: 268 base pairs
                (B) TYPE: nucleic acid
                (C) STRANDEDNESS: double
                (D) TOPOLOGY: linear
10

           (xi) SEQUENCE DESCRIPTION: SEQ ID :501:

15   AAAGGCATAG TAAAAATAAA ATCTACGTAA GTAACAATCT AATACTATAT   50

     TAAATNCGTT GCTACAAAGT GTTTTGTTTC TCTAAAAAGT AGTTTTTGCA   100

     TATCATTCGA CCTCTTCACC CATNTGCTGG CTTATTTGCT TTATATACAA   150
20
     CAGTTAAAAT TTGTGCACTA AGCTGAGCTG CCTTCACAAT GTGGTTCAGA   200

     CAAAATGCAC CCAAAGAACT ACATGTTAAG AGAGTTTATG TCCATGCTCA   250

25   ACCATGGCTT GCCCAAAT   268

     (2) INFORMATION FOR SEQ ID :502:

           (i) SEQUENCE CHARACTERISTICS:
30   (A) LENGTH: 152 base pairs
                (B) TYPE: nucleic acid
                (C) STRANDEDNESS: double
                (D) TOPOLOGY: linear

35

           (xi) SEQUENCE DESCRIPTION: SEQ ID :502:

     AAAAACTCTA ATCCAGACTA CAGTTGTCGA GATTCAAGTC GTGAGTGCAG   50
40
     GAGCGTACAC AGTGCCGTGC TGGCACATGC ACTGCACACG CTCTAGAGAC   100

263

```
GCTGACCTGG CTCTCGGAAA CGCAGGAGTC TTTCTGAGCC AGCTCAGAAA      150

CC                                                         152
```

5   (2) INFORMATION FOR SEQ ID :503:

           (i) SEQUENCE CHARACTERISTICS:
                (A) LENGTH: 141 base pairs
                (B) TYPE: nucleic acid
10   (C) STRANDEDNESS: double
                (D) TOPOLOGY: linear

15   (xi) SEQUENCE DESCRIPTION: SEQ ID :503:

```
CCCTGACCCC TCCTCACCAC CGCGCTGCAC CTCAGGGTTA CAAGAAGAAC      50

TAGGAAATAA CGCCGGCCAC CNGACCCCTG GAGAGGGGCC GGCTAGAACA      100
20
NTTCTAAGAT CCNGCACAGC AGGTCCCGNA TGTNGAACCT T               141
```

       (2) INFORMATION FOR SEQ ID :504:

25   (i) SEQUENCE CHARACTERISTICS:
                (A) LENGTH: 107 base pairs
                (B) TYPE: nucleic acid
                (C) STRANDEDNESS: double
                (D) TOPOLOGY: linear
30

           (xi) SEQUENCE DESCRIPTION: SEQ ID :504:

```
35  CACACGACAC ACGACACGCA CGCAAACACG CCAGACGCGA CAGAGCGCGC      50

    GCGGGAGCGG AGCAGCGGAA GCGCAGCAGC GCACACGAGA GATAAGGGCG      100

    GCCGAGC                                                   107
```
40
       (2) INFORMATION FOR SEQ ID :505:

(i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 193 base pairs
    (B) TYPE: nucleic acid
    (C) STRANDEDNESS: double
    (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :505:

ACCCTCTTCT GATAAATTTG AGGGCCCGTT TGTCCTTGGA GACCTTCAGT   50

AACTCCATGG CGCGCCATCG TACGGGGCAA ANACACACCT CCCGAATCAT   100

GTCCCGCACG AACTTGGTGT GTTTGGTCAG ACGCCCGCGT TNGGCNTGTG   150

CTGGGCTTGC TCACGTTCTT GTCACTTTGT GGCCCTTGTT GAG   193

(2) INFORMATION FOR SEQ ID :506:

(i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 274 base pairs
    (B) TYPE: nucleic acid
    (C) STRANDEDNESS: double
    (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :506:

ACATGGATAG GCGTATGCAT ACTACGCTAA GGAGAAACAA TGTTCCTACA   50

TATTACGGGT AGTGAGAACA TTATCTGTAT AACAGGGAAC TGTGATTATT   100

TAAAAATAGC AGAACTTATT ANCTGTGCTT TAGAAATAAC TGTATACAGT   150

GTTATAAGTT GAAAAGAACT CAAAATAACT AATAAATATA ACCTATGTAT   200

TAGAATTAAA AAAGCTGCTT TCTGTGAAGT CAATCAGCTA TATTAAAAAA   250

TGACACAAAT CCAAACAAGA TGCA   274

265

(2) INFORMATION FOR SEQ ID :507:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 281 base pairs
5   (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

10

    (xi) SEQUENCE DESCRIPTION: SEQ ID :507:

CAGGAGAAGG AAGGTTGTAC GTGGACACTA TAAAGGTCAG CAAATTGCAA   50

15 AGTAGTCCAG GTTTACAGGA AGAAATATGT TATCTACATC GAACGGGGCA   100

GCGGGAAAAG GCTAATGGCA CAACTGTCCA CGTAGGCATT CACCCCAGCA   150

AGTGGTTATC ACTAGGCTAA AACTGACAAA GACCGCAAAA AAACCTTCAA   200

20 CNGAAAGCCA AATGTNCCAG CCGGAAAGGA AAGNGCATAC AAGGAAGAAA   250

CCATTGAGAA GATGCAGGAG TAAAGTATTA T   281

25 (2) INFORMATION FOR SEQ ID :508:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 180 base pairs
        (B) TYPE: nucleic acid
30   (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

35   (xi) SEQUENCE DESCRIPTION: SEQ ID :508:

AGGGNTGCTA ANNTATTGGT GGGCAGGAGG CATCGCTGAT GATCTTGAGG   50

CTGTTGTCAT ACTTCTCATG GTTCACACCC ATGACGAACA TGAGGCATCA   100

40 GCAGAGGGGA CAGAGATGAT GACCCTTTCG CTCCCCCCTG CAAATGAGCC   150

266

CCAGCCTTCT CCATGGTGGT GAAGACGCCA   180

(2) INFORMATION FOR SEQ ID :509:

(i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 104 base pairs
    (B) TYPE: nucleic acid
    (C) STRANDEDNESS: double
    (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :509:

AAATGCAAAA CTCACCGTGC ACACTCCTAG ATCCCTGCCA CAAAGAAATC   50

TTTGAAAAAT GAAGTCTTCC TTTCGGACAA TATACCATTN GAGTTTCTCT   100

ATTT   104

(2) INFORMATION FOR SEQ ID :510:

(i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 171 base pairs
    (B) TYPE: nucleic acid
    (C) STRANDEDNESS: double
    (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :510:

GTNNATACAC AACTAAGTTC AAATAAAAAA ACCAAATNAA AAATNGGCAG   50

GGAAGCTAGA GCCAGAATCA GGAAAATCTG TTTCCTCGTC CCCAGACTCC   100

CGCCAAGCCT ACTCCACTAA CTAACANNGA CTCTATCAAG TTTCTATCAA   150

GACTTGCATC TGNATCTTGN A   171

(2) INFORMATION FOR SEQ ID :511:

267

(i) SEQUENCE CHARACTERISTICS:

    (A) LENGTH: 255 base pairs

    (B) TYPE: nucleic acid

    (C) STRANDEDNESS: double

    (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :511:

```
ACTGTACCTA TCATCCTGAA AAACTTTATG GGGGAGAAAG GTCAGCAGCT        50

TCTCTTTCTT TTNATCGAAA ATAATAAAAC TGCGTATTCT ACTTTAACTA       100

AATGTAAGGA AGAAAATATA CAAGCCCATA TTTAATGTAT TTCTATNCGA       150

GCAACAATAG TTCATATGTT CATGTTTGCT ACTATCACAA TTCAACATAT       200

GAACACAGAT CAGCTCTATA CCATGAATAC TGCTGGAAGT GATGGTTTAG       250

GATTA                                                        255
```

(2) INFORMATION FOR SEQ ID :512:

    (i) SEQUENCE CHARACTERISTICS:

        (A) LENGTH: 210 base pairs

        (B) TYPE: nucleic acid

        (C) STRANDEDNESS: double

        (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :512:

```
GAAAGATTGG ACATGATTGC GTTTATAAGA ATGAGAGTGT TAAATTGGAT        50

TTCTTGCTTT ATTTGTGACA TTTCAGTTTA TTAGAAATCA TGTTACCATT       100

AGAAAAATTG AAGTTTCCTA GTAACAAAGT AATTTGATTT GTGTAACTTG       150

ATAAAAGATT TACTGACTTA AGCTTTTGTT TTTTTTCATA AGCTGCTTTT       200
```

268

GAGCTTTGTC   210

(2) INFORMATION FOR SEQ ID :513:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 222 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID :513:

CTGTACAATC ATCCTGCAGA AAATTGTTTT GGAGAATTCT TGGTAATTGA   50

AGACCAGCAG AGCACCCCTC CCCACCCGCC CCGTAAAAGT GCTTACAATG   100

AACAGGGATT CTTTTCTTTA CAAAAGACCC AAAGATACGT GGACAAAAAA   150

AGAAAAGCTT GAAGTCTCAA TGCCTAATGT GTGCACATAA AACAGGCACG   200

AAGAAACAAA CGTGTGCATC CT   222

(2) INFORMATION FOR SEQ ID :514:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 240 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID :514:

GCAGGAGAAG GAAAAGACAG CAACTCATCC CAGAATTGCC NAATGAAGAT   50

GAGGAGAATC CCCTCAAAGG GATCTGTGTG CTTACAGTGG TGACAGTGAC   100

AATGAGGAGG ACTGATGAGA GACTCAAGAG TGAGGAAGAG AGCTAGCTGA   150

269

CTGNAAGAAA TGACCTGTCT NNTCTNCAGC GCCATTCCCN AACAGATGCC   200

CTAGTCAGGA CCACAACTCT TAAACCTCAT AGCNAAATAT   240

(2) INFORMATION FOR SEQ ID :515:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 183 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: double
            (D) TOPOLOGY: linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID :515:

CAATGCCCAA TCTGAGTGTA TACACATCTT AGGAAAAATA ATCTAANGTA   50

ACTTTTGAGG GTGAGAGNGG AAATAAGAGA TCACATTTAT TCAAGACTGA   100

TCCCTATNAG GAAGGAGAGG CCCAGGCACA GATACCACAA AAGAGCACAG   150

TACCCAGCTG TCCTGGNATT GNTTGAGTGT AAG   183

(2) INFORMATION FOR SEQ ID :516:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 215 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: double
            (D) TOPOLOGY: linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID :516:

TCGCAGCAGA AGGAAGTCGT TGACCTGGCA GCCAAGGGAA CACACAAACA   50

CACTCACACA CACATGCACT CACCTGCATA CACACACACT CATACACACG   100

AACACTCATA CACACANGCT TGTGCACACA TGTTCATGCA CATGCATGCA   150

270

CTCACACTCA TACAAACGCA CATTTAAACA CGTGTGNACA NTGTACTCAG   200

ACACACACAG GTGTG   215

5   (2) INFORMATION FOR SEQ ID :517:

         (i) SEQUENCE CHARACTERISTICS:
             (A) LENGTH: 181 base pairs
             (B) TYPE: nucleic acid
10   (C) STRANDEDNESS: double
             (D) TOPOLOGY: linear

15   (xi) SEQUENCE DESCRIPTION: SEQ ID :517:

         TCGCAGAGAA GGAACAATCA GGGCCATGAC AGGAACCGCA AAGAACCAGA   50

         GGGTATAGGC AGCAAAGAAG GGCACATAAA AAGGCTGCTT CTCAGGAAAG   100
20
         TGTCGCAGTG AGACAAACAC ACATACAGAC CACACACAGA CCACCACCTC   150

         AATCATGGGC CCTAGCCGNC CTNGTAATAC G   181

25   (2) INFORMATION FOR SEQ ID :518:

         (i) SEQUENCE CHARACTERISTICS:
             (A) LENGTH: 260 base pairs
             (B) TYPE: nucleic acid
30   (C) STRANDEDNESS: double
             (D) TOPOLOGY: linear

35   (xi) SEQUENCE DESCRIPTION: SEQ ID :518:

         ATGTAACTCA ATCCATCCGC AAGAAAACCA AACCAACAGA AAAGGAAGCT   50

         GAAGACATGG ACATCGCAAG CCACGCGGTA ATGCATACTT GGCACAGAGT   100
40
         AGCCAATATA GAAGACGTGT GCCTCACACG GTTCACTTTG TTCATCAATA   150

271

AAAGAATATA AAAATCTCGT TCACCCAGTG GTAAGTGTAT TAAAATAGAT   200

CTGTATCATA CACACAGTTT CTCCCGGAGT CGTGAGAATG ACAGGAGGGA   250

CCTGGCAACT   260

(2) INFORMATION FOR SEQ ID :519:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 115 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID :519:

AAGCTAATAC AATGGTCATT TCCAGACAAA TTTAAAGGAA ACACTAAGGC   50

TGCTTCAAAG ATTATCTGAT TCCTTTAAAA TATATGTCTA TATACACAGA   100

CATGCTCTTT TTTTA   115

(2) INFORMATION FOR SEQ ID :520:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 175 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID :520:

CANGTGGCTT CAATTAAACA ATNAGGAGCC TCNNAACATC CTGTCGCAGA   50

AACTCCCAAT ATAAACGCCC CCANACACTA ACACAAAACA GCCTTATTAA   100

CCAGATAAGT TCTCCACTAC CACTCCTAGA TTTGATGTAA CCCTGAATNT   150

272

GACTNATAGN TNGACCCACC TGTGA   175

(2) INFORMATION FOR SEQ ID :521:

5   (i) SEQUENCE CHARACTERISTICS:
                    (A) LENGTH: 136 base pairs
                    (B) TYPE: nucleic acid
                    (C) STRANDEDNESS: double
                    (D) TOPOLOGY: linear

10

                (xi) SEQUENCE DESCRIPTION: SEQ ID :521:

15   ATGGAATCAA ACAGCTCTAT AATGAAGATA ATGTCTCAGA AAATGTGGGT   50

        TCTGTGTGTG GCACTGATTT ATCAAGACAA GAGGGACATG CTTCCCCTTG   100

        TCCACCTTTG CAGCCTGTTT CTGTCATGTA GTTTCA   136

20

        (2) INFORMATION FOR SEQ ID :522:

                (i) SEQUENCE CHARACTERISTICS:
                    (A) LENGTH: 200 base pairs
25   (B) TYPE: nucleic acid
                    (C) STRANDEDNESS: double
                    (D) TOPOLOGY: linear

30
                (xi) SEQUENCE DESCRIPTION: SEQ ID :522:

        AATGGAGCAA TTCATCCAGT TCTTCTAGAA ACAGCTCAGA ATCAAAGCTG   50

35   GATATATTTT GTGTCTTCTG TGACTGTTCA TTCATGGAAG GAAGCAGACT   100

        GCTTTGGGCA GAATTATTCT CCTGACTACT TGAGCTAGTA GACTAGGAAC   150

        TATTCCATAA GAGGAAATCC TGTAAGTCTT AAATCCCCAC TGGAGAAAGC   200

40
        (2) INFORMATION FOR SEQ ID :523:

273

(i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 204 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :523:

AGTAAGGTTT TGCATCCTTT GATCAGCAGG TAACTGACGA ATTCTTGAGT   50

CGAAGATTAT ACCTTGATGA GCTTTGATGA GCTCTTGCAA ACGAATGAGA   100

CCAGTGCTGT CATCATACAC AACCATGACG TTTTCCACTT GAAAAACTGC   150

ACCAGGTCTA AAATGCACGC TGAGTGAAGA GAAGTCTGGG CAGAGACTGA   200

CATA   204

(2) INFORMATION FOR SEQ ID :524:

        (i) SEQUENCE CHARACTERISTICS:
                (A) LENGTH: 168 base pairs
                (B) TYPE: nucleic acid
                (C) STRANDEDNESS: double
                (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :524:

ATATCTGTCT CATCATCCCA AGGTTTCACA TCTAGTAAGA TGGAAGACTT   50

GGCAACAAGT GCAGGTTTTT TGGCTTTCTT TGATTCATAT TGTGCAAGAC   100

GTTCTTCCCT CAGCCTCTTT GCTTCTTCAC TTNNTCTAAN ATAATCCAAA   150

GAGGTCAATG TATCATCA   168

(2) INFORMATION FOR SEQ ID :525:

274

```
      (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 291 base pairs
          (B) TYPE: nucleic acid
          (C) STRANDEDNESS: double
          (D) TOPOLOGY: linear



      (xi) SEQUENCE DESCRIPTION: SEQ ID :525:


      AAACTGTTCT TTAAAAGGCC TCTCCTGGTT ATTAAGCCAG GAAGAGAAGT          50

      AGAATCTCGA ATCACCTAAN GGAAATGGTG ACACAGGTTG TCCTTTCTCA          100

      GCCGTTGGTT TCCTTTCATC TCTGAAGGCC TGTAGTACCA TGAGGAAAAC          150

      ATTTAATTTA GAGGGTGAAC CCAACAGTAG GAAGCTGAAA GCAGAAGTGT          200

      TTATCTCCCT CTGCATTCAG ACCAGGCTCC TTAGTGCACT CATCAGACTA          250

      TCGCTGCCCC TGCTGTCTGC TGTTGAGCCT TCACCACCAC T                  291


      (2) INFORMATION FOR SEQ ID :526:


          (i) SEQUENCE CHARACTERISTICS:
              (A) LENGTH: 207 base pairs
              (B) TYPE: nucleic acid
              (C) STRANDEDNESS: double
              (D) TOPOLOGY: linear



      (xi) SEQUENCE DESCRIPTION: SEQ ID :526:


      CATCCGCGTG CTGGACCCCT TCACCATCAA GCCCCTGGAC AGAAAACTCA          50

      TTCTCGACAG CGCTCGTGCC ACCAAGGGCA GGATCCTCAC CGTGGAGGAC          100

      CATTATTATG AAGATGGCAT TGGTGAGGCT GTGTCCNNNN GTAGTGGGCG          150

      AGCCTGGCAT CACTGTCACC CACCTGGCAG TTAACCGGGT ACCAAGAAGT          200
```

275

GGGAAGC   207

(2) INFORMATION FOR SEQ ID :527:

       (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 218 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: double
            (D) TOPOLOGY: linear

       (xi) SEQUENCE DESCRIPTION: SEQ ID :527:

AGCATTCCGT AAGGACGGAC GTGTTCAAGG ACAACTTTGA TGAGATGGAC   50

AGGTCTAGGG AGGTTGTTCA GGAGCTCATT GATGAGTACC ATGCGGCCAC   100

CCAGCCAGAC TACATTTCCT GGGGCACCCA GGAGCAGTGA TTTCCCTCCC   150

CACTACTTCT TTNCTTAGAT GGTAACCACA GCCTCGACCA TGCCTGCTCC   200

CTCTGACCCA GCTTCACC   218

(2) INFORMATION FOR SEQ ID :528:

       (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 229 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: double
            (D) TOPOLOGY: linear

       (xi) SEQUENCE DESCRIPTION: SEQ ID :528:

AACCTNATGA CTCTCCATCC CCTTGAACCA AACATCTAGC ACTCAGCTCC   50

AGCATATTTC ACCATTCAAC CCGAAATTCA CAAACGCTAC TTGTCGACTT   100

GTAACCAATT TACTCAGCAA GTGCTGACTC CTTAACGGAT CATCCCCATC   150

276

```
CTNCGCTGCA AGGTGACTCA CTAAAATCAT NTGTTAACAC CAACATTATT        200

TTTACACCCA GTGTGTAAGC CAGAAGGGC                               229
```

(2) INFORMATION FOR SEQ ID :529:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 117 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID :529:

```
ATATTATTCA TCATCCCAAG GTCACATCTA GTAAGATGGA AGACTTGGCA         50

ACAAGTGCAG GTTTTTGCTT TCTTTGATTC ATATCGTGCA AGACTTCTTC        100

CTTAGCCTCT TTGCTTC                                            117
```

(2) INFORMATION FOR SEQ ID :530:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 179 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID :530:

```
TCGCAGCAGA AGGAAGCTGA TCCACCATCC GGACAACCCG AACCCAAGCT         50

GAAGACGAGA AATGATCCAG AAAGAATGTG CTGCAATCCG GTCATCTTTT        100

AGAGAAGAAG ACAATACACA CCAATGTCGA AATGTGGCAA AATTACTGTA        150

TATGCACATG CTGGTGCTAC CCTCTCACT                               179
```

277

(2) INFORMATION FOR SEQ ID :531:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 204 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID :531:

AAAGCATTCA AGTAAGAATA TGGCAATAAA AAACAAAAAT ATCTTCTCAG   50

CATTCAAAAC AAAACGCATA AGTCATTCCT AACTTNAGAG CTTTATAGCA   100

TTTTCCTAGA CAGGAAGGGA AAAAACAGTT AGCATTTAAA AGTCCGGAAA   150

GCTTTTTCGT TGNNTTAATT ACATCAACNN TCTGCCTTTG TCCAAATCCC   200

TTAT   204

(2) INFORMATION FOR SEQ ID :532:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 183 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID :532:

AAAGGAGCTC AGAACTTCAG CTTGAGCAGG AAGAGGAGGA CGTGCCAGAC   50

CAGGAACAGA GCAGCAGCAT CGAGACCCCA TCAGAGGAGG CGGCCTCTCC   100

CCACAGCTGA GGGGCTGGGC TAGGGGTGGG TGGAGCCCTT TTAAAATACC   150

CTTTCTTCAA AACTTAGCTC TGAATGGAGA AAC   183

278

(2) INFORMATION FOR SEQ ID :533:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 287 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID :533:

GAAACAAGTT CTCGCTCATC CCTGCATTTC TGCCAACTTC AGCTTGCAAT   50

ATTTATACTC CAGACTATTT TCATCAGACA AAAACCAGTA AGCAGGGTCC   100

TCTTTGAGAA GAGTTCTCTC TTTGGGAGAC AGGCTGCCTT CGATGACACG   150

TTTCACAAGC TGGTTGATGG TGCCCACTAC CCGTGATCTG CTCGCTGGGG   200

GACAGCATCA CTCAGACTAC TTGGAGCCTT GCCTGAATTT CAGGTTTCGT   250

AGGAGGAATA ATTTTCTCCT TCTNTNGTAT CGNCTCT   287

(2) INFORMATION FOR SEQ ID :534:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 154 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID :534:

AGCCACTGCC CCTCTTGTCT ACGTATTCCC AAAATTAAAC TTTGATGCCT   50

GACTTTTTGC AGTCAGTTTT AAGTGAGCTC CCTGAGGTGC CAAGGCCATG   100

GTGTCCCCCT GCTGCGTCTG TTCGTCAGCT GAGTTCTTGT GAATCTNTGT   150

TTAG   154

(2) INFORMATION FOR SEQ ID :535:

     (i) SEQUENCE CHARACTERISTICS:

        (A) LENGTH: 212 base pairs

        (B) TYPE: nucleic acid

        (C) STRANDEDNESS: double

        (D) TOPOLOGY: linear

     (xi) SEQUENCE DESCRIPTION: SEQ ID :535:

GATTACCCTA TATCTACAAT TNGAGGTAAA ATAGAAGCAA CACATAAAAG   50

GGCCTATTTC TGCTACCATG TCATATAATT CTCCATAGTG AATATTGTGA   100

TAAAGCTACT GAAAACTATG CCTCACAGAG CCTAGCTTCT TGTAGAGCTG   150

GTATTTTACA ACTCGCATTG CTTGGAAATC TCAACACACG TAAGACTCTC   200

CTAGGAAGGC AC   212

(2) INFORMATION FOR SEQ ID :536:

     (i) SEQUENCE CHARACTERISTICS:

        (A) LENGTH: 168 base pairs

        (B) TYPE: nucleic acid

        (C) STRANDEDNESS: double

        (D) TOPOLOGY: linear

     (xi) SEQUENCE DESCRIPTION: SEQ ID :536:

GGAAGCTCAA TGTCCGGCAG GTCAATGCTT CNCGGACACG GATCATTTTT   50

ATCTGATTCC AGCCTGCTTG CAACCCTGGA ATCCTCTTGT TCCCTGCTGC   100

CTGCCCCTTG GGAAGGNACA GTGATGTCTT TAGGGGAAGG AGGAGCCCCT   150

NTCGGCAGTT GTCTTACT   168

(2) INFORMATION FOR SEQ ID :537:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 147 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: double
            (D) TOPOLOGY: linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID :537:

CGGATCATTT TTATCTGATT CCAGCCTGCT TGCAACCCTG GAATCCTCTT   50

GTTCCCTGCT GCCTGCCCCT TGGGAAGGNA CAGTGATGTC TTTAGGGGAA   100

GGAGGAGCCC CTNTCGGCAG TTGTCTTACT AGGNNNNTAA TGAAGTA   147

(2) INFORMATION FOR SEQ ID :538:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 250 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: double
            (D) TOPOLOGY: linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID :538:

GTGGAATCTC AATAATGACA CAAGGTACCA ACTGCCAGCA TTTCTGCGAG   50

GCAATCCTGC TCTTAATCTG CAAGATGGAC CCTTCTGCAG AGAGATTGCT   100

GTGGGTGATT CTAAGGACAG ATTGTTATAT ACGATGTGGG AGAGCAGATT   150

GCTGTTCCCC GCAATGATGA ATGGGCACGG TTTGGCCGAA CACTTGCAGA   200

AATNAATGTA AACCCNAACT GATGTAGAGA GGACGCAGCT GCCCNAATAC   250

281

(2) INFORMATION FOR SEQ ID :539:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 184 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: double
            (D) TOPOLOGY: linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID :539:

    AGAAGGTAAG GGAGTGGGAG GCAGGTGGGT GTTCTGGAGG GGGTATCCTT   50

    GTGCTCTAAG GGTGCTATGT TCGATGCTGG TGTTTCGGGG ATGGTGAATG   100

    CCCTTCTTTA ANNTTAGAGG GAAATCCAAA CCAATAGGCC CCAAGGTTGC   150

    CAGTGGGATA GGGGTGTAAA AAAGTAAATT GGGC   184

(2) INFORMATION FOR SEQ ID :540:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 154 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: double
            (D) TOPOLOGY: linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID :540:

    AACTTATAGA AAAGTAAAGG AAACCCCAAC ATGCATGCAC TGCCTTGTGA   50

    CCAGGGAAGT CACCCCACGG CTATGGGAAA TTAGCCCGAG GCTTANCTTT   100

    CATCATCATG TCTCCCAGGG NGTGCTTGCA AAGAGATATT CCGCCAAGCC   150

    AGAT   154

(2) INFORMATION FOR SEQ ID :541:

282

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 175 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: double
5   (D) TOPOLOGY: linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID :541:
10

    AATTGAATTC TTAAGAAGCT GTCAAATATG GCAGTCTTTT GATGTTAGTA   50

    ATTTTGTTTT CTTCTGTGTT ATTGGTTCAA AGTACTGGCC TTTTCCTTCA   100

15 TTTCCAGTAA TTATTTTATA ACTATCACTT TTAATTGAGT GGAAATTAGA   150

    TGATTTGGTT ATACTGTGAA ACAGC   175

    (2) INFORMATION FOR SEQ ID :542:
20

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 221 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: double
25   (D) TOPOLOGY: linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID :542:
30
    AAGTACCTTT TCCTGCAGCT GCCCGTATGC CTGAGTGACT AAGGGGCAGT   50

    CGTGAGAGGC AGAGTCCAAG ATCTCATTGG TCGTTTCCAG ACTGCCGTCC   100

35 AGCCGTGCTG CTTCATCAGG GCACACTCGC CGCCCTCCTG GGGCCAGGTT   150

    GCACATGTAC AGGTACCCGT CGGCGCACCC ACCAACAACG CGGTCTTCTG   200

    AATCGCGACT GGCNAACAGA T   221

40
    (2) INFORMATION FOR SEQ ID :543:

283

```
          (i) SEQUENCE CHARACTERISTICS:
               (A) LENGTH: 186 base pairs
               (B) TYPE: nucleic acid
               (C) STRANDEDNESS: double
5              (D) TOPOLOGY: linear


          (xi) SEQUENCE DESCRIPTION: SEQ ID :543:
10
     AAGTAGATAG CTTGCATCCT GACACCGTGG CAAAGTTAAG AAAGTTGAAG          50

     GAGAAACATA CCTTGAGAGG GGGTTTTCTT TAAAACTAGT GTTAGAAGCT         100

15   TAGGGATTTT TTTTTTTATT CCTTACTAAC TTTCACCCAG AACCGCTCTA         150

     TTTGACTTGT GCCGACATTG CAAACTTTNT GACAGG                       186

     (2) INFORMATION FOR SEQ ID :544:
20
          (i) SEQUENCE CHARACTERISTICS:
               (A) LENGTH: 153 base pairs
               (B) TYPE: nucleic acid
               (C) STRANDEDNESS: double
25             (D) TOPOLOGY: linear


          (xi) SEQUENCE DESCRIPTION: SEQ ID :544:
30
     AGCATCCTTG CCACCTCCCC ACCCGGGAGT CAAGGGTCGT GGTTCTGCCT          50

     TGAACAGGCC ACAGCCGTAG CTGTAGAGAG GCCAGTGGTA CATCAGCCCA         100

35   CCGACAGGAG GAGGAGCCCT GGCTTGAGGG AAGGGGAAGC CCAGGCCTGT         150

     GCC                                                           153

     (2) INFORMATION FOR SEQ ID :545:
40
          (i) SEQUENCE CHARACTERISTICS:
               (A) LENGTH: 161 base pairs
```

284

```
                    (B) TYPE: nucleic acid
                    (C) STRANDEDNESS: double
                    (D) TOPOLOGY: linear


5



               (xi) SEQUENCE DESCRIPTION: SEQ ID :545:


        GATTCAGCTC CAGCATCCTT GCCACCTCCC CACCCGGGAG TCAAGGGTCG        50
10

        TGGTTCTGCC TTGAACAGGC CACAGCCGTA GCTGTAGAGA GGCCAGTGGT        100


        ACATCAGCCC ACCGACAGGA GGAGGAGCCC TGGCTTGAGG GAAGGGGAAG        150


15      CCCAGGCCTG T                                                 161


        (2) INFORMATION FOR SEQ ID :546:


               (i) SEQUENCE CHARACTERISTICS:
20                 (A) LENGTH: 188 base pairs
                    (B) TYPE: nucleic acid
                    (C) STRANDEDNESS: double
                    (D) TOPOLOGY: linear


25



               (xi) SEQUENCE DESCRIPTION: SEQ ID :546:


        AATAGCCCTG AGGTCATCCT GCAAAGTGCG TATCAAAAAA TACGAAGTTA        50
30

        GGGTGACAAA GTTTGACAGT GATGTTATAC AAGTCAAACT TGGAAGGTCA        100


        TAGTAAGCAT ACCTATGCTG AGAGAAAGCA TCAAATCCTT TGTGTACACA        150


35      TTTAGTTTTA TTGTAACAAA GCAACTTGTA CACTTTTA                    188


        (2) INFORMATION FOR SEQ ID :547:


               (i) SEQUENCE CHARACTERISTICS:
40                 (A) LENGTH: 218 base pairs
                    (B) TYPE: nucleic acid
                    (C) STRANDEDNESS: double
```

285

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :547:

ATNCCTTCTC CATCCANTTA GTTANCAGAA ACTAATCAAA AGAAAGTCTG   50

ACAACTGCAC TCCCCCTTGC ATGCCATTCT CTCAAGCCCA TAATCTTGGA   100

GTATCCACAA CGTGCGAAGG CCTACCCTTT GTGTGTACTC ATCTCACGTT   150

TACGTATTTT GTNGTTGAGG AGCTCCTCTA CAAATGTTGC GTATCTTCCG   200

AATCACTCAT TTAGAAAA   218

(2) INFORMATION FOR SEQ ID :548:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 46 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :548:

GGAGGAGACC ATCAGNCCCG TGAAGACCAC TCCTGACGTC TCGTGT   46

(2) INFORMATION FOR SEQ ID :549:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 146 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :549:

286

AGGGGGCTAA NGGTTGGGGG CAGGAGGCAT TGCTGATGAT CTTGAGGCTG   50

TTGTCATACT TTTCACGGTT CACACCCACG ACGACACGGG GACTCAGCAG   100

AGGGGCAAGA CACGACCTTT AGTTTCCCCC TTGCGATAAN CTTCNC   146

(2) INFORMATION FOR SEQ ID :550:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 221 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID :550:

AAATATNGAN TATCCATCCC CTCAAGCATT TATCCTTTGT GTTACAAACA   50

ATCCAATTAT ACTCTTTCAG TTATTTTAAC ATGTACAATT AAATTATTAT   100

TGACTCTAGT CACCTTGTTG TGCGAGCAAG TACTAGGTCT TATTCATTCT   150

TTCTAACTAT TCCAGGCCCT TTTTAATCAA GAAGGCTCCC TAGACCAAAA   200

TTTTAAAAAG ACAATGCTAG G   221

(2) INFORMATION FOR SEQ ID :551:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 116 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID :551:

AAACATCGTT TATTCATCCA GCAGTGTTGC TCAGCTCCTA CCTCTGTGCC   50

287

AGGGCAGCAT TTTCATATCC AAGATCAATT CCCTCTCTCA GCACAGCCTG   100

GGGAGGGGGT CATTGT   116

5   (2) INFORMATION FOR SEQ ID :552:

            (i) SEQUENCE CHARACTERISTICS:
                (A) LENGTH: 150 base pairs
                (B) TYPE: nucleic acid
10   (C) STRANDEDNESS: double
                (D) TOPOLOGY: linear

15   (xi) SEQUENCE DESCRIPTION: SEQ ID :552:

CTCATCCTCT CCTATTACAT AGTGAAGCCC ATGNCAAATA GGAAGAAGCT   50

CAGTATCGCT CCTCCCACCA TAACCCCCCT TAATGCCTCC TGAACCATAG   100
20
TTNCCTCCAC TATATATCCC CCCATGTTCC TGCTACCCCA AGTTTTCACT   150

(2) INFORMATION FOR SEQ ID :553:

25   (i) SEQUENCE CHARACTERISTICS:
                (A) LENGTH: 189 base pairs
                (B) TYPE: nucleic acid
                (C) STRANDEDNESS: double
                (D) TOPOLOGY: linear
30

            (xi) SEQUENCE DESCRIPTION: SEQ ID :553:

35 ACTTATTGAA ATAGCAGACA TTTCGCTAGA CACTCCAATT AACCTGATAT   50

GAGGCGCTAA TCAATAAAAA AAGTTAAACA TTTGCATGAC TCTACTATGG   100

GAATAAATTA CCTGTTTAAT ACCTCGACTT TTTATAGAAA AATAATGATG   150
40
NCCAAGGTAA ACCAGGTAAC CCAGGCCTGT GAACTATAT   189

288

(2) INFORMATION FOR SEQ ID :554:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 198 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID :554:

ACTTATTGAA ATAGCAGACA TTTCGCTAGA CACTCCAATT AACCTGATAT   50

GAGGCGCTAA TCAATAAAAA AAGTTAAACA TTTGCATGAC TCTACTATGG   100

GAATAAATTA CCTGTTTAAT ACCTCGACTT TTTATAGAAA AATAATGATG   150

NCCAAGGTAA ACCAGGTAAC CCAGGCCTGT GAACTATATG CCTGGAAC   198

(2) INFORMATION FOR SEQ ID :555:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 97 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID :555:

CAAGCTGAGG AGCAAGGAGA GCCAGTCTGA GTCCCAAAAC TGAAGAACTT   50

GAGTCTGATG TTCGAGGGCA GGAAGCACCC AGCACAGGAG AAAGATG   97

(2) INFORMATION FOR SEQ ID :556:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 269 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double

289

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :556:

TCTGCTGTCT GTCGCAGGAG AAGGAATGTC AGAAACTTCA TCCTCTTGTT   50

GGGGAATGCA CCCTCNTGAG TAGGCTGACC CATGAGGCTG TGGGAATTGA   100

GTCTTAGGAC ACAGAGACCA GGGTGTTGAA TTTTCTTCCC TGCCCCTAGG   150

CTGTTCAGGT CTTCCTGCAG CAGTCAGGGC TGCAAGCCCT GGAAAGGCAT   200

CAAAAGAGGC CCAGCTCCAG GATCGTGTGT ATGCTCTCCA GCAGACAGCT   250

CTTCAAGGGT GATCTTGTT   269

(2) INFORMATION FOR SEQ ID :557:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 245 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :557:

ACTCCCTCAA GGTCGTGCGT CTAAGCCTAC AAGAAAGTTT GCCTATCTGG   50

ACCCTGNCTC ACGAGGTTGG CTGGAAGTAC CAGGCAGTGA CAGCCACCCT   100

GGAGGAGAAG AGGAAAGAGA AAGCCAAGAT CCACTACCGG AAGAAGAAAC   150

AGCTCATGAG GCTACGAAAC AGGCCGAGAA GAACGTGGAG AAGAAAATTG   200

ACAAATACAA AGGTTCTCAA GACCCACNNA CTCCTAGNTT NAGCC   245

(2) INFORMATION FOR SEQ ID :558:

290

            (i) SEQUENCE CHARACTERISTICS:
                (A) LENGTH: 183 base pairs
                (B) TYPE: nucleic acid
                (C) STRANDEDNESS: double
                (D) TOPOLOGY: linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID :558:

    GAATTTAAAA AAAAAGAAAG AAAGAAAGAA AGGTTCCATC TTAGATTCTC   50

    ACAACCTTCG TTCCGCAGTT CATTAATCCG ACTCTGATGC TAAGGTGACA   100

    GTGTATGTAA GTAGATTTTT GTTTTCAGTG AAGGAGACCT GGGAAAAGAT   150

    GGATTTCTCT CTGTATCTTA AGAGTTATCA GAT   183

    (2) INFORMATION FOR SEQ ID :559:

            (i) SEQUENCE CHARACTERISTICS:
                (A) LENGTH: 116 base pairs
                (B) TYPE: nucleic acid
                (C) STRANDEDNESS: double
                (D) TOPOLOGY: linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID :559:

    GTCATCTTTG GAAAGTGAGA TAACCAAGGA AATAATCGAA GGAGTTAGGG   50

    AGATGATTAC GTGATAATGA CTTTGGGCGC TTAACCTTTG ATCCCGGGTA   100

    TGCTNAAGAA GCTGAC   116

    (2) INFORMATION FOR SEQ ID :560:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 160 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: double

291

(D) TOPOLOGY: linear

5   (xi) SEQUENCE DESCRIPTION: SEQ ID :560:

CCTTGATGAT ACCATTATCC TCATTATAGA TGATGCACGG GCCCCTGCGC   50

TGGATACGGC GACGGTTTCT CATTTGCCTT TGTCAGCTCT CATTCGCTGA   100

10

GAGGCATAGA CCTTTTTGAT ATCATCAGGC TTTCCGTTTT TAGGAGCAAA   150

ACAGCTTCTT   160

15   (2) INFORMATION FOR SEQ ID :561:

          (i) SEQUENCE CHARACTERISTICS:
              (A) LENGTH: 101 base pairs
              (B) TYPE: nucleic acid
20   (C) STRANDEDNESS: double
              (D) TOPOLOGY: linear

25   (xi) SEQUENCE DESCRIPTION: SEQ ID :561:

GCAGTTGGCA GGTGCACTAT CCCAGATGGG CCACTAATAG AAAGTTCCGC   50

AAATGCACCC CGTTCCCCTG TGCGAGATCG TTTGAATNAG ACCAGAAACT   100

30

G   101

      (2) INFORMATION FOR SEQ ID :562:

35   (i) SEQUENCE CHARACTERISTICS:
              (A) LENGTH: 183 base pairs
              (B) TYPE: nucleic acid
              (C) STRANDEDNESS: double
              (D) TOPOLOGY: linear

40

292

(xi) SEQUENCE DESCRIPTION: SEQ ID :562:

ATAAGTTATA GCAAATACAG TCTTCACAGA TTTGAGTAAC TTTATTCGAT   50

TTTATAGTGA TTTCTTAAGG CCTATATCCA ATGAAACCAT TTCCAAGCTC   100

TATGAGGAGT GGAATTTTAG ATGTCTATTA CATTNGTCTT TTAAAAGAAA   150

AATGCTTAAC NNCTAGAATG AGCAAGATTA CTT   183

(2) INFORMATION FOR SEQ ID :563:

       (i) SEQUENCE CHARACTERISTICS:
           (A) LENGTH: 187 base pairs
           (B) TYPE: nucleic acid
           (C) STRANDEDNESS: double
           (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :563:

AGAGACACGT GAAATTCATA TCTCAAANNC ACAGAGCTGA GACTTTGGGC   50

CTAAATACTG TACCACTGGT TCCCTGAACC AAGGAAGAAA AGTGTCGGTA   100

AAGGCCCGTT AAGACAAGAT GGCAAGGAAA AGCACCTTAA ACAATGGTAA   150

GATTTATGTT AGATCAGTGG TAAGAGTTTC TAGTGAC   187

(2) INFORMATION FOR SEQ ID :564:

       (i) SEQUENCE CHARACTERISTICS:
           (A) LENGTH: 213 base pairs
           (B) TYPE: nucleic acid
           (C) STRANDEDNESS: double
           (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :564:

GGGACCCCAA ATCACATCCA GAATACTAGA GTGAGGCAGC TGCAACATGA   50

CACAGAAAAA TGGAATCAGG ATTTAGGGGA ATTGGATTTC AGTGCCTATT   100

GAGACACGAT CTAGGAAGCC TACCACTTTG GCTGCTCACT GTATGCACAC   150

AACCCNANNA NAATNGATGA AAACAAGAAT GTACAGCATG CTCCTAACAC   200

AANGTGACTA TTC   213

(2) INFORMATION FOR SEQ ID :565:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 167 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID :565:

TCCATCTGAC ATCGCATTTC CATAGAAATG GCCAAAGAAA GAAGGTCCTG   50

GGGTTTTTCA TAGAAAGCTC AAAAAGTTCA ACCTTGATGC TATCCCCCAG   100

CCCAATACAA AATACACAGA AAAAGCAATT ATTAAAATAC TGGCTTCGGT   150

TTCTTTTTTT CCTTTAA   167

(2) INFORMATION FOR SEQ ID :566:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 128 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID :566:

294

GAAGATACAG AACCATCCGT GAAAATCATT TAGCACTGGA GACCTTCTTT   50

GTATTACTTC CTNGTTACTA GACCTCTAA TTCAATGGGG CCCTGCTGGT   100

TTGTCGATGA ATTGAGCAAC TGAGAACG   128

(2) INFORMATION FOR SEQ ID :567:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 202 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID :567:

GGAGGCTCGG GAGTAGCATC CTCAGGAGTA GTGTAGCGAG CAAATTTGGA   50

AAGTAGTCCT CAATCTTCGA TTTCCCAGCA AGGACTTTCT CAGCNAGCGA   100

TCTCGNTTGT TGAGGAACGG ATCAAGAGAT GNNNGTNTAG CTGTNNTGTT   150

GTTTAGATGT CTTGAAGAGG TTAGAGCCTC CTGTAGGCGG TTGGNNTGGG   200

NG   202

(2) INFORMATION FOR SEQ ID :568:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 152 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID :568:

ATGTCATGAT GCCTAACTCA TACACTCTTT GCCTCAAATA TAATTACTAA   50

295

AAACAAATAT AGTATAAACA TTAAACAAAT GAACAATAAT CATCAATAGA   100

CGGGTTACTT TCAAGGAAGA GTTGTTTTGT GACAAATTCT ACTCTTGATC   150

TA   152

(2) INFORMATION FOR SEQ ID :569:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 181 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: double
            (D) TOPOLOGY: linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID :569:

CAGGTCCGCG TGCTCTCCGC ACCACCCCAC TTCATTCCGG CCAAACCAAC   50

CGCACCCCTG AATTTCTCCG CAAATTTCCT GCCGGCAAGG TCCCAGCATT   100

TGAGGGGATG ATGGATTCTG TGTGTTTGAG AGCAACGCCA TTGCCTATTA   150

CGCGAGCAAT GAGGAGCTGC GGGGAAGTAC T   181

(2) INFORMATION FOR SEQ ID :570:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 157 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: double
            (D) TOPOLOGY: linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID :570:

ATCCCTTGGG AGTTTATTCT CCTGGTAAGC TGTAATTGCA TATCCAGTTT   50

AACTGGACTG GGCTGTGTTG GGCGAGGATC NGCAGGGTTT TTTCCTCNNT   100

296

NGAAAGATGA AATAGATTNT TGAGCACTGG NTGCAGAGCC AAAATGCNTA   150

ATGCTTT   157

5   (2) INFORMATION FOR SEQ ID :571:

           (i) SEQUENCE CHARACTERISTICS:
               (A) LENGTH: 193 base pairs
               (B) TYPE: nucleic acid
10   (C) STRANDEDNESS: double
               (D) TOPOLOGY: linear

15   (xi) SEQUENCE DESCRIPTION: SEQ ID :571:

       GGCACTAAAG CCTTTAATAA TACGAGATGA AATGCAACNG TGNNATGACA   50

       AGTAAGTGAG CCTGACCTGG CATTGCCTCG CCTCACCGCT GGCTTTGACC   100
20
       AGGGTATGAT CTTTAACTTT TCTGAGCTGA TTTGATCGTG GTCTTTACAC   150

       ACAGGTGGTC GTTCCTGTTT GGACACTGTT TTATTTGTTT GAC   193

25   (2) INFORMATION FOR SEQ ID :572:

           (i) SEQUENCE CHARACTERISTICS:
               (A) LENGTH: 179 base pairs
               (B) TYPE: nucleic acid
30   (C) STRANDEDNESS: double
               (D) TOPOLOGY: linear

35   (xi) SEQUENCE DESCRIPTION: SEQ ID :572:

       TCGCAGGAGA AAGAGGTTTT CAGAGGCCCT GAGGACATGG CTGCCCTTGA   50

       GAAGGATTTG AGGAGGTTGG TGGAATTTGT TGAAGGAGAG GGCGAGGAAG   100
40
       AAGGAGAGGA TACTAAAGTT AAAACGTCAC AAGGTGTGCT TTTAAGGGAG   150

CTTTCCTGTT TTAAACATGA AAGTGTGGC   179

(2) INFORMATION FOR SEQ ID :573:

     (i) SEQUENCE CHARACTERISTICS:
         (A) LENGTH: 189 base pairs
         (B) TYPE: nucleic acid
         (C) STRANDEDNESS: double
         (D) TOPOLOGY: linear

     (xi) SEQUENCE DESCRIPTION: SEQ ID :573:

AGGACCTCTA AGACATCCTT ATGACGACAG TTTTGTCCAA GGGGATATCC   50

ACAGAGTACC TTGTGGCATT AGGTGATTGT AGTCATACAC TTTAAAAAGA   100

TTTTATTTCT GATCTTTTGG CGATCTTCTT CTTGCCCATG NNGCTGTTAC   150

TTNGCNCGGG NAGCGGTTAA TTCTANCCGC TAGGTGTGC   189

(2) INFORMATION FOR SEQ ID :574:

     (i) SEQUENCE CHARACTERISTICS:
         (A) LENGTH: 262 base pairs
         (B) TYPE: nucleic acid
         (C) STRANDEDNESS: double
         (D) TOPOLOGY: linear

     (xi) SEQUENCE DESCRIPTION: SEQ ID :574:

GTGCCTTCTA GGTTTTGAAC TTCTATGCAT TAGCGCAGAT GTGGAATGCG   50

TAAAGGTGTT CATAGTTTGA CTGTTTCTAT GATGTTTTTT CAAAGAATCG   100

TCCTTTTTTG AACTATAATN CCCCNCGGTT ATTTTACCAT CACAGTTTAA   150

ATGTATATCT TTTACGTCTC TACTCAGACC ATATTTNAAA GGGGCGCCTC   200

298

ATTATGGGGC AGAGAACCTT TTAATAAGTC TCATTAAGAT CTGAATTTTG   250

GTTCTAAGCA TT   262

5   (2) INFORMATION FOR SEQ ID :575:

              (i) SEQUENCE CHARACTERISTICS:
                     (A) LENGTH: 56 base pairs
                     (B) TYPE: nucleic acid
10   (C) STRANDEDNESS: double
                     (D) TOPOLOGY: linear

15   (xi) SEQUENCE DESCRIPTION: SEQ ID :575:

CCAAGGAACC ATCTGCGCCG CAAGCCAGAC CCCACAAGAC CTAGNTTGGT   50

CCTGAC   56
20
       (2) INFORMATION FOR SEQ ID :576:

              (i) SEQUENCE CHARACTERISTICS:
                     (A) LENGTH: 158 base pairs
25   (B) TYPE: nucleic acid
                     (C) STRANDEDNESS: double
                     (D) TOPOLOGY: linear

30
              (xi) SEQUENCE DESCRIPTION: SEQ ID :576:

GCGAGTCTCA AAGAGTAGAG GAGCGTCTAC TATCTTTCAA CTCCGATCTT   50

35   CTGATGNCGG ACTTTACCGT GACAGCGAAG TGGTATTGTA CGTCCAGGCC   100

CGCCAGCCAC TGTCTTCATG CAGGAACCAC AGTGCCAGAT CCCCACAGCT   150

CGTATCTT   158
40
       (2) INFORMATION FOR SEQ ID :577:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 255 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: double
            (D) TOPOLOGY: linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID :577:

    GGACCTTGAC CCACATCCAT GTTGAGGAAT GTCCTCTTGT CAAGGTCAGG   50

    GAACAGCACC CACAGAGGGC CTCTGGGTCC CTCTCTGCTC AACTCCCTCT   100

    CTCTCGGTTC CTGCGAGGCT CATAGGGTGC AGGGCCCAGC AGAAGGACTG   150

    AGTCTTCCTC CTGGACTTCT GGTCCTGGTA GGCTGTGCTT CATGCTCTCC   200

    TGTCACCTGT ACTGTAAGGA ACTATTATGA CAAACGCATA AAGAATATGA   250

    CTTTG   255

    (2) INFORMATION FOR SEQ ID :578:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 270 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: double
            (D) TOPOLOGY: linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID :578:

    GAGGAGTCCA TGCCATCCTT GATGGAAAAG AAACTGAAGA GAAAAGACAG   50

    CCTGTGGAAG AAGCTCAAAG GTTCTTTGAA GAAGAAGAGA GAAAATATGA   100

    CATGATATCT TTGCTTTTGA GTTCCTCACG CTCTCTGAAT TTATTAGTTG   150

    GACAATTCCA TATGCAGCAT TCTGCTTCAA TATANCTCTT NNGGTCTCTC   200

300

TCTCTNNAAT ATTTGCCTGT AGGTAAAAGC AAGCTCTGCA TATCTGTACC   250

TCTTGAGATA GTTTTGTTTT   270

(2) INFORMATION FOR SEQ ID :579:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 139 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: double
            (D) TOPOLOGY: linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID :579:

GAGTTTTCAG AGGCCCGTGA GGACATGGCT GCCCTTGAGA AGGATTATGA   50

GGAGGTTGGG TGGATCTGTT GAAGGAGAGG GNAGAAGAGG AGAGGAATGC   100

TAAAGTTAAA ACGTAATAAA GATGCTGCTC TTACGGAAG   139

(2) INFORMATION FOR SEQ ID :580:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 168 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: double
            (D) TOPOLOGY: linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID :580:

GGCAGGAATA CATATAGTCA TCATTGCCAG ACTTAATATG AGAGGTGAAA   50

TGTTCGATCC AATTTATTTC TTGGATAAGT TTTTCTTTCC TATNCCTNTN   100

GTTTTGATAA TATAATAAAG AAGATGAGGG GCCCA: .'A TATAGAGCTC   150

CTGAGNGAGT TTTNGGAG   168

301

(2) INFORMATION FOR SEQ ID :581:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 242 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID :581:

CGGAGGGCCC TGTTTGGGAA AAATAGGATT TTAAAAATAT GGTTCATTAA   50

TTTAGGTTTT CTAACATCTA CTTGGGGATG TAGCCTCCAG TGAGGTCAGT   100

TAAGTGGGAC AGAAACGGCA GAGGGAAGAG GTCTTTGCTT CCCCTGGGCC   150

CATTCTCCCT GGCTGCCAGC CCTTGAAGTC AGAACACCAT GGGAAAATTC   200

AGGAGTCGGC ACTGTAGCCG TCAAGTGGCG CTACTTTCCA CA   242

(2) INFORMATION FOR SEQ ID :582:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 37 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID :582:

GCATTTTTCT TGTGTGCTGT TTATAATAGC AAAGCAG   37

(2) INFORMATION FOR SEQ ID :583:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 179 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double

        (D) TOPOLOGY: linear

5   (xi) SEQUENCE DESCRIPTION: SEQ ID :583:

    GGAACAAAGA AAATGTACAG AGTTATATGC GCTTTTTTTT GGTATGGGGG   50

    ACAAGAAACA CTTACCAACA AAAATATTTC AACAACCCCA AAATAACTTA   100
10
    CTCACAAATA TGCAAAATTA TCTATGGCAT AGTATTTCGC ACTCGATGAC   150

    ATTTAGAGAT AAAAAATCAA ATGGAGCTT   179

15   (2) INFORMATION FOR SEQ ID :584:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 186 base pairs
            (B) TYPE: nucleic acid
20   (C) STRANDEDNESS: double
            (D) TOPOLOGY: linear

25   (xi) SEQUENCE DESCRIPTION: SEQ ID :584:

    AACTGCCATG AAGTAACCTG AAGGAGGCGC TGACTGGAGG GATTGATTAC   50

    AGGATCGGAA CACTCCACAC TCGCCATTCT CTGCATATAC CGGTTAGCGA   100
30
    GGCGAGCCTG GCGCTCTTCT TCGCGCTGAG CTAAAGCTAC ACACAATGCT   150

    TTGCGACCAC AATNCACCCT TCATTTCGTA ACTGCT   186

35   (2) INFORMATION FOR SEQ ID :585:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 180 base pairs
            (B) TYPE: nucleic acid
40   (C) STRANDEDNESS: double
            (D) TOPOLOGY: linear

·(xi) SEQUENCE DESCRIPTION: SEQ ID :585:

ACCCACGGTA CTTACATCCT ATGATATGGC CTGCAAACTA AACTACAAAC   50

5

GCACTCACAT CGCTATAATC CTTTTAAGGA CTTAAACTTT ACTCCATTAA   100

GACTTTTATG ACTTCTAACA ACCTCGCCAA CCTCCTCACC CCCCACTATA   150

10   CCTCGGAGAA CTTTCGCGTA ATAACCACGT   180

(2) INFORMATION FOR SEQ ID :586:

    (i) SEQUENCE CHARACTERISTICS:
15   (A) LENGTH: 183 base pairs
          (B) TYPE: nucleic acid
          (C) STRANDEDNESS: double
          (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :586:

ACCGACATCA CGANNGACTT GGTCTTAGTT GAGCAATTTG GCTAANNNNN   50
25

NTNCTNNTTA GCACGTTCTG AGTCTGTGGG ATAGCTGCCA TGAAGTAACC   100

TGAAGGAGGT GCTGGCTGGT AGGGGTTGAT TACAGGGTTG GGAACACTCG   150

30   AGANTGGCAT CCTGCATATA CTGGTTAGTG AGG   183

(2) INFORMATION FOR SEQ ID :587:

    (i) SEQUENCE CHARACTERISTICS:
35   (A) LENGTH: 280 base pairs
          (B) TYPE: nucleic acid
          (C) STRANDEDNESS: double
          (D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID :587:

304

AGGTCAAGTC TACAGCTGGA GACACCCACT TGGGNGNANG AAGATTTTGN   50

ACAACCGAAT NGTCAACCAT TTTAATTGCT GAGTTTAAGC GCACNTTAAA   100

GAAGGACATC AGNGAGAACA AGAGAGCTGT AAGACGCCTC CNTACTGCTT   150

GTGAACGTGC TAAGCGTACC CTCTCTTCCA GCACCCAGGN CAGTATTNAG   200

NTCGNTCTNT CTATGAAGGA ATCGACTCTN TACTCCATAC CNNNCCGATT   250

GAGACTGATG TGACNTTCCT GGGACTGNCA   280

(2) INFORMATION FOR SEQ ID :588:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 371 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: double
            (D) TOPOLOGY: linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID :588:

GGTGAAGAAA CTCCAGATAT CAAGGAATTG GGAAATCCTG GGCCAAACCA   50

CCCCAAGATG ATTACACTGA AATGTAGTAT TAGTACTNCT GCCAGATCTC   100

TTTTTAACAT CATGTGCGTC TCTTGGGATC CAGCAAAAGT GTTAAGCCAC   150

AATGCCCTTG TGCCTTTTAA TATACCACAG TGCCAGTTAA ACTAATATTT   200

TNTTTTGTTG CTTTTTGGGG TATTTTCATT AGTATTTCAG CAAATCTCAT   250

GATAAAGGNC AAGGNCAAGA ACTNCAGAGN ACTGAGCAGA GAGGCTNGTG   300

ATGAAANGTG AAGGCTTCNA CTGACTTTAN GCAGTGGCAG TCANGNTACT   350

GNGNNGCANG CTTANCTATG A   371

(2) INFORMATION FOR SEQ ID :589:

305

```
      (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 184 base pairs
          (B) TYPE: nucleic acid
          (C) STRANDEDNESS: double
          (D) TOPOLOGY: linear


      (xi) SEQUENCE DESCRIPTION: SEQ ID :589:


GAGAGAGAAC ACTCCCCTCC ATCCCAGCAC TATGCACAGT TCACGGCTCA        50

TATGCAAAGT GGAAGACACG TGGGACAAGA GCAAAGCACA AGTGACACAT        100

GGTCCCTCTC TAACACCTCA GCACACCAAC CCTGACGCTC CCATCACAGA        150

TGCTGNTCAT TCTTNCACGG NCCCCTTTTA TAAT                         184

(2) INFORMATION FOR SEQ ID :590:


      (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 243 base pairs
          (B) TYPE: nucleic acid
          (C) STRANDEDNESS: double
          (D) TOPOLOGY: linear


      (xi) SEQUENCE DESCRIPTION: SEQ ID :590:


GGGGGCCCGC CGTNCACNCC CCCACACTCT TGGTAGGCAA TGCTTGTCCC        50

NATATAGTTG NNGTCCTATC GAGTGACACT CTCGTTCATG GATANGGTGN        100

GTAAAACCCN TNGTNGCATC CNNATTGGGN GCANTGNGCC TNTCCCCTTN        150

AANGGTTTTT GCNTNCACTC GACCTNGGGA GGATTCAATG NACNNNCTNG        200

CANTGGNCAA GCNTTGNTTG CNNGNATTGA GAACCCNCCA ATT              243

(2) INFORMATION FOR SEQ ID :591:
```

306

(i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 247 base pairs
    (B) TYPE: nucleic acid
    (C) STRANDEDNESS: double
    (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :591:

ATTCGCCCNN TAAGTAAGTC GTNATTANAC GCGACGNCTA CTACTGAGAC   50

NCGCATGCGC TCTCTCTACA CTAAAGCTCG TCGCTNGNTN ACTTGCGNGN   100

NAAAAAAACC CCCTGGGNNC GCTTTTCACC CCCAAACTTT CAAATTCCGC   150

CCCTTTNGGC NANGCCCAAC CANNCCCCCC CCCTTTTTNC CGNCCCANNC   200

TTNGGNCNTA ANNATTNAGN CGGNANGNNN GGGCCCCCGG CCAACCC   247

(2) INFORMATION FOR SEQ ID :592:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 425 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :592:

GGAGGGGAGT AGAGGAAATT TTCATTCTGG AAAAAAATGC ATACTGTTTG   50

ATATATTACT CNTCATGCTT TCCACAGATA TTATACACAG ATATTATATT   100

CCANGGATTA CGTTGCAATG TCTTCAAAAA TAGANAATTC ATTTTATATT   150

TCTNGATGAA ATATAATAGT ANCTNNGCTA CCTTTGGGAA TGTGACAAAA   200

TACTATGATG ATTACAACTC ATTAAAGCAT AAATNTGCAT GATTTAACTN   250

307

CATGTTCCTT CTATGANCTN CGTGGNATAT AGGCATATTT ATTAATGCTA   300

TTTANGGCNT NNGTGCTTTG TAATGATTCG NCNTTAGGTG AAGGGNTACT   350

TTTNTNNTNC TTCNTAGTAG ATTNGNTTNN NTCTTTTTAA GAGGANTCNA   400

NTTTCATGNG TAANCATCAT CTTTT   425

(2) INFORMATION FOR SEQ ID :593:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 258 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: double
            (D) TOPOLOGY: linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID :593:

CGCTGCATGC GTCAGCGCNA CGCGACGACA GCGCGCGCGA CGCGCGCGAC   50

GCACAAAANA AATGCATGCC AACACGAANA TATGTGCACA CAAACGCAAA   100

CGCGTGTGAA CACATGCGCG CNNCGCGCNC GCGATNCAAA GCTGAAATGT   150

GCNNGNCNGT CGTGNGCGNA AATGTGAAAT GAACAAACAA CAATGAATGA   200

ATGAATGTGA AAAGAGNGN GNTTGAAAAT TNTANAGNNC CCCCCCNTNA   250

ANCAAAAG   258

(2) INFORMATION FOR SEQ ID :594:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 215 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: double
            (D) TOPOLOGY: linear

308

(xi) SEQUENCE DESCRIPTION: SEQ ID :594:

GACCCTAACA ATATGTACAA AAATATAAAA TGTAAATAAA AAATACAAAC　　50

AAATTTCCTT TTTAAAGTAC TTTTAAGAAA AAAAGCAGGG CCTTGGAAGT　　100

TTTGGTTCTT TTTTCCTCCC CTGTTGCAAA TTCTCATGGT TTGGGTTGGG　　150

TGGTGGAGAG CGCGTGTCAT CTGCGGGTGC CTGCCCACGT GGGCGGGCGG　　200

CTCTCTACTC GAAGG　　215

(2) INFORMATION FOR SEQ ID :595:

　　　(i) SEQUENCE CHARACTERISTICS:
　　　　　(A) LENGTH: 272 base pairs
　　　　　(B) TYPE: nucleic acid
　　　　　(C) STRANDEDNESS: double
　　　　　(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :595:

GGGGCTGGTT TGGTCATCCG AGATCATTAA AAATGGCTGA CCCTAACAAT　　50

ATGTACAAAA ATATAAAATG TAAATAAAAA ATACAAACAA ATTTCCTTTT　　100

TAAAGTACTT TTAAGAAAAA AAGCAGGGCC TTGGAAGTTT TGGTTCTTTT　　150

TTCCTCCCCT GTTGCAAATT CTCATGGTTT GGGTTGGGTG GTGGAGAGCG　　200

CGTGTCATCT GCGGGTGGCA CTGCCACGGT GGGCGGGCGG GCTCTCTACT　　250

CGAAGGTGAC CACGTTTAGA TT　　272

(2) INFORMATION FOR SEQ ID :596:

　　　(i) SEQUENCE CHARACTERISTICS:
　　　　　(A) LENGTH: 250 base pairs
　　　　　(B) TYPE: nucleic acid
　　　　　(C) STRANDEDNESS: double

309

(D) TOPOLOGY: linear

5   (xi) SEQUENCE DESCRIPTION: SEQ ID :596:

GACAAACTGT TGACACCCGG AGGCCTAAAC GAGGATTTCA GCTTCCATTA   50

TGCCCAACTC CAGTCCAACA TCATTGAGGC GATTAATGAG CTGCTAGTGG   100
10

AGCTGGAAGG GACAATGGAG AACATTGCAG CCCAGGCTCT GGAGCACATT   150

CACTCCAATG AGGTGATCAT GACCATTGGC TTCTCCCGAA CAGTAGAGGC   200

15   CTTCCTCAAA GAGGCTGCCC GAAAGAGGAA ATTCCATGTC ATTGTAGCAG   250

(2) INFORMATION FOR SEQ ID :597:

        (i) SEQUENCE CHARACTERISTICS:
20   (A) LENGTH: 225 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: double
            (D) TOPOLOGY: linear

25

        (xi) SEQUENCE DESCRIPTION: SEQ ID :597:

CTGCCAAATA CTTTCTTCAC CAACTCATGA GGAGAGGGAA CATGCTGAGA   50
30
AACTGATGAA GCTGCAGAAC CAACGAGGTG GCCGAATCTT CCTTCAGGAT   100

ATCAAGAAAC CAGACTGTGA TGACTGGGAG AGCGGGCTGA ATGCAATGAG   150

35   TGTGCATTAC ATTTGGAAAA GATGTGAATC AGTCACTACT GGAACTGCAC   200

AAACTGGCCA CTGACAAAAA TGACC   225

(2) INFORMATION FOR SEQ ID :598:

40   (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 210 base pairs

310

```
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: double
            (D) TOPOLOGY: linear
```

5

            (xi) SEQUENCE DESCRIPTION: SEQ ID :598:

```
        ACAAAACGCA GATATAAAAA AGTTACAAAG ATTTTTAGAT TTTCATTCAC          50
```
10

```
        AAAAAAAGTC ATTCACATTT TACACTATAC ACGTTATGAT ATAATACAGG          100
```

```
        AAAGTATTAT GTGCATTGTA AGAGAAGGAA AATAGAACTA CTAGATCACA          150
```

15

```
        CGTGTTGTTC TGTGCTCTAA AATACCTAAA GGTGGATTCA TTTAATGCAA          200
```

```
        CACCAGGGAC     .                                               210
```

            (2) INFORMATION FOR SEQ ID :599:
20

                (i) SEQUENCE CHARACTERISTICS:
                    (A) LENGTH: 116 base pairs
                    (B) TYPE: nucleic acid
                    (C) STRANDEDNESS: double
25   (D) TOPOLOGY: linear

            (xi) SEQUENCE DESCRIPTION: SEQ ID :599:
30

```
        AAAGGAGTTG AGTACTGTAA ACGCAGAGCT ACATAGAAAA AACGGGCTTC          50
```

```
        AAAAATCTGC ACAGAGGTTT GCTTGAGAAT TTAGCTACAC AAATATGTGT          100
```

35   AGAAGTGAAA AAAAAA   :   116

            (2) INFORMATION FOR SEQ ID :600:

                (i) SEQUENCE CHARACTERISTICS:
40   (A) LENGTH: 107 base pairs
                    (B) TYPE: nucleic acid
                    (C) STRANDEDNESS: double
```

311

(D) TOPOLOGY: linear


5              (xi) SEQUENCE DESCRIPTION: SEQ ID :600:

ACAGTGTGTG CCCTGTCAGC TCCGCAAATT GGCAGTCACT ACGTTTGTGC        50

CCCCTGTAAC CTTGTGATCT TCACTGCCAC TAGCGATGAA GTCTTCATTA        100

10

TGGCCTC                                                      107


(2) INFORMATION FOR SEQ ID :601:


15            (i) SEQUENCE CHARACTERISTICS:
                   (A) LENGTH: 173 base pairs
                   (B) TYPE: nucleic acid
                   (C) STRANDEDNESS: double
                   (D) TOPOLOGY: linear

20


              (xi) SEQUENCE DESCRIPTION: SEQ ID :601:


25   ACTGCTAGTG AAATTCACAT GACTCACAAT TCCCTTTAGC CAATGTTACC        50

GAAGTCAGTG TCAAGAAAAC TTAACAGAAA AAAAAAAGCA CAGAGTGAGT        100

TCCTACCATA AAAATCCAGG CTGCCCTGTT TCCTAGCTCT AATATAAGCC        150

30

ATTTTCTTTC CTTAGTGTAC CAA                                    173


(2) INFORMATION FOR SEQ ID :602:


35            (i) SEQUENCE CHARACTERISTICS:
                   (A) LENGTH: 216 base pairs
                   (B) TYPE: nucleic acid
                   (C) STRANDEDNESS: double
                   (D) TOPOLOGY: linear

40

312

(xi) SEQUENCE DESCRIPTION: SEQ ID :602:

GGAAGAGAAC ACATACACGA GGACCAGTAC CTGATGAGGA CAAGAGAGAT　　　　50

GGGAANNNGC TGTGGAATTC CTTTCGGCAC CCTGGATGTT AACCCCTGCT　　　100

CAGGAAAGGG TGCATCTGTC TTCATCATGC CTCTCTCTCC TCCTCCTCCA　　　150

GCCACCTCCC AAAGGCAGAG CTGCCGCAAC CTGCCTGGCC ATGTGGTGGC　　　200

AAGTACCCAG TAGGAG　　　　　　　　　　　　　　　　　　　　　　216

(2) INFORMATION FOR SEQ ID :603:

　　　　　(i) SEQUENCE CHARACTERISTICS:
　　　　　　　　(A) LENGTH: 213 base pairs
　　　　　　　　(B) TYPE: nucleic acid
　　　　　　　　(C) STRANDEDNESS: double
　　　　　　　　(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :603:

GAAAAAACAA TCATGACAGC AACTCTCCTA ACCACAAAAA TCACATATGT　　　50

TATCTTTCTT TCAGGACTAA TAATTAATAT TTAAGAGGAA AGCACATCAA　　　100

TTTCTAGGGC CCTTCTTGGG GAAAGGTTCA TATAATTTAG CATACATACA　　　150

TATTCAGTGA ATGCATTCAT ATATTACTAT ATAAACACTC TCAGCTACAA　　　200

TGGTAATATA ATG　　　　　　　　　　　　　　　　　　　　　　213

(2) INFORMATION FOR SEQ ID :604:

　　　　　(i) SEQUENCE CHARACTERISTICS:
　　　　　　　　(A) LENGTH: 219 base pairs
　　　　　　　　(B) TYPE: nucleic acid
　　　　　　　　(C) STRANDEDNESS: double
　　　　　　　　(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :604:

GACATCTGAT CATCTCACTG GACGCCACAG GGGCAAGAGG GTGGTTTTCC        50

TGAAGCAGCT GGCTAGTGGC TTATTACTTG TGACTGGACC TCTGGTCTCA       100

ATCGAGTTCC TCTACGAGAA CACACCAGAA ATTTGTCATT GCCACTTCAA       150

CAAAATCGAT ATCAGCAATG TAAAAATCCC AAACATCTTA CTGATGCTTA       200

CTTCAAGAAG AAGAGCTGC                                         219

(2) INFORMATION FOR SEQ ID :605:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 104 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: double
            (D) TOPOLOGY: linear




    (xi) SEQUENCE DESCRIPTION: SEQ ID :605:

AGCGAACACG AGCACAGCGA GCGCACAGAG AGCAGCAGGG AGGGCAGCCA        50

CCGCCGGGAC GCCGGCAGGG GCACGAGAAG GCAAGGAGCG GACACCCGNG       100

NNGA                                                        104

(2) INFORMATION FOR SEQ ID :606:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 189 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: double
            (D) TOPOLOGY: linear




    (xi) SEQUENCE DESCRIPTION: SEQ ID :606:

314

```
AATAAAGCAT TCTCACAACC TTTGTTGGGT CAATGATTCC TTTTTACCAC        50

ANNTACAGAA TCTCCACCAT AGCATCAT.A CCAACTCTGA GGAACTTCGC       100

ATAATTCTTA ACTACAAAGA TCCTTCAACA CCCGCATTCT TACAATGTCA       150

TCGCCGGAAT TTTGAGTGTT CTTTCAATAA CCTACANTA                   189
```

(2) INFORMATION FOR SEQ ID :607:

    (i)· SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 171 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID :607:

```
GGAAAAGNTC ATTACATAAG CACCAAGNCA TTGATTATGA TCCACCGGAA        50

GAGCTCGTAT TTATCCTTTG CTTTNATNTG AGACCAAGCT AGCCCTGAGT       100

AATTTTANNT GGTTCCTAAA ACATATGGCT TATCGTACTC TAAGAAAAAT       150

GCCTTACGCA CATTCCTTTN T                                      171
```

(2) INFORMATION FOR SEQ ID :608:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 184 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID :608:

```
GGAAAAGTNC GCATATAGCG TGCNATAATA CTACGNCTAA GGAGAAACAA        50
```

315

TTTCCTACAC ATAAAGTAGT GAGAACATCA TCCTATAACA GGGAACTGTG   100

ATTATTTAAA AAACGCAGAA CTTATTTATT TGGCTTTAGA AATAACTGCA   150

TACAATGTCA TAAGTCGAAA AGAACTCAAA ATAA   184

(2) INFORMATION FOR SEQ ID :609:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 191 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID :609:

GGGGACAGCT NNNNNGTTGT TTTGGAGCCT GTTGACTTTG TATTCTCTGC   50

CTGTGATTTT CNNTTCTAAA TGAAACTCCA TGTNNNAACC AGGACGAAGN   100

TGAGAAGGAA AACGCCAAAT GCTTTGGTTA TTAGAGNTTA ATAGGNAAGC   150

TCTGTTACAC TAGGTGTAGA GTTCCAGAAT GTTCTTTTGT T   191

(2) INFORMATION FOR SEQ ID :610:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 172 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID :610:

GCAACTGTGC AAACATCCAT CAGTGTGGAG GAATGGTAAA CTTGGTACAT   50

GCATGCANTN GNNNCATATT TTTGTGGTTA AGATNNTGAT GTATAGGCAT   100

316

GGAATGTTAT CAAAAGCACA TTAAGTGGTC AAAGCCAGAT ACAGAAGAGT   150

AGGTATGATT TTATAGGNAT AA   172

(2) INFORMATION FOR SEQ ID :611:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 51 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: double
            (D) TOPOLOGY: linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID :611:

    TCCACCTTAC AGACCTGATT TGGCTGCTTC TGACGTCTGT TTCCTAATCT   50

    T   51

(2) INFORMATION FOR SEQ ID :612:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 60 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: double
            (D) TOPOLOGY: linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID :612:

    CGCCTGAAAC TTTGAGGATA AACTTTTTCA AAAAAATAAA ACAGTATCTC   50

    TTAATCACTG   60

(2) INFORMATION FOR SEQ ID :613:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 75 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

5   (xi) SEQUENCE DESCRIPTION: SEQ ID :613:

TTGAAGCTGG GAGGCAGAGG TTGCAGCGTG CAGAGTCGTG CCACTGCACT   50

CCTGGGCGCA CAGCGAGACT GTCTC   75

10   (2) INFORMATION FOR SEQ ID :614:

          (i) SEQUENCE CHARACTERISTICS:
               (A) LENGTH: 25 base pairs
15   (B) TYPE: nucleic acid
               (C) STRANDEDNESS: double
               (D) TOPOLOGY: linear

20   (xi) SEQUENCE DESCRIPTION: SEQ ID :614:

ACGGGATTCT CTTCTTCGGC CGCCA   25

25   (2) INFORMATION FOR SEQ ID :615:

          (i) SEQUENCE CHARACTERISTICS:
               (A) LENGTH: 72 base pairs
               (B) TYPE: nucleic acid
30   (C) STRANDEDNESS: double
               (D) TOPOLOGY: linear

35   (xi) SEQUENCE DESCRIPTION: SEQ ID :615:

GCAGTGTACT ATGTTCGCAT CTGTGAATAG CCACTGCACT CTAGCCTGGA   50

TAATATAGTG AGAACCCATC TC   72

40
          (2) INFORMATION FOR SEQ ID :616:

318

(i) SEQUENCE CHARACTERISTICS:

    (A) LENGTH: 137 base pairs

    (B) TYPE: nucleic acid

    (C) STRANDEDNESS: double

    (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :616:

```
TCTAACTGAT TTCAAAGCAA ACTCTCTCTT AATTAGGCTG CCTCTCCAGG        50

GGAAATTTAG TGGCAGGGTC CCAGTGAGCC TGTAAGAAGT GTTCTACTCA       100

CCAGAGTCAC TACTCCAGGT TGAGGACATG AGGCAGG                     137
```

(2) INFORMATION FOR SEQ ID :617:

    (i) SEQUENCE CHARACTERISTICS:

        (A) LENGTH: 139 base pairs

        (B) TYPE: nucleic acid

        (C) STRANDEDNESS: double

        (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :617:

```
GCAGGGCAGT CTTGGTGTGC AGCCCCTCTC CTCTCTGTCC CCTGACACTC        50

CACAGTGTGC CTGCAACCCA AGTGGCCTTA TCCGTGCAGT GGTGGCAGTT       100

CAGAAATAAA GGGCCCATTT GAGGGATGAC CGCATTCAC                   139
```

(2) INFORMATION FOR SEQ ID :618:

    (i) SEQUENCE CHARACTERISTICS:

        (A) LENGTH: 178 base pairs

        (B) TYPE: nucleic acid

        (C) STRANDEDNESS: double

        (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :618:

5

TCTTCTTACT ACACTGGAAG TCTGAACTGG GTGCCTGTTA CCGTCGAGGG   50

TTACTGGCAG ATCACCGTGG ACAGCATCAC CATGAACGGA GAGGCCATCG·   100

CCTNCNCTGA GGNCNGCCAG GCCATTGTTG ACACCNNCAC CTCTCNNCTG   150

10   ANNNNCCCAA CCAGCCCCAT TNCCAACA   178

(2) INFORMATION FOR SEQ ID :619:

(i) SEQUENCE CHARACTERISTICS:
15   (A) LENGTH: 73 base pairs
         (B) TYPE: nucleic acid
         (C) STRANDEDNESS: double
         (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :619:

ACCACCCCTT CCTTTTCTTC ATCCAGCACA GCAAGACCAA CGGGATTCTC   50
25

TTCTGCGGCC GCCACCGCGT GGA   73

(2) INFORMATION FOR SEQ ID :620:

30   (i) SEQUENCE CHARACTERISTICS:
         (A) LENGTH: 139 base pairs
         (B) TYPE: nucleic.acid
         (C) STRANDEDNESS: double
         (D) TOPOLOGY: linear
35

(xi) SEQUENCE DESCRIPTION: SEQ ID :620:

40   TGCCTTACAC ACTCAGGGAG ACCTCGGGTT GTACCTAGGC CTAGTGGACA   50

AACTTTGGTA GAGGGTTCGG TACGACTTAC GACACCTGGC CCTACGTCAT   100

AGTCCGTACC CTCAGTAACA GTGTAGTAGC TCTTCCTGT   139

(2) INFORMATION FOR SEQ ID :621:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 123 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID :621:

TTCAAAAACA ACTTTATTCA TGACACATAT TAANNNAAAA CCCCACCCCT   50

GGAAATGAGC TAAAAAAATA AACAAAATCC ACCTCCCACC TCCCTGNNCC   100

CACTTCCTCC CATGCCCTCC AAA   123

(2) INFORMATION FOR SEQ ID :622:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 173 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID :622:

CACCCAAGAC CATCCTTTAT TGTAGTATTA GTTCATGGTA ACTGCATGAA   50

AAAACATTTC NNGAGGAATT TTCAATTTCC AGCTTAAAGA ACNNNCCCAC   100

CAACATAACC AATTTATGAA ANNNAATTCA TTAAAAGGTA TAGAACCTCT   150

TGTNNNCATG ATGGCAAGGG ACA   173

(2) INFORMATION FOR SEQ ID :623:

(i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 112 base pairs
    (B) TYPE: nucleic acid
    (C) STRANDEDNESS: double
    (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :623:

TTTATTGTAT CATGAGGCAT TGAAACATCT GAATAAATCA ATGTCTGGGC   50

GGTGAAGGCA GCTGCTTTCT CCTTCACTTC TTTGGGTTAC TAGAGCAACT   100

TGTCAGTAGA TT   112

(2) INFORMATION FOR SEQ ID :624:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 119 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :624:

ACTCCTTCTG CCCCCGTTCT TCTAGTGAGA GGGGCGGACA AGGGGGCGGC   50

GAAAAGAGGA GAAAGGAGAG AAACAAGAGT CGAGGGGGAC AGGGGAGTCG   100

AGGTCTGCAT CCCCTCCCC   119

(2) INFORMATION FOR SEQ ID :625:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 39 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

322

(xi) SEQUENCE DESCRIPTION: SEQ ID :625:

AACAGCACGG AGATTGCGTT TATATATCAG ACCAAGCTC   39

(2) INFORMATION FOR SEQ ID :626:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 72 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: double
            (D) TOPOLOGY: linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID :626:

CCAGCGCCGA GGTTGTATAT TTCTAGGTGC AGGTATATGA TTGCCATATA   50

ATAAAAATCT GAAAACATCC CC   72

(2) INFORMATION FOR SEQ ID :627:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 153 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: double
            (D) TOPOLOGY: linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID :627:

CCTCCGCCGG AGCTATCTGC ACTACATCCG CAAGTACAAC CGTCTTCGAG   50

AAGCGCCACA AGAACATGTC TGTACACCTG TCCCCCTGCT TCAGGGACGT   100

CCAGATCGGT GACATCGTCA CAGTGGGCGA GTGCGGCCTC TAGACAAGAC   150   r

AGT   153   ŗ

(2) INFORMATION FOR SEQ ID :628:

323

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 108 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: double
    5   (D) TOPOLOGY: linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID :628:

    10

        AAAAGAAGTA GGTCGTGTCG TTCTGGTTGC CCTAAGAGAA GAAGANNNCG   50

        GTGGCCACCT CGAGGTTAAG AGGGATATCA CTCAGCATAA TGTTAAGTGA   100

    15 CCGGCAGC   108

        (2) INFORMATION FOR SEQ ID :629:

            (i) SEQUENCE CHARACTERISTICS:
    20   (A) LENGTH: 95 base pairs
                (B) TYPE: nucleic acid
                (C) STRANDEDNESS: double
                (D) TOPOLOGY: linear

    25

        (xi) SEQUENCE DESCRIPTION: SEQ ID :629:

        TCGCACCACT AGAAANCACC GTGACTGAGA AGAATGATGT GACCTTCAGA   50
    30
        CTTGACCCNN GGACAATGNC AGCTCCCAAT GNCCGTCTAG TGGCA   95

        (2) INFORMATION FOR SEQ ID :630:

    35   (i) SEQUENCE CHARACTERISTICS:
                (A) LENGTH: 139 base pairs
                (B) TYPE: nucleic acid
                (C) STRANDEDNESS: double
                (D) TOPOLOGY: linear

    40

324

(xi) SEQUENCE DESCRIPTION: SEQ ID :630:

CCAGCNCCGA AAAGCCAAGA CTTCATCAAC TACATAGGTC TTACCATTGA   50

5   CCTAAGATCA ATCTGAACTA TCTTAGCCCA GTCAGGGAGC TCTGCTTCCT   100

AGAAAGGCAT CTTTCGCCAG TGGATTCGCC TCAAGGTTG   139

(2) INFORMATION FOR SEQ ID :631:

10

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 117 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: double
15   (D) TOPOLOGY: linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID :631:

20

CCACCGCCCC GAGCGAATGT AACCCGGCCT TGGACGACCC GACGCCGGAC   50

TACATGAACC TGCTGGGCAT GATCTTCAGC ATGTNCNNCC TCATGCTTAA   100

25   GCTGAAGTGG TGTGCTT   117

(2) INFORMATION FOR SEQ ID :632:

        (i) SEQUENCE CHARACTERISTICS:
30   (A) LENGTH: 161 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: double
            (D) TOPOLOGY: linear

35

        (xi) SEQUENCE DESCRIPTION: SEQ ID :632:

CCAGCNCCGA AAAGCCAAGA CTTCATGAAC TACATAGGTC TTACCATTGA   50
40
CCTAAGATCA ATCTGAACTA TCTTAGCCCA GTCAGGGAGC TCTGCTTCCT   100

325

AGAAAGGCAT CTTTCGCCAG TGGATTCGCC TCAAGGTTGA GGCCGCCATT   150

GGAAGATGAA A   161

5   (2) INFORMATION FOR SEQ ID :633:

             (i) SEQUENCE CHARACTERISTICS:
                 (A) LENGTH: 97 base pairs
                 (B) TYPE: nucleic acid
10   (C) STRANDEDNESS: double
                 (D) TOPOLOGY: linear

15   (xi) SEQUENCE DESCRIPTION: SEQ ID :633:

         CCTGCNCCGA CGATGCCCAG AATCCAGAAC TTTGTCTATC ACTCTCCCCA   50

         ACAACCTAGA TGTGAAAACA GAATAAACTT CACCCAGAAA AACAAAC   97
20
         (2) INFORMATION FOR SEQ ID :634:

             (i) SEQUENCE CHARACTERISTICS:
                 (A) LENGTH: 178 base pairs
25   (B) TYPE: nucleic acid
                 (C) STRANDEDNESS: double
                 (D) TOPOLOGY: linear

30
             (xi) SEQUENCE DESCRIPTION: SEQ ID :634:

         CCAGCNCCGA AGCATTGGAT GCTTGACAAA CTAACGGGTG TATTTGCACC   50

35   TCGTCCATCG ACAGGTCCCC AGAAGCTGAG GGAATGTCTT TCCTCTGATC   100

         TTCTTCCTCA GGAATAGACT CAAGTATGCG TTGACTGGAG ATGAGGTAAA   150

         GAAGATATGT ATGCAACGTT CATTCAAA   178
40
         (2) INFORMATION FOR SEQ ID :635:

326

(i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 90 base pairs
    (B) TYPE: nucleic acid
    (C) STRANDEDNESS: double
5   (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID :635:
10
    CCTGCNCCGA TGCACCCGCC ATCCAGCCTG TCCTTTGGAC CACGCCACCC   50

    CTCCAGCATG GTCACCGCCA TGGGTTAGAN CCCTGCTCGA   90

15 (2) INFORMATION FOR SEQ ID :636:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 101 base pairs
        (B) TYPE: nucleic acid
20   (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

25   (xi) SEQUENCE DESCRIPTION: SEQ ID :636:

    CAGGAGACAC AGACAATAGT CACTACATCA CAGCCTTGTT CTTTCCGAAG   50

    GATAAAATGT CATTCAAGAA TGGGGTGAGG TGGTTAGAGG GACTAGGTAC   100
30
    T   101

    (2) INFORMATION FOR SEQ ID :637:

35   (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 70 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear
40

327

(xi) SEQUENCE DESCRIPTION: SEQ ID :637:

CCGAGCACGA GACCCTGATG CACATTCTAA AATAAAAGAA TGATGCACAT   50

5   TTTAATAAAG CACAGCACAA   70

(2) INFORMATION FOR SEQ ID :638:

        (i) SEQUENCE CHARACTERISTICS:
10   (A) LENGTH: 160 base pairs
                (B) TYPE: nucleic acid
                (C) STRANDEDNESS: double
                (D) TOPOLOGY: linear

15

        (xi) SEQUENCE DESCRIPTION: SEQ ID :638:

CCGAGCANAN TCTAACCCGG CCTTGGACGA CCCGACGCCG GACTACATGA   50
20
ACCTGCTGGG CATGATCTTC AGCATGTGCG GCCTCATGCT TAAGCTGAAG   100

TGGTGTGCTT GGGTCGCTGT CTACTGCTCC TTCATCAGCT TTGCCAACTC   150

25   TCGGAGCTCG   160

(2) INFORMATION FOR SEQ ID :639:

        (i) SEQUENCE CHARACTERISTICS:
30   (A) LENGTH: 138 base pairs
                (B) TYPE: nucleic acid
                (C) STRANDEDNESS: double
                (D) TOPOLOGY: linear

35

        (xi) SEQUENCE DESCRIPTION: SEQ ID :639:

CCGAACAAAT GTACGGAATG TGTGAGTCCC TCTGGAGCCC AACATGGATC   50
40
CGGATCACCT GTTTGAAACC ATCTCCCAAG CCATGCTGAA TGCTGTGGGC   100

328

CGGGATGCAT GTGCAGGCAT GGAGTCATTG TCACATCA   138

(2) INFORMATION FOR SEQ ID :640:

5   (i) SEQUENCE CHARACTERISTICS:
                 (A) LENGTH: 80 base pairs
                 (B) TYPE: nucleic acid
                 (C) STRANDEDNESS: double
                 (D) TOPOLOGY: linear

10

            (xi) SEQUENCE DESCRIPTION: SEQ ID :640:

15 CCGACCACCC CTTCCTTTTC TTCGTCCATC CAGCACAGCA AGACCAACGG   50

    GATTCTCTTC TGCGGCCGCC ACCGCGTGGA   80

    (2) INFORMATION FOR SEQ ID :641:
20
            (i) SEQUENCE CHARACTERISTICS:
                 (A) LENGTH: 100 base pairs
                 (B) TYPE: nucleic acid
                 (C) STRANDEDNESS: double
25   (D) TOPOLOGY: linear

            (xi) SEQUENCE DESCRIPTION: SEQ ID :641:
30
    AACTAAACTG TTACCTTCCC TCGCTCCACA GAAGAAGACA GCCAGCTTCA   50

    GGGGTCCCTG TTGCTGGCCA AGCCAGTGAG CCTGCTGGGA GGCTGGTCCA   100

35 (2) INFORMATION FOR SEQ ID :642:

            (i) SEQUENCE CHARACTERISTICS:
                 (A) LENGTH: 77 base pairs
                 (B) TYPE: nucleic acid
40   (C) STRANDEDNESS: double
                 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :642:

AGAGGACAGA AAGGAACAGA ATGATCTTCC TACNCACAAC ACAAACGTCA   50

GTTAATGTTC CATCCATGCT GCTTAAA   77

(2) INFORMATION FOR SEQ ID :643:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 127 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :643:

CCAGCGCCGA GAGCAGCCCC AGTAGCAGCN CATGGCCGGG TCCAACGCCT   50

ACATCGACAA CCTTCATGGC GGACGGGACC TGTCAGGACN GGCCATCGTG   100

GGCTACAAGG ACTCGCCCTC CGTCTGG   127

(2) INFORMATION FOR SEQ ID :644:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 116 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :644:

GTAGCCAGAC CACAACACCG AGTTGTACCC AGATAGCTGG GATTGGAAGT   50

GAGGAGGTTT CTCACCCCAC AGATAACCCA AGACACAAAT GTGCAATTAA   100

AAGTTTATTT TAGACC   116

(2) INFORMATION FOR SEQ ID :645:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 182 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: double
            (D) TOPOLOGY: linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID :645:

CCACCACCCG ATTCGTGACC AAGAAGGCTC TGTGCATTCG GGTTTTCCAG   50

GAGACTCAAA AGCCGAAGAA GCGAAGAAGA GCCTTAAAGG CTGCAGCAGC   100

CAGAAAAACA AGCAAAGGAG GAACCCAGAC AGCCCTGCAA AGCATACAAG   150

ACACTCAAGA CAGCAATTAA TCTGTCATCA TT   182

(2) INFORMATION FOR SEQ ID :646:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 66 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: double
            (D) TOPOLOGY: linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID :646:

CCAGCGCCGA GGTTGTATAT TTCTAGGTGC AGGTATATGA TTGCCATATA   50

ATAAAAATCT GAAAAC   66

(2) INFORMATION FOR SEQ ID :647:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 93 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: double

331

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :647:

CAAGACAATA GTCACATCAT CGCAGCCTTG TTCTTTCCGA AGGATAAAAT   50

GTCATTCAAG AATGGGGTGA GGTGGTTAGA GGGAGTAGGT ACT   93

(2) INFORMATION FOR SEQ ID :648:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 114 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: double
            (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :648:

CCCCTTTTTG TCCCCACTGA GATGTATGAA GGTTTTGGTC TCCCTGGGAG   50

TGGGTGGAGG CAGCCAGGGC TTACCTGTAC ACTGACTTGA GACCAGTTGA   100

AAAGTGCACA CCTT   114

(2) INFORMATION FOR SEQ ID :649:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 81 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: double
            (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :649:

CTGCNCCGAC CACCCCTTCC TTTTCTTCAT CCAGCACAGC AAGACCAACG   50

332

GGATTCTCTT CTGCGGCCGC CACCGCGTGG A   81

(2) INFORMATION FOR SEQ ID :650:

(i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 159 base pairs
    (B) TYPE: nucleic acid
    (C) STRANDEDNESS: double
    (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :650:

AGGAGCNCCG ACAAAAGACA CATTGGACCT GTCAGCTCCT CTGTTTCACC   50

AAGCAGACAC AATAACCTTA CCAACAAAGC AGAGTAAGCC AAGTGCCTCT   100

GTGTGACACC ACCGCATNNT GATGACGCAT AATAAAAATA TAACTAATTT   150

AGACTAGAG   159

(2) INFORMATION FOR SEQ ID :651:

(i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 78 base pairs
    (B) TYPE: nucleic acid
    (C) STRANDEDNESS: double
    (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :651:

CCGACCACCC CTTCCTTTTC TTCATCCAGC ACAGCAAGAC CAACGGGATT   50

CTCTTCTGCG GCCGCCACCG CTGGAGCT   78

(2) INFORMATION FOR SEQ ID :652:

(i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 198 base pairs

333

(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :652:

CCGACAGACG GTCATTGATT ACAACGGGGA ACGCACGCTG GATGGTTTTA   50

AGAAATTCCT GGAGAGCGGT GGCCAGGATG GGGCAGGGGA TGATGACGAT   100

CTCGAGGACC TGGAAGAAGC AGAGGAGCCA GACATGGAGG AAGACNATGA   150

TCAGAAAGCT GTGAAAGATG AACTGTAATA CGCAAAGCCA GACCCGGG   198

(2) INFORMATION FOR SEQ ID :653:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 224 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: double
            (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :653:

CCGAAAAGCC AAGACTTCAT GAACTACATA GGTCTTACCA TTGACCTAAG   50

ATCAATCTGA ACTATCTTAG CCCAGTCAGG GAGCTCTGCT TCCTAGAAAG   100

GCATCTTTCG CCAGTGGATT CGCCTCAAGG TTGAGGCCGC CATTGGAAGA   150

TGAAAAATTG CACTCCCTTG GTGTAGACAA TACCAGTTCC ATTGGTGTTG   200

TTGCTATAAT AACACTTTTC TTTT   224

(2) INFORMATION FOR SEQ ID :654:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 226 base pairs

334

```
                 (B)  TYPE: nucleic acid
                 (C)  STRANDEDNESS: double
                 (D)  TOPOLOGY: linear
```

```
         (xi)  SEQUENCE DESCRIPTION: SEQ ID :654:

    CCGCCTCAGA CTCTGGACCA GCCACTGTCC CAGAAGCCAG GCCGGGCAGT      50

    GGCCTTCTCC ACTCCCCTCT GACTTCTCCA AGGGGCTCAG TGGCCAGTGC     100

    CCCCCAGGAG GCTCCACCCT CAACTCAACC CAAGCAAGAG GGACAGATGA     150

    AAAACAAAAT CCAATCAGGG CGATAAATGG CGGGGGGTTT AATTTGGTTT     200

    CTGAGCGCAT AAAGCTAAGG AGGGGT                               226
```

```
    (2)  INFORMATION FOR SEQ ID :655:

         (i)  SEQUENCE CHARACTERISTICS:
                 (A)  LENGTH: 167 base pairs
                 (B)  TYPE: nucleic acid
                 (C)  STRANDEDNESS: double
                 (D)  TOPOLOGY: linear
```

```
         (xi)  SEQUENCE DESCRIPTION: SEQ ID :655:

    TTAAAAAAAT TCCCCCCTTT AATTGACCAA AGTAAAGCCA TGACATTTCA      50

    TTTGGTAACC TGTTTAGAAT TATAAAAATC ATTTCATTTG GCCCAGCCCA     100

    TACGCCCAAG AGAAAACTTC CAGACTTTTC TGATGCCATC CAGTTTTGTT     150

    CTTACAAAAT GCATATT                                        167
```

```
    (2)  INFORMATION FOR SEQ ID :656:

         (i)  SEQUENCE CHARACTERISTICS:
                 (A)  LENGTH: 72 base pairs
```

335

```
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: double
            (D) TOPOLOGY: linear
```

5

```
        (xi) SEQUENCE DESCRIPTION: SEQ ID :656:
```

```
    CCACCCCTTC CTTTTCTTCA TCCAGCACAG CAAGACCAAC GGGATTCTCT        50
```
10
```
    TCTGCGGCCG CCACCGCGTG GA                                      72
```

```
    (2) INFORMATION FOR SEQ ID :657:
```

15
```
        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 178 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: double
            (D) TOPOLOGY: linear
```
20

```
        (xi) SEQUENCE DESCRIPTION: SEQ ID :657:
```

25
```
    AGAGGGTTTT CTATATGTAA TTCTTTTATT CTGTAAAAGG TAACAAAATA        50
```

```
    TACAGAACAA AAAAACTTTC CCTTTTTAAA ACTAATGTTA CAAATCTGTA        100
```

```
    TTATCACTTG TATATAAATA GTATATAGCT GATCATTAAT AAGGTGTATA        150
```
30
```
    GTACAATGTA TTCTAAAACT GTTCCGCC                                178
```

```
    (2) INFORMATION FOR SEQ ID :658:
```

35
```
        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 76 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: double
            (D) TOPOLOGY: linear
```
40

:

336

(xi) SEQUENCE DESCRIPTION: SEQ ID :658:

CCGACCACCC CTTCCTTTTC TTCATCCAGC ACAGCAAGAC CAACGGGATT   50

5   CTCTTCTGCG GCCGCCACCG CGTGGA   76

(2) INFORMATION FOR SEQ ID :659:

(i) SEQUENCE CHARACTERISTICS:
10   (A) LENGTH: 68 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: double
            (D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID :659:

GCCAGCGCCG AGGTCGCATA TTTCTAGGCG CAGGTATATG ACTGCCATAT   50
20
AACAAAAACC NTGAAAAC   68

(2) INFORMATION FOR SEQ ID :660:

25   (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 151 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: double
            (D) TOPOLOGY: linear
30

(xi) SEQUENCE DESCRIPTION: SEQ ID :660:

35   CCCAAACTTC TTTAAAAATC AAGTAATGTT TACAAGAAAG AATAAAATCT   50

TAATCCTTTT CACTTTTAAA GACAATCAGA TAAGATTACC CACTGCGATT   100

AAACACTGAT CAAACTCAGT TGTCCTTACG TTAGCATTAC TCTGTCATAG   150
40
C   151

(2) INFORMATION FOR SEQ ID :661:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 245 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID :661:

AGGCACTGAC CCCTGCCACC CCTCACTGCA TTAACTTCAG CCACGTCTCC   50

TCCTTCCTCT GCGCTTCCAG TGATAAGGGT ACTGTCCATA TCTTTGCTCT   100

CAAGGATACC CGCCTCAACC GCCGCTCCGG CCTGGCTCGC GTGGGCAAGG   150

TGGGGCCTAT GATTGGGCAG TACGTGGACT CTCAGTGGAG CCTGGCGAGC   200

TTCACTGTGC CTGCTGAGTC AGCTTGCATC TGCGCCTTCG GTGCG   245

(2) INFORMATION FOR SEQ ID :662:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 72 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID :662:

GCCAGCGCCG AGGTCGCATA TTTCTAGGCG CAGGTATATG ATTGCCATAT   50

AATAAAAACM TGAAAACACC CC   72

(2) INFORMATION FOR SEQ ID :663:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 88 base pairs

338

```
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: double
            (D) TOPOLOGY: linear


5


        (xi) SEQUENCE DESCRIPTION: SEQ ID :663:


    GCCTGCGCCG ACGATGACCA GAATCCAGAA CTTTGCCTAT CACTCTCCCC        50

10

    AACAACCTAG ACGCGAAAAC AGAATAAACT TCACCCAG                      88


    (2) INFORMATION FOR SEQ ID :664:

15      (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 223 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: double
            (D) TOPOLOGY: linear

20



        (xi) SEQUENCE DESCRIPTION: SEQ ID :664:


25  GCCTGCGCCG ACAAACAAAA CCTGGAGGCC ATTCTGCACA GCCTGCCCGA        50

    GAACTGTGCC AGCTGGCGGT GAGGGCTGCC CAGATCCCCG GCACACACTC       100

    CCCCACCTGC TGTTTACATG ACCCAGGGGG CGCACACTAC CCCACAGGCG       150

30  CGCCCATACA GACATTCCCC GGAGCCGGCT GCTGCGAACT CGACCCCGTG       200

    CGGATAGTCA CACTCCCTGC CGA                                    223

35  (2) INFORMATION FOR SEQ ID :665:


        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 70 base pairs
            (B) TYPE: nucleic acid
40          (C) STRANDEDNESS: double
            (D) TOPOLOGY: linear
```

339

        (xi) SEQUENCE DESCRIPTION: SEQ ID :665:

GCCAGCGCCG AGGTTGCATA TTTCTAGGCG CAGGTATATG ATTGCCATAT   50

AATAAAAATC TGAAAACACC   70

(2) INFORMATION FOR SEQ ID :666:

        (i) SEQUENCE CHARACTERISTICS:
             (A) LENGTH: 118 base pairs
             (B) TYPE: nucleic acid
             (C) STRANDEDNESS: double
             (D) TOPOLOGY: linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID :666:

GCCAGCGCCG ACCGCCCCAA AAATACTCCC ACCGGGATCA GGGCGATTAA   50

TGAAGACTCA ACGGGGACTA AAAGGGGCC CCAAAAAAAA CCAAACCACC   100

TTTCTACGTA CCGTATAG   118

(2) INFORMATION FOR SEQ ID :667:

        (i) SEQUENCE CHARACTERISTICS:
             (A) LENGTH: 88 base pairs
             (B) TYPE: nucleic acid
             (C) STRANDEDNESS: double
             (D) TOPOLOGY: linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID :667:

GCCAGCGCCG ACGATGCCCA GAATCCAGGA CTTTGCCTAT CACTCTCCCC   50

AACAACCTAG ACGCGAAAAC AGAATAAACT TCACCCAG   88

(2) INFORMATION FOR SEQ ID :668:

340

        (i) SEQUENCE CHARACTERISTICS:

           (A) LENGTH: 59 base pairs

           (B) TYPE: nucleic acid

           (C) STRANDEDNESS: double

5   (D) TOPOLOGY: linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID :668:

10

    GCCACCGCCG ACTCCAGGCA CTCACTCAAA CTTGATCTTC AACTCTGCAT   50

    ACAAGCAGA   59

15   (2) INFORMATION FOR SEQ ID :669:

        (i) SEQUENCE CHARACTERISTICS:

           (A) LENGTH: 223 base pairs

           (B) TYPE: nucleic acid

20   (C) STRANDEDNESS: double

           (D) TOPOLOGY: linear

25   (xi) SEQUENCE DESCRIPTION: SEQ ID :669:

    GCCTGCGCCG AACAAATATA CAGAATGCGC GAGTCCCTCT GGAAGCCCAA   50

    CATGGATCCG GATCACCTGT TTGAAACCAT CTCCCAAGCC ATGCTGAATG   100

30

    CTGCGGACCA GGATGCAGTG CCAGGCATGG GAGTCATTGC CCACATCACC   150

    GAGAAGGACA AAATCACCAC CAGGACACTG AAGGCCCGAA TGGACTCGCC   200

35   CTGCTCCCAG AGCCCACTTT TTT   223

    (2) INFORMATION FOR SEQ ID :670:

        (i) SEQUENCE CHARACTERISTICS:

40   (A) LENGTH: 37 base pairs

           (B) TYPE: nucleic acid

           (C) STRANDEDNESS: double

341

    (D) TOPOLOGY: linear

5   (xi) SEQUENCE DESCRIPTION: SEQ ID :670:

GCCAGCGCCG AAAACACACA CTTTGCTTCT TACCTGC   37

    (2) INFORMATION FOR SEQ ID :671:

10   (i) SEQUENCE CHARACTERISTICS:
         (A) LENGTH: 37 base pairs
         (B) TYPE: nucleic acid
         (C) STRANDEDNESS: double
15   (D) TOPOLOGY: linear

         (xi) SEQUENCE DESCRIPTION: SEQ ID :671:
20

GCCAGCGCCG AAAACACACA CTCTGCTTCT TACCTGC   37

    (2) INFORMATION FOR SEQ ID :672:

25   (i) SEQUENCE CHARACTERISTICS:
         (A) LENGTH: 59 base pairs
         (B) TYPE: nucleic acid
         (C) STRANDEDNESS: double
         (D) TOPOLOGY: linear
30

         (xi) SEQUENCE DESCRIPTION: SEQ ID :672:

35   GCCACCGCCG ACTCCAGGCA CTCACTCAAA CTCGATCTTC AACTCTGCAT   50

ACAAGCAGA   59

    (2) INFORMATION FOR SEQ ID :673:

40   (i) SEQUENCE CHARACTERISTICS:
         (A) LENGTH: 177 base pairs

342

```
              (B) TYPE: nucleic acid
              (C) STRANDEDNESS: double
              (D) TOPOLOGY: linear
```

5


```
         (xi) SEQUENCE DESCRIPTION: SEQ ID :673:
```

```
     GCCTGCGCCG ANGCATTCCC TTTGACCTGA GTCTGCAGCA GGTCCCTTTT          50
```
10
```
     GCGCTTCCTT CCCCTCAGGT AGCCTCTCTC CCCCTGGGCC ACTCCCGGGG          100
```

```
     GTGAGGGGGT TACCCCTTCC CAGTGTTTTT TATTTCCGTG GGGCTCACCC          150
```

15
```
     CAAAGTATTA AAAGCAACTT TGCAATT                                   177
```


```
     (2) INFORMATION FOR SEQ ID :674:
```

20
```
         (i) SEQUENCE CHARACTERISTICS:
              (A) LENGTH: 77 base pairs
              (B) TYPE: nucleic acid
              (C) STRANDEDNESS: double
              (D) TOPOLOGY: linear
```
25


```
         (xi) SEQUENCE DESCRIPTION: SEQ ID :674:
```

30
```
     GCCTGCGCCG AGCACAAGAC AATGACGAAC ATTTTAAAAA AAAAGAATGA          50
```

```
     CGCACATTTT AATAAAGCAC AGCACAA                                   77
```

```
     (2) INFORMATION FOR SEQ ID :675:
```
35
```
         (i) SEQUENCE CHARACTERISTICS:
              (A) LENGTH: 176 base pairs
              (B) TYPE: nucleic acid
              (C) STRANDEDNESS: double
40            (D) TOPOLOGY: linear
```

343

(xi) SEQUENCE DESCRIPTION: SEQ ID :675:

GCCAGCGCCG ACACCCAGAG ACTACAGTAC TTAGGGGTTA CACACAACAG   50

5   CCGTAACTGG CGGCTATCTG TTCATAACAA ACAAACCATA GCATATTTAC   100

ACCGCATCAC ATCGAGTGAT TATAGAAATC CATACACACA CCGATTGCAT   150

AAAATCTTTT TTTAGGAAAA AAACAC   176

10   (2) INFORMATION FOR SEQ ID :676:

          (i) SEQUENCE CHARACTERISTICS:
              (A) LENGTH: 141 base pairs
15   (B) TYPE: nucleic acid
              (C) STRANDEDNESS: double
              (D) TOPOLOGY: linear

20
          (xi) SEQUENCE DESCRIPTION: SEQ ID :676:

GCCAGCGCCG ACGCCCAGAG AATACAGTAC TTAGGGGTTA CACACAACAG   50

25   CCGTAACTGG CGGCTATCTG CTCATAACAA ACAAACCACA GCATATCTAT   100

ACCGTATCAC ATCGAGTGAT TATAGAAATC CACAGAGAGA C   141

          (2) INFORMATION FOR SEQ ID :677:
30
              (i) SEQUENCE CHARACTERISTICS:
                  (A) LENGTH: 365 base pairs
                  (B) TYPE: nucleic acid
                  (C) STRANDEDNESS: double
35   (D) TOPOLOGY: linear

          (xi) SEQUENCE DESCRIPTION: SEQ ID :677:
40
CTCTGAACAG ACACGAAGCT GCCCCTCGTA CAGCCACTCG GGCGCTGACC   50

344

```
ACCAGGGAAG GCAAAGGCAT AGGACTTCCA CACAGTCCAG ACACTGCACG        100

CTGACAAGCG CCTCCGCGGC GGCTGCGAGC CGGACTCAGG CGGATCTTGA        150

CAGCCTTGCC CGCGAGTGCC CGGGGATAGA ACCCGTGCGC GTGGACCTAG        200

GTGACTGGGA GGCCACCAAG CAGGCACTGG GCAGCGTGGG CCCCGTGGAC        250

CTGCTGGAGA ACAACACCAC CGTCGCCCTG CCGCAGCCCT TCCAGGAGGT        300

CACCAAGGAG GCCTTCGACA GATCCTTTGA GGTGAGCTTG CGTGCGATCA        350

TCCAGGTGCT GTAGA                                             365
```

(2) INFORMATION FOR SEQ ID :678:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 366 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: double
            (D) TOPOLOGY: linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID :678:

```
GCCTGCCCCG ACACGAAGAT GACCCTCGAC AGCCGCCGGG CGCTGATCAC         50

CAGGGAAGGC AAAGGCATAG GACTTCTGCA CGGTCCAGAC CCATGTACGC        100

GACGGGCGCC TNCGCGGTGG CTGCGAGCCG GATTCAGGCA GATCTTGACA        150

GCCTTGCCCG CGAGTGCCCG GGGATAGAAC CCGTGTGCGT GGACCTNGGG        200

TGACTGGGAG GCCACCAAGC AGGCACTGGG GTAGCATGGG CCCCGCGGAC        250

CTGCCGGAGA ACAATACCAC CGCCGCCTNT GCCGCAGTCT TTCCCGGAGG        300

TCACCAAGGA GGCCTNTTGA TAGATCTTTT GAGGTGAGCT TGCGTGCGGT        350

CATCTAGGTG CTGTAG                                            366
```

345

(2) INFORMATION FOR SEQ ID :679:

  (i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 253 base pairs
    (B) TYPE: nucleic acid
    (C) STRANDEDNESS: double
    (D) TOPOLOGY: linear

  (xi) SEQUENCE DESCRIPTION: SEQ ID :679:

```
GCCTGCCCCG ACACGAAGAT GACCCTCGAC AGCCGCCGGG CGCTGATCAC         50

CAGGGAAGGC AAAGGCATAG GCCAGCACCG ATGAATTCCC TTTGACCTAA        100

GTCTGCAGCA GGCCCCTTTT GCGCTTCCTT CCCCTCAGGC AGCCTCTCTC        150

CCCCCGGGCC ACTCCCGGGG GCGAGGGGGT TACCCCTTTC CCAGTGCTTT        200

TTATTCCCGC GGGGCTCACC CCAAAGCATT AAAAGCAGCT TTGCAATTCC        250

TTG                                                           253
```

(2) INFORMATION FOR SEQ ID :680:

  (i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 294 base pairs
    (B) TYPE: nucleic acid
    (C) STRANDEDNESS: double
    (D) TOPOLOGY: linear

  (xi) SEQUENCE DESCRIPTION: SEQ ID :680:

```
GCCAGCGCCG AGGCTTCTCC TAGGGCTGCT CCTGGGCCTA GCTCTTACAG         50

GCTCGTCCCC CAGGCCTGCC CTTCTCCACT GCCCCCTCCC GTGCCTGGGC        100

CCACACACCC TTCAGGAAGG GGGAGCACTG AGAAGCACAG CACAGGGGCT        150
```

346

CAGCCTGGGA TCCGGTGACG GCCTAGGCAG AGGCTGGGCC AGGAGTCCCA   200

AAGGTCAGTG ACAGTTTCTC AGAAGGGGCC CAGCGTCCAC CTCTCTCCCA   250

5   GGACCAGACA CCCCTTCCAG GCTCCCCCAC CCCCCTACGG GCTC   294

(2) INFORMATION FOR SEQ ID :681:

    (i) SEQUENCE CHARACTERISTICS:
10   (A) LENGTH: 268 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

15

    (xi) SEQUENCE DESCRIPTION: SEQ ID :681:

CCGCCAAGTG ACACCAAAGC CCTGGTTGAC TTTGACAGCC CCGTGGGCGC   50
20
GCGGGAGGCC GGGCACTCTA GGGTCTACCT ACCAGTGCAA TCGTTTAGCG   100

CTTTTTCAGT GGGGCAGGGC AGGAAGCAGG CGGGACCAGG CAGCCAGTTC   150

25 TCAAAGGCTG CGGGGCCAAC TAGAGGCCAC AGCCCCTCAC CCCTAGACAC   200

TGCCAACCAG AACTGACACG CGACCTCCTG GGCGCTGACG CCATTAAAAC   250

CAACGTTGGC GCCCGGCG   268
30
(2) INFORMATION FOR SEQ ID :682:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 354 base pairs
35   (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

40

    (xi) SEQUENCE DESCRIPTION: SEQ ID :682:

347

GCCACCGCCG AGGAAAACCG TGCACTGTTA GCCATGATCA ACCCCACCGT   50

GCTCTTCGAC ATTGACATCG ACGGCTGAGC CCTTGACCTA GTCTCCTTTG   100

AGCTGTTTGC AGACAAGGTC CCAAAGACAG CAGAAAATTT TCGTGCTCTA   150

AGCACTGGAG AGAAAGGATT TGGTTATAAG GGTTCCTGCT TTCACAGAAT   200

TATTCCAGGG TTTATGCGCC AGGGTGGTGA CTTCACACGC CATAATGGCA   250

CTGGTGGCAA GTCCATCCAT GGGGAGAAAT TTGAAGACGA GAACTTCATC   300

CTAAAGCATA CGGGCCCTGG CATCTTGCCC ATGGCAAATG CTGATCCTGA   350

TACA   354

(2) INFORMATION FOR SEQ ID :683:

     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 148 base pairs
          (B) TYPE: nucleic acid
          (C) STRANDEDNESS: double
          (D) TOPOLOGY: linear

     (xi) SEQUENCE DESCRIPTION: SEQ ID :683:

CCTCTCCGTG AGGACAGGGC AGTCTTGGTG CGCAGCCCCT CTCCTCTCTG   50

TCCCCTGACA CTCCACAGTG CGCCTGCAAC CCAGGCGGCC TTATCCGCGC   100

AGTGGCGGCA GTTCAGAAAT AAAGGGCCCA TTTGCGGGAT GCCGCATT   148

(2) INFORMATION FOR SEQ ID :684:

     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 307 base pairs
          (B) TYPE: nucleic acid
          (C) STRANDEDNESS: double
          (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :684:

AGCACCGAGG CGCTCAAGGT CCTGGGGAAC CCCAAGAGCG ACGAGACGAA   50

CGCGAAGGCG CTGGACTTTG AGCACTTTCT GCCCATGCTG CAGACAGTGG   100

CCAAGAACAA GGACCAGGGC ACCTATGAGG ATTATGCCGA AGGACTTCGG   150

GCGCTTGACA AGGAAGGAAA TGGCACCGTC ATGGGCGCTG AAACCCGGCA   200

TGCTCTTGCC ACACTGGGCG AGAAGACGAC AGAGGAAGAA GCAGAGACGC   250

TGGCGGCAGG GCATGAGGAC AGCAATGGTT GCATCAACTA CGAAGCATTT   300

GTGAGGC   307

(2) INFORMATION FOR SEQ ID :685:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 174 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: double
            (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :685:

CCATCTCAAG GCGATCCATG GAAAGCTTCC TGGGGAACGT ATGCTAGCAG   50

AGCTTCTCCC CGTGAATCAC ATGCCGGAGA TCCCACTCTT AGCTGGCAAA   100

TGAATCCGAA TTGACACAGC AGCCCCATAA GCATCAGCCC TGTAGAGTGA   150

GGAGCCATCT CTAGCGGGCC CTTC   174

(2) INFORMATION FOR SEQ ID :686:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 106 base pairs
            (B) TYPE: nucleic acid

                    (C) STRANDEDNESS: double
                    (D) TOPOLOGY: linear

5

            (xi) SEQUENCE DESCRIPTION: SEQ ID :686:

    ACATGCCAAA GAAAGCGTGC ATATTAGCCT ATAGAACCAC AGTAATCACA   50

10 CTAGAGAAAT TCCACTGCTA CAATAAAATG TAATCGGAAG CATCTTTACT   100

    TATAAA   106

15   (2) INFORMATION FOR SEQ ID :687:

            (i) SEQUENCE CHARACTERISTICS:
                (A) LENGTH: 97 base pairs
                (B) TYPE: nucleic acid
20   (C) STRANDEDNESS: double
                (D) TOPOLOGY: linear

25   (xi) SEQUENCE DESCRIPTION: SEQ ID :687:

    CAGATTTTTT TCAATTCTCC ACCCGCCAAA AGGGGAAGGG CTTTTCCCCA   50

    GAGAAAAGGA AAGGGGGGAA AAGGGGAAAA AACCCAACCC AAAACCA   97

30   (2) INFORMATION FOR SEQ ID :688:

            (i) SEQUENCE CHARACTERISTICS:
                (A) LENGTH: 172 base pairs
35   (B) TYPE: nucleic acid
                (C) STRANDEDNESS: double
                (D) TOPOLOGY: linear

40
            (xi) SEQUENCE DESCRIPTION: SEQ ID :688:

350

GCCTCTCTCT GGGCAAGTTC ATGGCTTCTG TGAGCCCTTT NACTGACCTC   50

CAGACACTGT TAGGCTGGAG CCTCGGTAGC CGTTCCTCCT GCCCACTGGA   100

CCTTCCAACA GGCCCTCCTC CCCTCCTTGA ACCGGCCCTT CCTGGCCTTT   150

GAATAGAGTC TAAGCGAACG AC   172

(2) INFORMATION FOR SEQ ID :689:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 200 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: double
            (D) TOPOLOGY: linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID :689:

GCCACCGCCG AGCTCACCCC TGCGGTGCAC GCCTTCCTTG ACAAGTTTT   50

TGGCTTCTGC GAGCCTTTTA CTGACCTCCA AACGCTGTTA AGCCGGAGCC   100

TCGGTAGCCG TTCCTCCTGC CCACTGGACN TCCCAACGGG CCCTCCTCCC   150

CTCCTTGAAC CAGCCCTTCC TGGCCTTTGA ATAAAGTTTA AGCGAGTAGC   200

(2) INFORMATION FOR SEQ ID :690:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 81 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: double
            (D) TOPOLOGY: linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID :690:

GCCACCGCCG AGCAGCAGCT TACAGCCAGG GCAGCTTTGA ATGCGGCCCA   50

351

ACACAAATTC ACAAGTGNTC TCAAAAAACT C   81

(2) INFORMATION FOR SEQ ID :691:

5   (i) SEQUENCE CHARACTERISTICS:
                  (A) LENGTH: 217 base pairs
                  (B) TYPE: nucleic acid
                  (C) STRANDEDNESS: double
                  (D) TOPOLOGY: linear
10

             (xi) SEQUENCE DESCRIPTION: SEQ ID :691:

15   TTCCTAACCG ATCGAATGAA GGATTCAAAA TTAACCACTC CAAGGGGGGA   50

      TTGAAGGAAG AACCACTCTT AACGGACAAA AAGAAAGAAA GGGGAGGGAG   100

      TAACAGGGAT ATGAGCTCTA GCCGCCCAAG CTAGCAATGG CAACCCTTCT   150
20
      GGGTCCCCTT TCAGCATGCG GAAGCTTTTC TTCGACTTCA CTCCATAAAC   200

      AGCTGACGCT CAAAAAG   217

25   (2) INFORMATION FOR SEQ ID :692:

             (i) SEQUENCE CHARACTERISTICS:
                  (A) LENGTH: 72 base pairs
                  (B) TYPE: nucleic acid
30   (C) STRANDEDNESS: double
                  (D) TOPOLOGY: linear

35   (xi) SEQUENCE DESCRIPTION: SEQ ID :692:

      CGGCCTTCTG GAAACCCATG AAAAAAAAAA GTTCCGCACC TCCAAGGGGA   50

      GAAGAGTAAG AGACAGCTTT CA   72
40
      (2) INFORMATION FOR SEQ ID :693:

352

```
          (i). SEQUENCE CHARACTERISTICS:
                (A) LENGTH: 329 base pairs
                (B) TYPE: nucleic acid
                (C) STRANDEDNESS: double
  5             (D) TOPOLOGY: linear




          (xi) SEQUENCE DESCRIPTION: SEQ ID :693:
 10

      TCTGCTGCCG CCCGCAAGCA GAGGGACTCG GAGATCATGC AGGGGAAGCA          50

      GAAAAAGGCA AACAAGAAGA AGGAGGAACC CAAGCAGCTT TGCGGCTTCG         100

 15   CGTCCAACCC TCTTGCCCTT CACCTACGCG CCTAGAGCCA GTCCCACCAC         150

      GCTCGCGTTT CCTCCTGTAG CGCTCACAGG CCCCAGCACC GATGGCATTC         200

      CCTTTGACCT AAGCCTACAG CAGGCCCCTT TTGTGCTTCC TTCCCCTCAG         250
 20
      GCAGCCTCTT TCCCCCTGGG CCACTCCCGG GGGTGAGGGG GTTGTCCTTC         300

      CCGATGCTTT TTGTTACCGT GGGGTTTGC                              329

 25   (2) INFORMATION FOR SEQ ID :694:


          .(i) SEQUENCE CHARACTERISTICS:
                (A) LENGTH: 296 base pairs
                (B) TYPE: nucleic acid
 30             (C) STRANDEDNESS: double
                (D) TOPOLOGY: linear




 35       (xi) SEQUENCE DESCRIPTION: SEQ ID :694:

      TCTGCTGCCG CCCGCAAGCA GAGGGACTCG GAGATCATGG CCTGCGCCGA          50

      ACAAATGTAC GGAATGCGTG AGTCCCTCTG GGAGGC....A CACGGATCCG        100
 40
      GATCACCTGT TTGAAACCAT CTCCCAAGCC ATGCTGAATG CTGCGGACCA        150
```

GGATGCAGTG TCAGGCATGG GAGTCATTGC CCACATCATC GAGAAGGACA   200

AAATCACCAC CAGGACACTG AAGGCCCGAA TGGACTAACC CTGTTCCCAG   250

AGCCCACTTT TTTTTTTTTT TTGGAAATAA AATAGCCTAT CTTTCG   296

(2) INFORMATION FOR SEQ ID :695:

      (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 211 base pairs
          (B) TYPE: nucleic acid
          (C) STRANDEDNESS: double
          (D) TOPOLOGY: linear

      (xi) SEQUENCE DESCRIPTION: SEQ ID :695:

GCCAGCACCG ACCTAGCCTA AGCCGTCTAG AACCACCTAA GCCCCTAAGG   50

AAACCTGTGG TCACACTGGG CCCTCCTCAG GAACTCTCCC TGCGCAGAGG   100

CGTGTCTTAG CACTAACCTC CTCCCTAGCC CCTTATTTGG TGGCAGAAGT   150

GGCCTCCACC CCTTCACCGT TTAAAAATAC TCCGTGGAGA AAAGAAAGCT   200

TNAAGGAGTA G   211

(2) INFORMATION FOR SEQ ID :696:

      (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 92 base pairs
          (B) TYPE: nucleic acid
          (C) STRANDEDNESS: double
          (D) TOPOLOGY: linear

      (xi) SEQUENCE DESCRIPTION: SEQ ID :696:

GCCTGCACCG ACAATGCCCA GAACTCCAGA ACTTCACCTA TCACGTATCC   50

CCAACAACAC AGACGGCGAA AACAAAACAA ACTTAAACCT AG   92

    (2) INFORMATION FOR SEQ ID :697:

         (i) SEQUENCE CHARACTERISTICS:
             (A) LENGTH: 314 base pairs
             (B) TYPE: nucleic acid
             (C) STRANDEDNESS: double
             (D) TOPOLOGY: linear

         (xi) SEQUENCE DESCRIPTION: SEQ ID :697:

GCCAGCACCG AGGCCTAGGG TAGAGCAGAC TGTGGCTTTA CCTCGGTGTC   50

CTACCAGCAA GGGGTCCTAT CTACCACCAT CCTCTATGAG ATCCTGCTAG   100

GGAAGGCCAC CCTGCATGCT GCGTTGGTCA GCACCCTTGC GCTGATGGCC   150

ATAGTCAAGA GAAAGGATTT CTGAAGGCAG CCCTAGAAGC GGAGTTAGGA   200

GCTTCTAACC CGTCATGGTT TAAATACACA CCCTTTTTTG GACAGCGCTT   250

CTGAAGAGCT GCTCTTACCT CTCTGCATCC CAATAGATAT CCCCCTATGC   300

GCATGCGTAC CTGT   314

    (2) INFORMATION FOR SEQ ID :698:

         (i) SEQUENCE CHARACTERISTICS:
             (A) LENGTH: 198 base pairs
             (B) TYPE: nucleic acid
             (C) STRANDEDNESS: double
             (D) TOPOLOGY: linear

         (xi) SEQUENCE DESCRIPTION: SEQ ID :698:

GCCACCGCCG AGTTCACCCC TGCAGTGCAC GCCTCCCTGG ACAAGTTCCT   50

355

GGCTTCTGTG AGCACCGTGC TGACCTCCAA ACACCGTTAA GCTGGAGCCT   100

CGGTAGCCGT TCCTCCTGCC CACTGGACTC CCAACAGGCC CTCCTCCCCT   150

CCTTGCACCG GCCCTTCCTG GTCTTTGAAT AAAGTCTAAG CGGGCAGC   198

(2) INFORMATION FOR SEQ ID :699:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 230 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID :699:

GCCAGCACCG ACAGCAACAA AAATGTTCCC ACAGAGATCA GGATGACTTG   50

CTGAAGCTCA GTGGAGGCTA AAAAGAGGAC ACAAAAGTGA ACAGAATGAC   100

CTTCCTACGC ACAACACAAA CACCAGTTAA TGCTCCATCC ACGCTGCTTA   150

AAGAGCATTC CTGTCCTAGC AAAATGGGCA AGTCCCTCTA CCCCCCACCC   200

TTAGCCGGCA TGCTTACATT AATAGCTAGA   230

(2) INFORMATION FOR SEQ ID :700:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 282 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID :700:

AGCAACAAAA ATGTTTCCAC GGAGATCAGG ATGACTTGCT GAAGCTCAGT   50

356

GGAGGCTCAA AAGAGGACAC AAAAGTGAAC AGAATGATCT TCCTACGCAC   100

AACACAAACA TCAGTTAATG CTCCATCCAC GCTGCTTAAA GAGCATTCCT   150

GTCCTAGCAA AATGGGCAAG TCCCTCTACC CCCCACCCTC ACTTGGCATG   200

CTTACATTAA TAGCTAAAGT CAATCCTGTA ATGAAATAAA GCAAATGGCA   250

GCTGTCTAGT AGCCTCCACT ACCGCAAATA TC   282

(2) INFORMATION FOR SEQ ID :701:

     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 255 base pairs
          (B) TYPE: nucleic acid
          (C) STRANDEDNESS: double
          (D) TOPOLOGY: linear

     (xi) SEQUENCE DESCRIPTION: SEQ ID :701:

GCCTGCGCCG AACAAACGCA CGGAATGAGC GAGTCCCTCT GGGAGCCCAA   50

CATGGATCCG AATCACCTGT TTGAAACCAT CTCCCAAGCC ATGCTGAATG   100

CTGCGGACCA GGATGCAGTG CCAGGCATGG GAGTCATTGC CCACATCACC   150

GAGAAGGACA AAATCACCAC CAGGACACTG AAGGCCCGAA TGGACTAACC   200

CTGTTCCCAG AGCCCACTTT TCCCCTATTT TGGAAATAAA ATAGCCTGTC   250

TTTCG   255

(2) INFORMATION FOR SEQ ID :702:

     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 89 base pairs
          (B) TYPE: nucleic acid
          (C) STRANDEDNESS: double
          (D) TOPOLOGY: linear

357

(xi) SEQUENCE DESCRIPTION: SEQ ID :702:

GCCTGCGCCG AGCACAAGAC AATGATGAAC ATTCTAAAAA AAAAGAATGA   50

CGCACATTTT AATAAAGCAC AGCACAAACT GTTCTTTCC   89

(2) INFORMATION FOR SEQ ID :703:

       (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 96 base pairs
          (B) TYPE: nucleic acid
          (C) STRANDEDNESS: double
          (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :703:

GCCAGCGCCG AGATCCTGGC GGCCTACCGC CCCCCGCCGC ACCCCCGCTA   50

GCGCCCCACC CCGCGTCTAT CGCCCAATAA AGGCATCTTT GTCGGG   96

(2) INFORMATION FOR SEQ ID :704:

      (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 123 base pairs
          (B) TYPE: nucleic acid
          (C) STRANDEDNESS: double
          (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :704:

GCCTGCGCCG AACAAACATA CAGAACGCAA CGAGTCCCTC TGAAGGCCCA   50

ACACGGATCC GAATCACCTG GCCCGAAACC ACCTACCTAG CCATGATGAA   100

TGCTGAGGAC CCAGATGCAG TAC   123

(2) INFORMATION FOR SEQ ID :705:

358

```
        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 262 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: double
            (D) TOPOLOGY: linear
```

```
        (xi) SEQUENCE DESCRIPTION: SEQ ID :705:

GCTTGATGCC TGCGCCGAAC AAACATACAG AATGCGGCGA GTCCCTCTGG        50

ACGCCCAACA CGGATCCGGA TCACCTATCT GAAACCATCT CCCAAGCCAT        100

GCTGAATGCT GCGGACCAGG ATGCAGTGCC AGGCATGGGA GCCATTGCCC        150

ACATCACCGA GAAGGACAAA ATCACCACCA GGACACTGAA GGCCCGAATG        200

GACTAACCCT GTTCCCAGAG CCCACTTTTT TTCTTTTTCA GAAATAAAAC        250

AGCCTGTCTT TC                                                262
```

```
    (2) INFORMATION FOR SEQ ID :706:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 209 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: double
            (D) TOPOLOGY: linear
```

```
        (xi) SEQUENCE DESCRIPTION: SEQ ID :706:

GCCAGCACCG ACCTAGCCTA AGCCGTCTAA AACCACCTGA GCCCCTGAGG        50

AAACCTGTGG TCACACTGGG CCCTCCTCAG GAACTCTCCC TGCGCAGAGG        100

CGTGTCTTAG CACTGCCCCC CTCCCTAGCC CCTTATTTGG CGGCGGAAGC        150

GGCCTCCACC CCTTCCCTGT TTGCAAACAC TCTGCGGAGA AAAGAGGACT        200
```

359

TCAGGGAGT   209

(2) INFORMATION FOR SEQ ID :707:

5   (i) SEQUENCE CHARACTERISTICS:
                (A) LENGTH: 170 base pairs
                (B) TYPE: nucleic acid
                (C) STRANDEDNESS: double
                (D) TOPOLOGY: linear
10

            (xi) SEQUENCE DESCRIPTION: SEQ ID :707:

15   GCCAGCACCG AGATGACGAG CTTTCTGCTG CCACCCACAA GCAGAGGGAC   50

        TCGGAGATCA CGCAGCAGAA GCAGAAAAAG GCAAACAAGA AGAAGGAGGA   100

        ACCCAAGCAG CTTTGCGGCT TCACGCCCAA CCCTCTCGCC CTTCACCTGT   150
20
        GAGCCTGGAG CCAGTCCCAC   170

        (2) INFORMATION FOR SEQ ID :708:

25   (i) SEQUENCE CHARACTERISTICS:
                (A) LENGTH: 160 base pairs
                (B) TYPE: nucleic acid
                (C) STRANDEDNESS: double
                (D) TOPOLOGY: linear
30

            (xi) SEQUENCE DESCRIPTION: SEQ ID :708:

35   GCCACCGTCG AGGATTCAGC AGCCTCCCCC TTGAGCCCCC TCACTTCCCG   50

        ACGTTCCGTT TCCCCCTGCC CGCCTTTTTC CGCCACCACC GCCGCCGCCT   100

        TCTGCAGGCC GTTTCCACCG AGGAAAAGGA ATCGTATTGT ATACCCGCTA   150
40
        CCCAGAACCT   160

(2) INFORMATION FOR SEQ ID :709:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 51 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID :709:

GCCAGCACCG AGCAACCTGG GTCCAAATAA AAACTAAACT GCAAACTCCT   50

G   51

(2) INFORMATION FOR SEQ ID :710:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 64 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID :710:

GCCTGCGCCG ACCACCCCTT CCTTTTCTTC ATCCAGCACA GCAAGACCAA   50

CAGGATTCTC TTCT   64

(2) INFORMATION FOR SEQ ID :711:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 104 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

361

(xi) SEQUENCE DESCRIPTION: SEQ ID :711:

CCAGCCAAAG ATTCCCAGGC TTTCTTGTCT CAGCAACTTT CCCATCTTCT   50

CTCTCTTGGA TGATGTTTGC CGTCAGCATT CACCAAATAA ACTTGCTCTC   100

TGGG   104

(2) INFORMATION FOR SEQ ID :712:

     (i) SEQUENCE CHARACTERISTICS:
         (A) LENGTH: 68 base pairs
         (B) TYPE: nucleic acid
         (C) STRANDEDNESS: double
         (D) TOPOLOGY: linear

     (xi) SEQUENCE DESCRIPTION: SEQ ID :712:

CTAGAAATAG ACCCACAATT TAGAGACAAT CTATACTAGA TTTATCTCCT   50

TTGTTTTTAG TTGAAGGC   68

(2) INFORMATION FOR SEQ ID :713:

     (i) SEQUENCE CHARACTERISTICS:
         (A) LENGTH: 127 base pairs
         (B) TYPE: nucleic acid
         (C) STRANDEDNESS: double
         (D) TOPOLOGY: linear

     (xi) SEQUENCE DESCRIPTION: SEQ ID :713:

AGCGAATGTA AGGGGGCCTT GGACGACCCG ACGCCGGACT ACATGAACCT   50

GCTGGGCATG ATCTTCAGCA TGTGCGGCCT CATGCTTAAG CTGAAGTGGT   100

GTGCTTGGGT CGCTGTCTAC TGCTCCT   127

362

(2) INFORMATION FOR SEQ ID :714:

  (i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 90 base pairs
    (B) TYPE: nucleic acid
    (C) STRANDEDNESS: double
    (D) TOPOLOGY: linear

  (xi) SEQUENCE DESCRIPTION: SEQ ID :714:

CTTGGGAGAT AACAGTTTCC CCTCTCCCTC CCCCTGCAGA TTTCCAGCGC   50

CCGGACCAAG GCCAAGTAAG CCTCTACAAA CCTAGCATTT   90

(2) INFORMATION FOR SEQ ID :715:

  (i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 69 base pairs
    (B) TYPE: nucleic acid
    (C) STRANDEDNESS: double
    (D) TOPOLOGY: linear

  (xi) SEQUENCE DESCRIPTION: SEQ ID :715:

CCAGCGCCGA GGTTGTATAT TTGTAGGTGC AGGCACACGA CCAGGACACA   50

ACAAAAATCT GAAAACATC   69

(2) INFORMATION FOR SEQ ID :716:

  (i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 102 base pairs
    (B) TYPE: nucleic acid
    (C) STRANDEDNESS: double
    (D) TOPOLOGY: linear

363

(xi) SEQUENCE DESCRIPTION: SEQ ID :716:

GCCGAGGAGA ACCCCCGCTC CCTGAGGAGG ACCTGTCCAA ACTCTTCAAA   50

CCACCACAGC CGCCTGCCAG GATGGACTCG CTGCTCATTG CAGGCCAGAT   100

AA   102

(2) INFORMATION FOR SEQ ID :717:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 124 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :717:

AGCGAATGTA ACCCGGCCTT GGACGACCCG ACGCCGGACT ACATGAACCT   50

GCTGGGCATG ATCTTCAGCA TGTGCGGCCT CATGCTTAAG CTGAAGTGGT   100

GTGCTTGGGA TACGCTGTCT ACAG   124

(2) INFORMATION FOR SEQ ID :718:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 123 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :718:

GGAAAACCGT GTACTATTAG CCATGGTCAA CCCCACCGTG TTCTTCGACA   50

TTGCCGTCGA CGGGAGCCCT TGGCGCGCGT CTCCTTTGAG CTGTTTGCAG   100

364

ACAAGGTCCC AAAGACAGCA GAA   123

(2) INFORMATION FOR SEQ ID :719:

5   (i) SEQUENCE CHARACTERISTICS:
                    (A) LENGTH: 54 base pairs
                    (B) TYPE: nucleic acid
                    (C) STRANDEDNESS: double
                    (D) TOPOLOGY: linear
10

               (xi) SEQUENCE DESCRIPTION: SEQ ID :719:

15   ACCACCCCTT CCTTTTCTTC ATCCAGCACA GCAAGACCAA CGGGATTCTC   50

        TTCT   54

        (2) INFORMATION FOR SEQ ID :720:
20
               (i) SEQUENCE CHARACTERISTICS:
                    (A) LENGTH: 117 base pairs
                    (B) TYPE: nucleic acid
                    (C) STRANDEDNESS: double
25   (D) TOPOLOGY: linear

               (xi) SEQUENCE DESCRIPTION: SEQ ID :720:
30
        GACCACAGGG CCTTCAATCC TTTTTTGTTT TCAACAGTCT TGCTGAATTA   50

        AGCAGAAAGG GCCTTGAATC CTGGCCTGGA ATTTGGGCAG ATATAGCATT   100

35   AATAAAACTG TGCACTC   117

        (2) INFORMATION FOR SEQ ID :721:

               (i) SEQUENCE CHARACTERISTICS:
40   (A) LENGTH: 55 base pairs
                    (B) TYPE: nucleic acid
                    (C) STRANDEDNESS: double

365

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :721:

GACCACCCCT TCCTTTTCTT CATCCAGCAC AGCAAGACCA ACGGGATTCT   50

CTTCT   55

(2) INFORMATION FOR SEQ ID :722:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 92 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :722:

GACTTCACGA ACTACACAGG TCTTACCATT GACCTAAGAT CAATCTGAAC   50

ATTCTTAGCC CAGTCAGGGA GCTCTGCTTC CTAGAAAGGC AT   92

(2) INFORMATION FOR SEQ ID :723:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 55 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :723:

TATTTCTAGG TGCAGGTATA TGATTGCCAT ATAATAAAAA TCTGAAAACA   50

TCCCC   55

366

(2) INFORMATION FOR SEQ ID :724:

        (i) SEQUENCE CHARACTERISTICS:
             (A) LENGTH: 164 base pairs
             (B) TYPE: nucleic acid
             (C) STRANDEDNESS: double
             (D) TOPOLOGY: linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID :724:

GTGTACTATT AGCCATGGTC AACCCCACCG TGTTCTTCGA CATTGCCGTC   50

GACGGGCGAG CCCTTGGCGC GCGTCCTTTG AGCTGTTTGC AGACAAGGTC   100

CCAAAGACAG CAGAAAAATT TTTCGTGCTC TGAGCACTGG AGAGAAAGGA   150

TTTGGTTATA AGGG   164

(2) INFORMATION FOR SEQ ID :725:

        (i) SEQUENCE CHARACTERISTICS:
             (A) LENGTH: 110 base pairs
             (B) TYPE: nucleic acid
             (C) STRANDEDNESS: double
             (D) TOPOLOGY: linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID :725:

GTGAGAAGCT GCAGCGGTGA CCTGGAGGCT GCGATGTGGA GGTGGAGGAC   50

ACACCCTCAA CCGTTGCTCC TGTAGCTTCC GAGTCCTGGT GGTGTCGGCC   100

AAGTTCAGTA   110

(2) INFORMATION FOR SEQ ID :726:

        (i) SEQUENCE CHARACTERISTICS:
             (A) LENGTH: 163 base pairs

367

```
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: double
            (D) TOPOLOGY: linear


    5


            (xi) SEQUENCE DESCRIPTION: SEQ ID :726:


    CCGTGTACTA TTAGCCATGG TCAACCCCAC CGTGTTCTTC GACATTGCCG        50
10

    TCGACGGGAG CCCTTGGCGC GCGTCTCCTT TGAGCTGTTT GCAGACAAGG        100


    TCCCAAAGAC AGCAGAAAAT TTTCGTGCTC TGAGCACTGG AGAGAAAGGA        150


15  TTTGGTTATA AGG                                               163


    (2) INFORMATION FOR SEQ ID :727:


            (i) SEQUENCE CHARACTERISTICS:
20              (A) LENGTH: 105 base pairs
                (B) TYPE: nucleic acid
                (C) STRANDEDNESS: double
                (D) TOPOLOGY: linear


25


            (xi) SEQUENCE DESCRIPTION: SEQ ID :727:


    GAGGGCGAGT TCGAGGAGGA GGCTGAGGAG GAGGTGGCCT AGAGCCTTCA        50
30

    GTCACTGGGG AAAGCAGGGA AGCAGTGTGA ACTCTTTATT CACTCCCAGC       100


    CTGTT                                                        105


35  (2) INFORMATION FOR SEQ ID :728:


            (i) SEQUENCE CHARACTERISTICS:
                (A) LENGTH: 186 base pairs
                (B) TYPE: nucleic acid
40              (C) STRANDEDNESS: double
                (D) TOPOLOGY: linear
```

368

(xi) SEQUENCE DESCRIPTION: SEQ ID :728:

GCCAGCGCCG AAAAGCCAAG ACTTCATGAA CTACACAGGT CTTACCATTG   50

ACCTAAGATC AATCTAAACT ATCTTAGCCC AGTCAGGGAG CTCTATTCCT   100

AGGAAGGCAT CTTTCGCCAG TGGATTCGCC TCAAGGTCGA GGCCGCCACT   150

GGAAGACGAA AAATAGAACT CCCTTAGAGT AGACAA.. ..   186

(2) INFORMATION FOR SEQ ID :729:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 167 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :729:

GCCAGCGCCG AGGTTGCATA TTCTAGGCGC AGGTATATGA TTGCCATATA   50

ATAAAAACCT GAAAACATCC CACCCGGGAA AAAAAAAAAA AAAAAAAAAA   100

AAAAACACCC CCCCCCCACA AAAAACTCAA ATTCCCCTCC CAAAAAACCC   150

CCTCAAAATC AAAAAAC   167

(2) INFORMATION FOR SEQ ID :730:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 64 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :730:

369

```
GCCTGCGCCG ACCACCCCTT CCTTTTCTTC ATCCAGCACA GCAAGACCAA        50

CAGGATTCTC TTCT                                               64
```

5   (2) INFORMATION FOR SEQ ID :731:

            (i) SEQUENCE CHARACTERISTICS:
                (A) LENGTH: 96 base pairs
                (B) TYPE: nucleic acid
10   (C) STRANDEDNESS: double
                (D) TOPOLOGY: linear

15   (xi) SEQUENCE DESCRIPTION: SEQ ID :731:

```
GCCAGCGCCG AGACCCTGGC GGCCTACCGG CCCCCCGTGC ACCCCCGCTA        50

GCGCCCCACC CCGCGTCTAT CGCCCAATAA AGGCATCTTT GCCGGG           96
```
20
        (2) INFORMATION FOR SEQ ID :732:

            (i) SEQUENCE CHARACTERISTICS:
                (A) LENGTH: 84 base pairs
25   (B) TYPE: nucleic acid
                (C) STRANDEDNESS: double
                (D) TOPOLOGY: linear

30
            (xi) SEQUENCE DESCRIPTION: SEQ ID :732:

```
GCCTGCGCCG ACCACCCCTT CCTTTTCTTC ATCCAGCACA GCAAGACCAA        50

35  CAGGATTCTC TTCTGCAGCC GCCACCGCGT CGGA                        84
```

        (2) INFORMATION FOR SEQ ID :733:

            (i) SEQUENCE CHARACTERISTICS:
40   (A) LENGTH: 96 base pairs
                (B) TYPE: nucleic acid
                (C) STRANDEDNESS: double

370

        (D) TOPOLOGY: linear

5   (xi) SEQUENCE DESCRIPTION: SEQ ID :733:

    GCCAGCGCCG AGATCCTGGC GGCCTACCGG CCCTCAGTGC ACCCCCGCTA   50

    GCGCCCCACC CCGCGTCTAT CGCCCAATAA AGGCATCTTT GCCGGG   96

10 (2) INFORMATION FOR SEQ ID :734:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 96 base pairs
15   (B) TYPE: nucleic acid
            (C) STRANDEDNESS: double
            (D) TOPOLOGY: linear

20
        (xi) SEQUENCE DESCRIPTION: SEQ ID :734:

    GCCAGCGCCG AGATCCTGGC GGCCTACCAG CCCTCCGTGC ACCCCCGCTA   50

25 GCGCCCCACC CCGCGTCTAT CGCCCAATAA AGGCATCTTT GCCGGG   96

    (2) INFORMATION FOR SEQ ID :735:

        (i) SEQUENCE CHARACTERISTICS:
30   (A) LENGTH: 97 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: double
            (D) TOPOLOGY: linear

35
        (xi) SEQUENCE DESCRIPTION: SEQ ID :735:

    GCCAGCGCCG AGATCCTGGC GGCCTACCAG CTCCTCAGTG CACCCCCACT   50
40
    AGCACCCCAC CCCGCATCTA TCGCCCAATA AAGGCATCTT TGCCGGG   97

371

(2) INFORMATION FOR SEQ ID :736:

   (i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 127 base pairs
    (B) TYPE: nucleic acid
    (C) STRANDEDNESS: double
    (D) TOPOLOGY: linear

   (xi) SEQUENCE DESCRIPTION: SEQ ID :736:

GCCAGCGCCG ACCACAGGGC CTTGAATCCT TTTTTGTTTT CAACAGTCTT   50

GCTGAATTAA GCAGAAAGGG CCTTGAATCC TGGCCTAGAA TTTGGGCAGA   100

TACAGCATTA ACAAAACCGC GCATCTC   127

(2) INFORMATION FOR SEQ ID :737:

   (i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 64 base pairs
    (B) TYPE: nucleic acid
    (C) STRANDEDNESS: double
    (D) TOPOLOGY: linear

   (xi) SEQUENCE DESCRIPTION: SEQ ID :737:

GCCTGCGCCG ACCACCCCTT CCTTTTCTTC ATCCAGCACA GCAAGACCAA   50

CAGGATTCTC TTCT   64

(2) INFORMATION FOR SEQ ID :738:

   (i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 88 base pairs
    (B) TYPE: nucleic acid
    (C) STRANDEDNESS: double
    (D) TOPOLOGY: linear

372

(xi) SEQUENCE DESCRIPTION: SEQ ID :738:

GCCAGCGCCG ACAATGCCCA GAATCCAGAA CTTTGCCTAT CACTCTCCCC   50

AACAACCTAG ACGCGAAAAC AGAATAAACT TCACCCAG   88

(2) INFORMATION FOR SEQ ID :739:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 95 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: double
            (D) TOPOLOGY: linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID :739:

GCCAGCGCCG AGATCCTGGC GGCCTACCGC CCCCCGTGCA CCCCCGCTAG   50

CGCCCCACCC CGCGTCTACC GCCCAATAAA GGCATCTTTG CCGGG   95

(2) INFORMATION FOR SEQ ID :740:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 245 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: double
            (D) TOPOLOGY: linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID :740:

GCCACCCCGA AGACGTATCA AGGCCCTCGA ACAACCCCGA GAGCTGATGA   50

GATGAATGAG AAGATGCCGA ACTTTGCGCA CTCCATGCCC CTGCTGCAGA   100

CAGTAACCAA GAGCAAGGAC CAGGGCACCC ATGAGGATTA TGTCGAAGGA   150

CTTCGGGTGT TTGACAAGGA AGGAAATGGC ACCGTCATGG GTGCTGAAAT   200

CCGGCATGTT CTTGTCACAC TGGGTGAGAA GATGACAGAG GAAGA   245

(2) INFORMATION FOR SEQ ID :741:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 88 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: double
            (D) TOPOLOGY: linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID :741:

GCCTGCGCCG ACGATGCCCA GAATCCAGAA CTTCGTCTAT CACTCTCCCC   50

AACAACCTAG ATGTGAAAAC AGAATAAACT TCACCCAG   88

(2) INFORMATION FOR SEQ ID :742:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 242 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: double
            (D) TOPOLOGY: linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID :742:

GCCGGAGCCA AAGCAAGCCA GAAGACTAAC AGTACTAACT ACAAATATTC   50

GCACCTCGAT CGCAGTACCC AGGTTCTCAC GTAGCTGAAG NAATGTATTA   100

CTCTGATAGT CTTCATTCGG ATAGACTAAA GCGTGTGCTG ACTGGAGATG   150

AGGTAAAGAA GATATGTATG CAACGTCCAG TCAAAACGGA TGGCAAGGTT   200

CGAGTCATGT CATATACCTT GCTGGATTAA TGGATGTCAT TA   242

(2) INFORMATION FOR SEQ ID :743:

374

(i) SEQUENCE CHARACTERISTICS:
         (A) LENGTH: 64 base pairs
         (B) TYPE: nucleic acid
         (C) STRANDEDNESS: double
    5   (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID :743:

10
    GCCTGCGCCG ACCACCCCTT CCTTTTCTTG ATCTAGCACA GCAAGACCAA   50

    CGGGATTCTC TTCT   64

15 (2) INFORMATION FOR SEQ ID :744:

         (i) SEQUENCE CHARACTERISTICS:
             (A) LENGTH: 69 base pairs
             (B) TYPE: nucleic acid
20   (C) STRANDEDNESS: double
             (D) TOPOLOGY: linear

25   (xi) SEQUENCE DESCRIPTION: SEQ ID :744:

    GCCAGCGCCG AGGTTGTATA TTTCTAGGTG CAGGTATATG ATTGCCATAT   50

    AATAAAAATT TGAAAACAT   69
30
    (2) INFORMATION FOR SEQ ID :745:

         (i) SEQUENCE CHARACTERISTICS:
             (A) LENGTH: 74 base pairs
35   (B) TYPE: nucleic acid
             (C) STRANDEDNESS: double
             (D) TOPOLOGY: linear

40
        (xi) SEQUENCE DESCRIPTION: SEQ ID :745:

GCCAGCTCCG AGGTTGTATA TTTCCAGGTG CAGATATATG ATTGCCATAT   50

AATAAAAATC TGAAAACATC CCAC   74

(2) INFORMATION FOR SEQ ID :746:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 88 base pairs
        (B) TYPE: nucleic acid
       .(C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID :746:

GCCTGCGCCG ACGATGCCCA GAATCCAGAA CTTTGTCTAT CACTCTCCCC   50

AACAACCTAG ATGTGAAAAC AGGATAAACT TCACCCAG   88

(2) INFORMATION FOR SEQ ID :747:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 88 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID :747:

GCCTGCGCCG ACGATGCCCA GAATCCAGAA CTTTGTCTAT CACTCTCCCC   50

AACAACCTAG ATGTGAAAAC AGAATAAACT TCACCCAG   88

(2) INFORMATION FOR SEQ ID :748:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 178 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double

376

(D) TOPOLOGY: linear

5　　　　　　(xi) SEQUENCE DESCRIPTION: SEQ ID :748:

GCCAGCACCG ATGAATTCCC TTTGACCCAA GTCTGCAGCA GGTCCCTTTT　　　　50

GCGCTTCCTT CCCCTCAGGC AGCCTCTTTC CCCCTGGGCC ACTCCCGGGG　　　100

10

GCGAGGGGGC TACCCCTTTC CCAGGCTTTT TATTCCCGTG GGGCTCACCC　　　150

CAAAGCATTA AAAGCAGCTT TGCAATTC　　　　　　　　　　　　　　　178

15　　　　(2) INFORMATION FOR SEQ ID :749:

　　　　　　　(i) SEQUENCE CHARACTERISTICS:
　　　　　　　　　(A) LENGTH: 235 base pairs
　　　　　　　　　(B) TYPE: nucleic acid
20　　　　　　　　(C) STRANDEDNESS: double
　　　　　　　　　(D) TOPOLOGY: linear

25　　　　　　(xi) SEQUENCE DESCRIPTION: SEQ ID :749:

GCCAGCACCG AAAAGCCAAG ACTTCATGAA CTACACAGGT CTTACCATTG　　　50

ACCTAAGATC AATCTGAACT ATCTTAGCCC AGTCAGGGAG CTCTATTCCT　　　100

30

AGAAAGGCAT CTTTCGCCAG TGGATTCGCC CCAAGGTTGA GGCCGCCATT　　　150

GGAAGACGAA AAATTGCACT CCCTTGGCGC AGACAAACAC CAGTTCCCAT　　　200

35　　TGGCGCTGCT GCCTATAACA AACACTTTTT TTTTT　　　　　　　　　　235

　　　　(2) INFORMATION FOR SEQ ID :750:

　　　　　　　(i) SEQUENCE CHARACTERISTICS:
40　　　　　　　　(A) LENGTH: 87 base pairs
　　　　　　　　　(B) TYPE: nucleic acid
　　　　　　　　　(C) STRANDEDNESS: double

    (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID :750:

GCCTACGCCG AAAACCCCTT CCTTTTTTTC ATCCAGAAAA GCAAGAGAAA   50

AAGGATTCTC TTCTGCGGCC GCCAACGCGT CGGAGAT   87

(2) INFORMATION FOR SEQ ID :751:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 170 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID :751:

GCCTCCGCCG ATTCGTGACC AAGAAGGCTC TATGCATTCA GGCTTTCCAG   50

GAGACTCAAA AGCTGAAGAA GCAAAGAAGA GCCTTAAAGG CTGCAGCAGC   100

AGTCCNAAAA ACAAGCAGAG CAGAGGAACC CAGACAGCCC TGCCAAAGCC   150

ATGCCAAAGA CACTCAAAGA   170

(2) INFORMATION FOR SEQ ID :752:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 72 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID :752:

378

```
GCCAGCACCG AGGTTGCATA TTTCTAGGCG CAGGCATATG ATTGCCATAT          50

AATAAAAAAA TGAAAACACC CC                                        72
```

(2) INFORMATION FOR SEQ ID :753:

    (i) SEQUENCE CHARACTERISTICS:
       (A) LENGTH: 122 base pairs
       (B) TYPE: nucleic acid
       (C) STRANDEDNESS: double
       (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID :753:

```
GCCAGCGCCG AGGACACCAA GAAGGTTTTG GACAGCGTGG GCATCGAGGC          50

GGACAACAAC CAGCTCAACA AGGCCATTAG TGAGCTGAAT GAAAAAAACA          100

TTGAAGACGT TATTGNCCAG GA                                        122
```

(2) INFORMATION FOR SEQ ID :754:

    (i) SEQUENCE CHARACTERISTICS:
       (A) LENGTH 243 base pairs
       (B) TYPE: nucleic acid
       (C) STRANDEDNESS: double
       (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID :754:

```
GCCACCGCCG ACTGAAACTG CACCGACCCC CCCTCGAGGA CCTGCTCTTA          50

GGTTCAGAAG CAAACCTCAC GTGCACACTG ACCGACCTAA GAGACGCCTC          100

AGGCGCCACC TTCACCTGGA CACCCTCAAG CGGGAAGAGC ACTGTTCAAG          150

GACCACCTAA GCATGACCTC TACGGCTGCT ACAGCGTGTC CAGTGCCCTG          200
```

379

CCGGGCTGCG CCGAGCCATG GAACCATGGG AAGACCTTCA CTT   243

(2) INFORMATION FOR SEQ ID :755:

        (i) SEQUENCE CHARACTERISTICS:
                (A) LENGTH: 71 base pairs
                (B) TYPE: nucleic acid
                (C) STRANDEDNESS: double
                (D) TOPOLOGY: linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID :755:

GCCAGCGCCG AGGTTGCATA TTTCTAGGCG CAGGCATATG ATTGCCATAT   50

AACAAAAACC TGAAAGCATC A   71

(2) INFORMATION FOR SEQ ID :756:

        (i) SEQUENCE CHARACTERISTICS:
                (A) LENGTH: 243 base pairs
                (B) TYPE: nucleic acid
                (C) STRANDEDNESS: double
                (D) TOPOLOGY: linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID :756:

GCCACCGCCG AGTGACGCCA AAGCCCTTGG TTGACTCTAA CAGCCCCGTG   50

GGCGCGCGGG AGGCCGGGCG CTCTAGGGTC TACCTATCAG CGCAATCGTT   100

TAGTGCTTTT TCAGTGGGGC GGGGCGGGAA GCAGGCGGGA CCAGGCAGCC   150

AGTTCTCAAA GGCTGCGGGG CCGACTAGAG GCCACAGCCC CTCACCCCTA   200

GACGTCGCCA ACCAGAACTG ACGCGCGACC TCCTGGGCGC TGA   243

(2) INFORMATION FOR SEQ ID :757:

380

(i) SEQUENCE CHARACTERISTICS:
       (A) LENGTH: 64 base pairs
       (B) TYPE: nucleic acid
       (C) STRANDEDNESS: double
       (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :757:

GCCTGCGCCG ACCACCCCTT CCTTTTTTTT ATCCAGCACA GCAAGACCAA   50

CAGGATTCTC TTCC   64

(2) INFORMATION FOR SEQ ID :758:

       (i) SEQUENCE CHARACTERISTICS:
              (A) LENGTH: 243 base pairs
              (B) TYPE: nucleic acid
              (C) STRANDEDNESS: double
              (D) TOPOLOGY: linear

       (xi) SEQUENCE DESCRIPTION: SEQ ID :758:

GCCAGCACCA AGTGACGCCA AAGCCCCTAG TTGACTCTAA CAGCCCCGTG   50

GGCGCGCGGG AGGCCGAGCG CTCTAGGGTC TACCTATCAG CGCAATCGTT   100

TAGCGCTTTT TCAATGGGGC AGGGCAGGAA GCAGGCGGGA CCAGGCAGCC   150

AGTTCTCAAA GGCTGCGGGG CCGACTAGAG GCCACAGCCC CTCACCCCTA   200

GACGTCGACA ACCAGAACTG ACGTGCGACC TCCCGGGCGC CGA   243

(2) INFORMATION FOR SEQ ID :759:

       (i) SEQUENCE CHARACTERISTICS:
              (A) LENGTH: 245 base pairs
              (B) TYPE: nucleic acid
              (C) STRANDEDNESS: double

381

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :759:

GCCACACCAG ACTTTCGACC CCCCAACCCT CTGAGGAAGA TGGGGGCAAG   50

AAGATCACGC TCCCCGCCTG TTCCCCCGCC GCTTTTCTCC TCTCTTCTCT   100

CTTCGCTCTC AGCTCCCCCT GTCCCCTCAG CTCCAGACGT AGGGGAGGGG   150

TTGCCACAGA CTCCCTGCTT GAAGCCTGCC CTTGCCTAAG ATGCTGGTAA   200

TGGCCATGGT ACCCCCTTCC GGGCATCTAC TCTGGTTTTC GGCCA   245

(2) INFORMATION FOR SEQ ID :760:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 68 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: double
            (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :760:

GCCAGCGCCG AGGTCGCATA TTTCTAGGCG CAGGTATATG ACTGCCATAT   50

AACAAAAACC NTGAAAAC   68

(2) INFORMATION FOR SEQ ID :761:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 71 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: double
            (D) TOPOLOGY: linear

382

(xi) SEQUENCE DESCRIPTION: SEQ ID :761:

GCCAGCGCCG AGGTCGCATA TTTCTAGGCG CAGGTATATG ATTGCCATAT   50

5   AATAAAAACT GAAAACACCC C   71

(2) INFORMATION FOR SEQ ID :762:

        (i) SEQUENCE CHARACTERISTICS:
10   (A) LENGTH: 88 base pairs
                (B) TYPE: nucleic acid
                (C) STRANDEDNESS: double
                (D) TOPOLOGY: linear

15

        (xi) SEQUENCE DESCRIPTION: SEQ ID :762:

GCCTGCGCCG ACGATGACCA GAATCCAGAA CTTTGCCTAT CACTCTCCCC   50
20
AACAACCTAG ACGCGAAAAC AGAATAAACT TCACCCAG   88

(2) INFORMATION FOR SEQ ID :763:

25   (i) SEQUENCE CHARACTERISTICS:
                (A) LENGTH: 223 base pairs
                (B) TYPE: nucleic acid
                (C) STRANDEDNESS: double
                (D) TOPOLOGY: linear

30

        (xi) SEQUENCE DESCRIPTION: SEQ ID :763:

35   GCCTGCGCCG ACAAACAAAA CCTGGAGGCC ATTCTGCACA GCCTGCCCGA   50

        GAACTGTGCC AGCTGGCGGT GAGGGCTGCC CAGATCCCCG GCACACACTC   100

        CCCCACCTGC TGTTTACATG ACCCAGGGGG CGCACACTAC CCCACAGGCG   150
40
        CGCCCATACA GACATTCCCC GGAGCCGGCT GCTGCGAACT CGACCCCGTG   200

CGGATAGTCA CACTCCCTGC CGA   223

(2) INFORMATION FOR SEQ ID :764:

(i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 70 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :764:

GCCAGCGCCG AGGTTGCATA TTTCTAGGCG CAGGTATATG ATTGCCATAT   50

AATAAAAATC TGAAAACACC   70

(2) INFORMATION FOR SEQ ID :765:

(i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 118 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :765:

GCCAGCGCCG ACCGCCCCAA AAATACTCCC ACCGGGATCA GGGCGATTAA   50

TGAAGACTCA ACGGGGACTA AAAAGGGGCC CCAAAAAAAA CCAAACCACC   100

TTTCTACGTA CCGTATAG   118

(2) INFORMATION FOR SEQ ID :766:

(i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 88 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double

384

(D) TOPOLOGY: linear

5   (xi) SEQUENCE DESCRIPTION: SEQ ID :766:

GCCAGCGCCG ACGATGCCCA GAATCCAGGA CTTTGCCTAT CACTCTCCCC   50

AACAACCTAG ACGCGAAAAC AGAATAAACT TCACCCAG   88

10   (2) INFORMATION FOR SEQ ID :767:

           (i) SEQUENCE CHARACTERISTICS:
                (A) LENGTH: 91 base pairs
15   (B) TYPE: nucleic acid
                (C) STRANDEDNESS: double
                (D) TOPOLOGY: linear

20   (xi) SEQUENCE DESCRIPTION: SEQ ID :767:

GCCACCGCCG ACTCCAGGCA CTCACTCAAA CTTGATCTTC AACTCTGCAT   50

25   ACAAGCAGAA GCAATAAACC AATCTGATTT TCTTTTCAAT T   91

        (2) INFORMATION FOR SEQ ID :768:

           (i) SEQUENCE CHARACTERISTICS:
30   (A) LENGTH: 223 base pairs
                (B) TYPE: nucleic acid
                (C) STRANDEDNESS: double
                (D) TOPOLOGY: linear

35

           (xi) SEQUENCE DESCRIPTION: SEQ ID :768:

GCCTGCGCCG AACAAATATA CAGAATGCGC GAGTCCCTCT GGAAGCCCAA   50
40
CATGGATCCG GATCACCTGT TTGAAACCAT CTCCCAAGCC ATGCTGAATG   100

385

CTGCGGACCA GGATGCAGTG CCAGGCATGG GAGTCATTGC CCACATCACC   150

GAGAAGGACA AAATCACCAC CAGGACACTG AAGGCCCGAA TGGACTCGCC   200

CTGCTCCCAG AGCCCACTTT TTT   223

(2) INFORMATION FOR SEQ ID :769:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 37 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: double
            (D) TOPOLOGY: linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID :769:

GCCAGCGCCG AAAACACACA CTTTGCTTCT TACCTGC   37

(2) INFORMATION FOR SEQ ID :770:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 37 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: double
            (D) TOPOLOGY: linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID :770:

GCCAGCGCCG AAAACACACA CTCTGCTTCT TACCTGC   37

(2) INFORMATION FOR SEQ ID :771:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 91 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: double
            (D) TOPOLOGY: linear

386

(xi) SEQUENCE DESCRIPTION: SEQ ID :771:

GCCACCGCCG ACTCCAGGCA CTCACTCAAA CTCGATCTTC AACTCTGCAT   50

ACAAGCAGAA GCAATAAACC AATCTGATTT TCTTTTCAAT T   91

(2) INFORMATION FOR SEQ ID :772:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 177 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: double
            (D) TOPOLOGY: linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID :772:

GCCTGCGCCG ANGCATTCCC TTTGACCTGA GTCTGCAGCA GGTCCCTTTT   50

GCGCTTCCTT CCCCTCAGGT AGCCTCTCTC CCCCTGGGCC ACTCCCGGGG   100

GTGAGGGGGT TACCCCTTCC CAGTGTTTTT TATTTCCGTG GGGCTCACCC   150

CAAAGTATTA AAAGCAACTT TGCAATT   177

(2) INFORMATION FOR SEQ ID :773:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 151 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: double
            (D) TOPOLOGY: linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID :773:

AACATAAGAG GAGAAAGGAA GGGACATGAG GCATACCATT CCCCCCCCCA   50

387

GAATTAGAGG TAAAGGAATC CTAAAATAAA GAGCACAGCA GCAATCACAC   100

TCACAGGGTC CAGAGGCGTA TTCCTGGCCA TCTTCCTAGT ACTCGGTCCG   150

T   151

(2) INFORMATION FOR SEQ ID :774:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 299 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID :774:

ATCTTAATGA ACATGGCATT TAAAATCCTG TAATTTCAAA CAGTGAACCA   50

CAATGCCGTA TGATCTAAAG GCTGCTGAAC CACAGCGTGG ATACACTTAA   100

CTGAGCTCCT CGCTGGGTCA AAGCACTCAT CTCCGAGTCT AAAGCTACAC   150

ACTATGGAGC ACACAACTCT GCCTCGCGCT GACACCAGAC AAACACGGCG   200

GGAGCTGAGG CGGACAGCTA CAGGACCACG AGCATAGACC ACGGCACCTG   250

AGACCATCTC TACGCAAGGA CTTAAGGAAG CAAATATAAT ATTAAAATA.   299

(2) INFORMATION FOR SEQ ID :775:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 185 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID :775:

388

TGAAGGAAAT GACTACCTTG CACTACATGA AAAGGATATC GTTGCCATTG   50

TGGCGTAATT TTCGTGCCGA GTGAATGTGG CGCAAACAAC TATATATCNA   100

AACCGTATAT TTAAAATGAA TTACTAGAGA GGGAATGTAA TCATGGCAAA   150

AGAAATTAAG TTTTAAGAAG ATGCTAGTGC TAAGC   185

(2) INFORMATION FOR SEQ ID :776:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 255 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID :776:

ATCCAAGCCC ATACCCATCA ACAATGGGAC AGCGATTGGA TCACCAGCCA   50

TTTCACCACA CATGGCAACA AACTTACCTT CTTTAAGAGC GGCAGTAATC   100

ACATCGTCGA TCAAACGCAA AATCGATGGG TTATAAGGTC GATACAAATA   150

AGCAACCTTA TCATTACCAC GATCTGCAGC CATCGTATAA CCAATCAAAT   200

CGTCGGTACC AATCGAGAAG AAGTCCAATC CCTTAGCAAA CTCATCAGCC   250

AACAT   255

(2) INFORMATION FOR SEQ ID :777:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 239 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

389

(xi) SEQUENCE DESCRIPTION: SEQ ID :777:

AGATTCTGCA GTGTAATATG ACCAAATCAA ATCCGTTGTA TGATCGAATA   50

5   AGGCCGTCAT AAAGTAAGTT GAAAATTTCG TTCTTGGCTG AATCGTGTTA   100

AACCGTTGTA CACAACGTAG TAAAATTCAT AACCCATCTG CATACCAATC   150

GTCAGCCGTG ATGCATTTAC TCACTTTACG TCGATGAATG TCAAACATCG   200

10 CACCTTTTCA ATGTTTACTA AAAACATAGC ACGCAATAT   239

(2) INFORMATION FOR SEQ ID :778:

15   (i) SEQUENCE CHARACTERISTICS:
                (A) LENGTH: 252 base pairs
                (B) TYPE: nucleic acid
                (C) STRANDEDNESS: double
                (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :778:

25 ACTGAACAAC GTAAGGTCTT GACTGACACT TACAAGTTGG ATGAATCTGA   50

AATAAAGTTG GTATTGTTTG AAGCAGCCCA ACAATTTCGA ACATGCTACA   100

AGACCGTCGT TTGACTGACA AGGCCTTGAA GTACATGACT GACAACAACG   150

30 TCGATCTTCG CCTAGGCGCC ATGGTCACTG GTGTTGACGA AAATGGCGTG   200

ATTTTTAAGG ATGACTCAAC TTCGCCAACT CGGTTCCTCA TTAGGACAAC   250

35 TA   252

(2) INFORMATION FOR SEQ ID :779:

            (i) SEQUENCE CHARACTERISTICS:
40   (A) LENGTH: 265 base pairs
                (B) TYPE: nucleic acid
                (C) STRANDEDNESS: double

390

(D) TOPOLOGY: linear

5   (xi) SEQUENCE DESCRIPTION: SEQ ID :779:

TCGGATTTAT ACGGCTGTTA GTGCTATCGG CGTCTGGTAT GTGTTATATA   50

TCGCCTATCG TTTTTTGGCC AATGGGCGTT GGCTACGCGG GGCAATGATT   100
10
GCCATCGTTT TTGTTATCTT GACTTATTTC GTCATTTTAA ATATTATTTA   150

ACTATTTTAC AAATAAAGTG GTCAAATGGG ATATTTTGCC AAAAATAGAG   200
15
AAAGTGTTAG GCGGCCCACA GCTGGAGGAA GAGAAAGCGG CTGTGCATGA   250

AGTTATTGCA CCCGC   265

(2) INFORMATION FOR SEQ ID :780:
20
          (i) SEQUENCE CHARACTERISTICS:
               (A) LENGTH: 249 base pairs
               (B) TYPE: nucleic acid
               (C) STRANDEDNESS: double
25   (D) TOPOLOGY: linear

          (xi) SEQUENCE DESCRIPTION: SEQ ID :780:
30
CTCAGCTGGA CCAAATTAGT TGAATTACTC ACCATCAATA AACTATAAAT   50

GGCGCCAATG ACCAACCCGC CAACGATTCC CGTTGTCAAA GAACCTAATA   100

35 ACAAGTAACC AACCGCAGCC CCAACAAGCC CAACTAGGTT TAAAAAAACC   150

AAGCAAAAGG CCAACTGTCC GTCGTTTATT GGATTGTATC TGCTCATATA   200

ACATTAAAAC TTAACCGTTG GCACTTCTTT CTCAGACCCG CCGATACTG   249
40
(2) INFORMATION FOR SEQ ID :781:

(i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 188 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: double
            (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID :781:

GAGAGAACCC ACCATAGTAC TGTCTCCTGC AGACAAGACC AACGGCAAGG   50

CCGCCTGGGG TAAGGTCGGC GCGCACCTGG CGAGTATGGT GCGGAGGCCC   100

TGGAGAGGAT GTTCCTGTCC TTCCCCACCA CCANNNACTA CTTCCCGCAC   150

TTCGACCTGA GCCACGGCTC TGCCCAGGTT AAGGGCCA   188

(2) INFORMATION FOR SEQ ID :782:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 182 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: double
            (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID :782:

AATATTTATT TCATTTGTTT ACTACCACTT CATTTTATTT GTTTGCTGCT   50

GCCGTTTTAT TTATTTTTAC TGAAAGTGAG AGGGAACTTT TGTGGCCTCC   100

AACCTTTTTC TGTAGGCCGC CTTAAGCTTT CTAAATTTGG AACATCTAAC   150

AAGCTGAAGN GGAAAAGGGG GTTTCGCAAA AT   182

(2) INFORMATION FOR SEQ ID :783:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 295 base pairs

392

```
                  (B) TYPE: nucleic acid
                  (C) STRANDEDNESS: double
                  (D) TOPOLOGY: linear
```

5

```
        (xi) SEQUENCE DESCRIPTION: SEQ ID :783:
```

10
```
        CACAGCCAGA GCTTCGTCCT CAGTGACCAC AGGGCTGAGC CAGGCTCAAC       50
```

```
        CGGCTTCTGG CTCTTGTTTT GCAGAAGAAG AACTAGAAGC AAGGNGCTTT      100
```

```
        CCTCCGGGTC CCAGAGCTGT TAGTGATGGA GCCAGGCCTG GGATCCAGCT      150
```

15
```
        TTCCTGAGTT CCTGACCCCT GCTATTTTAT TAGTCAGCTC TCAGCACTTA      200
```

```
        CCAGAGGAAC AGGCAGCCTT TTGGCTACTG CCTTCAGAGA AAGAGAGATG      250
```

```
        AGAGAATTCA AATGCGTGTT GGTGTTCCTG TTAGTACAAG CAGCA           295
```

20
```
    (2) INFORMATION FOR SEQ ID :784:
```

```
        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 295 base pairs
```
25
```
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: double
            (D) TOPOLOGY: linear
```

30
```
        (xi) SEQUENCE DESCRIPTION: SEQ ID :784:
```

```
        CAATAGCGAC TTCTGGTGTC AATTCGATAA TCGGCCAATG GATACTTCAC       50
```

35
```
        GTGTGTTTCA TCGTCTGTAA TAACGGCGAA TGGTGTCACT TCAGAACCAG      100
```

```
        TACCTGATGT TGTTGGAATG GCAACCATTT GTGTCAAACG CACTGGTAGA      150
```

```
        ACTTCACGAT ACGCTTACGG ATGTCCATGA ACTTTGTTC TATTTCCATG       200
```
40
```
        AACAATTCCT TGATACCTTC TTCGTCTGAC AAAATACCTT CGTGACGTGT      250
```

TGAGTATTCG TACAAGAAGC GACCAATCTT ACCGGCATCA AGTGC   295

(2) INFORMATION FOR SEQ ID :785:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 303 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID :785:

GTGTAAAGCG AGTAGCCCCC AAATCAGTCA TCTTGGCCTG AAGATGTAAA   50

CAAGGAGGTT TGCTTCCTGC AAGATGAGTA CTTCACTGAG TTTGGTTTTC   100

ATTTTTCCTA CACCGAAGCC ACCTCTGTCC ATCCAATGTT CATGTCTGTC   150

CGAGGCTGCG CAGGAGGTTA CGTCAAGATG TGGCCAATAA AGTCCAAAAA   200

GCGCTTTGAA TACTGTTCTG GGTTCACGGT GGAGATCTCC GCGCAGCCAT   250

GTTTAACAGT TTTTGCAGCA TGGGCAGCTT TCTTTTTTGC ATCATAATGA   300

GTA   303

(2) INFORMATION FOR SEQ ID :786:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 255 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID :786:

TATGGCGCGG ATCCTAACGG CTGGAATGAA GATATGCCAA CGTACAGCCT   50

394

```
CTATGACCCA GCCATGGGAT CAGGCTCATT GCTTTTGACG ACTGCTTCAT        100

ACATGAAGAA TGATGGTGTT CGTGGGGCCA TTAAGTACTA AGCCAAGAAG        150

TTATCACGAC AACCTATAAC TTGGGCCGAA TTAACTTGAT GATGCACGGG        200

GTGGAGTATA ACGATATCAA TATCCATAAT GCAGATACCT TGAGTTCAGA        250

CTGGC                                                        255
```

(2) INFORMATION FOR SEQ ID :787:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 206 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID :787:

```
CATTGAAAAG TGCCTGAAAA ATGGTAAATT CTTAAATGTG TGTGAGATTG        50

TCAGAATCAA CAAAACTAGG TTGGTTAAAC ATATCTCTGG TACATCAAGG        100

GGCATGATAC AAACCAGTCT AAAGACTGTT TATAAAGGAG AGAGCTGGCG        150

ACTTATTTTT ATTTTTTTTT TTTTGGACAG ACTCCCTTTG TCCCCAGGCC        200

GGAGTG                                                       206
```

(2) INFORMATION FOR SEQ ID :788:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 260 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

395

(xi) SEQUENCE DESCRIPTION: SEQ ID :788:

ACAAATAGCG ACCTCCTGGA GAAAAATCGA AAACGGCCAA GTGGATACCT   50

5   CACGTGGTTC ACGTCTGAAC AACGGCGAAT GTGAGCTACC TCAGAACCAG   100

TACCCGAAGT TGCTGGAAGG CAACCACATT TGGTTCAAAC GAGGCGTGGA   150

AGAACCTCAC GACACGCTTA CGGAGTCCAT GAACGCTTGT TGCAATCCAG   200

10   GAACAATTCC GCGACACCCT TCGTCTGACA AAAAACCTTC GTGACGCGTC   250

GAGTATCCGC   260

15   (2) INFORMATION FOR SEQ ID :789:

(i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 208 base pairs
            (B) TYPE: nucleic acid
20   (C) STRANDEDNESS: double
            (D) TOPOLOGY: linear

25   (xi) SEQUENCE DESCRIPTION: SEQ ID :789:

AACCCACCAT GGTGCTGTCT CCTGCCGACA AGACCAACGT CAAGGCCGCC   50

TGGGGTAAGG TCGGCCTGCG CACTATGCGT GAGTATGATG CAGAGGCCCT   100

30   GGAGAGGATG TTCCTGTCCT TCCCCACCAC CAAGCCCTAC TTCCCGCACT   150

TCGACCTGAG CCACGGCTCT GCCGAGGTTA GGGGCCACGA CAAGAAGGTG   200

35   ATCGACGC   208

(2) INFORMATION FOR SEQ ID :790:

(i) SEQUENCE CHARACTERISTICS:
40   (A) LENGTH: 289 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: double

396

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :790:

AAAAGAAGTA CGGTAAGGCA AATCCTGAAA TTAAGAGTTA CTATGTGCCT   50

GAAAATACAT TGTTCTACTC ATTTAGTGTG ATGGCAATGG GCGCCGGCGC   100

ACTCTTGCTA TCGACCATCG TCGCGCTTTG GATGAACCGT CGTAAGTCAC   150

AATTAATGTA GACACAACGT CGATTCTCGT GACTTATGGG GATCGCAACT   200

TTCGCGCCAT TCTCGATCAA CACAGCCGGT TGGTCAGTGA CTGAATTAGG   250

TCGTTATCCA TGGGTTGTTT ATGGCTTGAT GCTAATAGC   289

(2) INFORMATION FOR SEQ ID :791:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 232 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :791:

TTTCCTGTGG AAGTAGTTAA ATTGATAAAT TCCAAAAATT TGGCAATTAA   50

TTGCTCATTA TTAATGGTAG AGTTTCCATT AATGAAGTTG GAAAATACGG   100

TGAATCTTTC AATGAACTCA GTTAGACATT CGGAATGAGC TTCATACATT   150

GTCTTATTAT CTTTCTTCAA TTTATCCTCC AAATCTGGGA ATTCTGATAA   200

CCAAATTGAA GCACCTTATC TATGATCCGG GC   232

(2) INFORMATION FOR SEQ ID :792:

(i) SEQUENCE CHARACTERISTICS:

    (A) LENGTH: 232 base pairs

    (B) TYPE: nucleic acid

    (C) STRANDEDNESS: double

5   (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :792:

10

TTTCAACAAA CAGAAACCAA TTTCCAACCA GAGGGCGATT TCTCCTTGTC   50

TGGTAATATC GAACAAACTA TTTTTAAGAA CTTGATTTCT GGCAACATTA   100

15   AGAGCGCTGT GAAAAATTCT CTAGAGAATG ACTTACTAAC GGAGGCCATG   150

GCGATCGCAT TAGATTCAAA TAACGAAAGA TCAAAGGAAA GTGTCAAGAA   200

TGCCTATTTC GCGAAGTATG GATCTAAATA AC   232

20

(2) INFORMATION FOR SEQ ID :793:

    (i) SEQUENCE CHARACTERISTICS:

        (A) LENGTH: 292 base pairs

25   (B) TYPE: nucleic acid

        (C) STRANDEDNESS: double

        (D) TOPOLOGY: linear

30

    (xi) SEQUENCE DESCRIPTION: SEQ ID :793:

GGGAACATAT CTTCACGGTA GTGANCCCAG TGACCAGATG TCTTATACAA   50

35   GTTCAAGTTA GACAAAACGG GTGTATACAC GTGTTGGTAA CCATTGGCCA   100

ATTCTTTGTC GGTGATGTAA CGTTCAACTT GACGGCGAAG CGATTGCCCC   150

ATTTGGTAAC CAAACTGGCA AACCTGAACC CACTTCTTGA CTCGTAAAGA   200

40

ACAAGTCCAT GTCACGACCA ATCGTCCGGT GGTCACGTTC TTTAGCTTCT   250

```
         TCACGACGTG CAATTCTGCT TCAACGTCGG CTTGCTTCCA TT                    292
```

(2) INFORMATION FOR SEQ ID :794:

5   (i) SEQUENCE CHARACTERISTICS:
                    (A) LENGTH: 288 base pairs
                    (B) TYPE: nucleic acid
                    (C) STRANDEDNESS: double
                    (D) TOPOLOGY: linear
10

            (xi) SEQUENCE DESCRIPTION: SEQ ID :794:

```
15       CAGCAGGCAC AACACCATCG GTTGTCGCTG AAAGTATTTT TAAGTCTTTG          50

         GCCAAGAAGT CAGTTTCAGC TAAGTTAGAC GGCACTTATG CGGGTATGCA          100

         TGATGTCATT CCTGCATCCG ATGATTTTTA ATTAATTACA ACAACTGATG          150
20
         ATGAAGCGTC GAATTCGTCG CGTCATTCTG CCTCACACTC ACAGGCACAA          200

         GCCTTAAAGC ATTTGCCAAA GTTTGCTAAC ATGCACTTTG GCGCGGCAAC          250

25       CATTTATTGA AAATGGTTTC TACTATGATA CAAATAAC                       288
```

(2) INFORMATION FOR SEQ ID :795:

               (i) SEQUENCE CHARACTERISTICS:
30   (A) LENGTH: 258 base pairs
                    (B) TYPE: nucleic acid
                    (C) STRANDEDNESS: double
                    (D) TOPOLOGY: linear

35

            (xi) SEQUENCE DESCRIPTION: SEQ ID :795:

```
         GTGGCTATGT ATAAGCAGAT ATTATCTAGT AAATGTAAAG TGAACCCAAT          .50
40
         CGATAGACCC AAAAAGTGTT TTAACTGGAA AACACCTTAT GAGGTTTATT          100
```

399

TTGATGAAGT GTTGCAGTTG GTTTGATAAT TCAAGGCATT AAGGCAATAT   150

CTCAATCACC GCATTTTCCA CAACCGGCCA CAAAACAGCT CGTCTATTTC   200

GAGGTCAGTT ACGGCGTCCA GTCTTTGAGC AGATGATTTG CCCCGAGTGA   250

TCGTCGGC   258

(2) INFORMATION FOR SEQ ID :796:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 270 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: double
            (D) TOPOLOGY: linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID :796:

TGCTTCAAAG CCTGGCTTAA CCCGCTTGCC CACCAACTTC AATTATACCT   50

GCCCCTTTGC CTAACATCTC ACCGACTCGG GCAACCATCG TATCAACACC   100

CGCGACTCGA TCCCCATCGT AAAATGATTC CGAACTAACA TTTAACACAC   150

AATAGATAAT ACCATCAGCA TAATGCAAGG TTTTACCATC CACGACCCAG   200

AGGCGATCAA TCGCGACTAA CCGTCGTTGT AATTCAGGAC TAGCGGTACG   250

CTCATGTAAC GCGACAATAT   270

(2) INFORMATION FOR SEQ ID :797:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 210 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: double
            (D) TOPOLOGY: linear

400

(xi) SEQUENCE DESCRIPTION: SEQ ID :797:

AAATATCGCT GCGTGCAGCT GAGTTACTAG CTGTTGAAAC TTATCGTTAC   50

TTGTGTAGGT TGTCTGAAAC GGTCGCAGTC ACCGGTTAGC TTGATAAGTC   100

AGGTTTTCAG CAACTGTCAT CAAGCCATCA CGACCTATAT AAGCCACTGC   150

AATCGCACTT TACATCATTA AGACCCTTAC TAGAAGTAAC TGGCCATCCT   200

GCCACCGCTT   210

(2) INFORMATION FOR SEQ ID :798:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 218 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :798:

ATCATAAGCG CTGGAACTTG GGGCATTGTA CAGGGACAAC TTCGGCCTTT   50

GTTAGCCCCA AGAGTCTACA CTCTGCCAAT GGTGCGCTCC ATAGGAAAAA   100

CCACGGTCCA AGGCAAAAAC TACGAACCTC AGATAACCGC AAAGAGGATA   150

TCAACCAGAG GACGGAAATG TAAGCCTATT TTAGCCCAAA TAACGAGACA   200

AGTAGTTGAG CTAAATGC   218

(2) INFORMATION FOR SEQ ID :799:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 176 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

401

        (xi) SEQUENCE DESCRIPTION: SEQ ID .:799:

        CCTATCAGAA TCCAATGAGA ACTACAATGG TGTGCCCAGA CGTAGAGCTG   50

        AGAATAGCAT TACCAAATGG AACAACGTGC TACAGTCAGG ATTAAAAAGA   100

        ACAATACTAC AAACCAAGTA TATCAGGCTA TTATAGCAAA GGCTGCCATG   150

        AACAATACAA CACTGAATTA CTCGGC   176

        (2) INFORMATION FOR SEQ ID :800:

            (i) SEQUENCE CHARACTERISTICS:
                (A) LENGTH: 254 base pairs
                (B) TYPE: nucleic acid
                (C) STRANDEDNESS: double
                (D) TOPOLOGY: linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID :800:

        GCAATTGCTT AATTTGTTCT TCCTTCTTAG CATTTTGCTG AGAAGCCAAA   50

        CGTTGCGCCA ATTCAGAAGA TTCACGCCAG AAGTCGTAGT TACCAACGAA   100

        TGGTGTGATC TTACCAAAGT CAACATCCAA GATGTTGGTT GACACGGCGT   150

        TTAGGAAGTG ACGGTCGTGG GATACCACAA TCACTAGGTT CGGGAAATCA   200

        GCCAAGAAAT CTTCTAACCA GTTAATTGTC TGCACATCCA GACCGTTGGT   250

        TCGA   254

        (2) INFORMATION FOR SEQ ID :801:

            (i) SEQUENCE CHARACTERISTICS:
                (A) LENGTH: 203 base pairs
                (B) TYPE: nucleic acid
                (C) STRANDEDNESS: double
                (D) TOPOLOGY: linear

402

(xi) SEQUENCE DESCRIPTION: SEQ ID :801:

5   ATCCAGGCCC ATACCCATCA ACCCTGAAAC AACGATTGAA TCACCAGCCA   50

        TTTAACCACA CATTGCAACA AACTCACATT GGGTTCCGAG CGGCAGTAAT   100

        AACACAGTCG ATCAAACGCA AAATAGATGG GCAATAAGGT CGATACAAAT   150
10
        AGGCAACCTT ACAATTACCA CGATCTGTAG CTATCGTATA ACCAATGAAA   200

        ATG   203

15   (2) INFORMATION FOR SEQ ID :802:

            (i) SEQUENCE CHARACTERISTICS:
                (A) LENGTH: 193 base pairs
                (B) TYPE: nucleic acid
20   (C) STRANDEDNESS: double
                (D) TOPOLOGY: linear

25   (xi) SEQUENCE DESCRIPTION: SEQ ID :802:

        GACACAACTG TGTTCACTAG CAACCTCAAA CAGACACCAT GGTGCACCTG   50

        ACTCCTGAGG AGAAGTCTGC CGTTACTGCC CTGTGGGCTA GGCGAACGTG   100
30
        GATGAAGTCG ATGGCGAGGC CCTGGGCAGG CTGCTGGCGA TCTACCCTTG   150

        GACCCAGAGG TTCTTTGAGT CCTTTGAGGA TCTGTCAACT TCC   193

35   (2) INFORMATION FOR SEQ ID :803:

            (i) SEQUENCE CHARACTERISTICS:
                (A) LENGTH: 290 base pairs
                (B) TYPE: nucleic acid
40   (C) STRANDEDNESS: double
                (D) TOPOLOGY: linear

403

(xi) SEQUENCE DESCRIPTION: SEQ ID :803:

AACAAAAGTT GAAAATTTTA AATGGTCTTT TTATGGTTTG CGTGACCTAA   50

AAAGACAAAG TTTATCCTTG CCTTACTGTA TAGAAATGCG TCGTATCCAC   100

AATAGCGTAC AGATTTTTCC GCATTAATCC GTGTTTATAT TAACAGATTC   150

GTTAAGTATC GTTTAAAAAG GGAGAGAGGG GATACCCTCT CTCTAGATAA   200

ATGGGTCATC ATTTAATCCC AAGAATGATG TCGATAAGTA CTTTTCTAAA   250

CGATAACAAG AACCCCAGTA GGTAGTATAG CAGTCTTTAA   290

(2) INFORMATION FOR SEQ ID :804:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 256 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: double
            (D) TOPOLOGY: linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID :804:

AACTTGATGG TCGAGGCCAT CTCCTGGGCC GCCTGACGAT ACCGTGGCTA   50

AACAGGTACT GCTGGGCCGG AAGGTGGTGG TCGTACGCTG TGAAGGCATC   100

AACATTTCCG GCAATTTCTA CAGAAACAAG TTGAAGTACC TGACTTTCCT   150

CCGCAAGCGA ATGAACACCA ACCCTTCCCG AGGCCCCTAC CACTTCCGGG   200

CCCCCAGCCG CATATTCCGG CGGACCGTGC GAGGTATGCT GTCCCACAAA   250

ACAGGG   256

(2) INFORMATION FOR SEQ ID :805:

        (i) SEQUENCE CHARACTERISTICS:

404

```
        (A) LENGTH: 286 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear
```

5

        (xi) SEQUENCE DESCRIPTION: SEQ ID :805:

10   AGCAACCTCA AACAGACACC ATGGCGCACC TGACTCCTGA GGAGAAGTCT   50

      GCCGTTACTG CCCCTGTGGG ACCAGACGAA CGCGGATGAA GTCGGCGGCG   100

      AGGCCCTGGG CAGGCTGCTG ACCGATTTAC CCTTGGACCC AGAGATTCTT   150
15
      TGAGTCCTTT GAGAATCTGT CCACTTCTGA TGCTGTTATG GGCAACCCTA   200

      AGACGAAGGC TCATGGCAAG AAAGTGTTCG GTGCCTTTAG TGATGACCTG   250

20   GCTCACCTGG ACGACCTCAA GGGCACCTTT GCACAC   286

      (2) INFORMATION FOR SEQ ID :806:

          (i) SEQUENCE CHARACTERISTICS:
25   (A) LENGTH: 291 base pairs
              (B) TYPE: nucleic acid
              (C) STRANDEDNESS: double
              (D) TOPOLOGY: linear

30

        (xi) SEQUENCE DESCRIPTION: SEQ ID :806:

      TTCTTCATCA GATTTTACAT CTGCCTGATT AGAATCTTCT ACACTGGCCT   50
35
      CAGAAGATGA TTGTTCAAAA CTTTTTCTAA GTTGCTGTAA AAAAACTTCC   100

      ACGGACAAAG TAAAATGCAG TTCTTTATCG TTTAGCCAGT GTACAACAAA   150

40   AGGTCCAATC TTCTCTTCAT TTTAATTCAG ACTCAGAGAT GTAATAGATG   200

      GAAGAAGTGA AATGTCTGTG GCTGGGTTGA TGCTGGCTGC AATATGAAAG   250

405

TGGCAAAGTG CATTGCTATG CAGTGGAGTG TTACTGTGGA C   291

(2) INFORMATION FOR SEQ ID :807:

(i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 276 base pairs
    (B) TYPE: nucleic acid
    (C) STRANDEDNESS: double
    (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :807:

AGTTTAATCA GCTGCAATGA AAACAAACGT CTTTTATTAG GCAGAATCCA   50

GATGCTCAAG GCCCTTCATA ATATCCCTTA ATTTAGTAGT CGAACTTAGG   100

GAACAAAGGA ACCTTTAACA GAAATAGAAC AACAAGAAAG CGAACTTAGC   150

GATACTCGCG GGCCAGGGCA TTAGCCACAC CAACCACCAC TTTACGATAG   200

GCAACCTGCA CTGGAGGGGC GACTTCTCCG CCAAAGCGAC GGGCCAGCAC   250

ACAGACCAGC ACGTCGCCCA GGAGCC   276

(2) INFORMATION FOR SEQ ID :808:

(i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 218 base pairs
    (B) TYPE: nucleic acid
    (C) STRANDEDNESS: double
    (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :808:

GGCCTGCCAA CAGCATAGGG AAGAATCTCA TTGTTATACA TATTAAGAAT   50

CGATTCTAAA TAGACCTTTT TACCAGTCGC TGAAACTCTT AAATTAAGTA   100

406

ACATCGCTAG CTAATTTTCG TAATGGCCGA TTAATCTTGA AACGGCGGCG   150

AAGCTTGTTC TTCACACGTT TCCCTTCAGG TCCTTTGATG AATCATACTG   200

5   ACGTGATCGC TTATCGTA   218

(2) INFORMATION FOR SEQ ID :809:

        (i) SEQUENCE CHARACTERISTICS:
10   (A) LENGTH: 276 base pairs
                (B) TYPE: nucleic acid
                (C) STRANDEDNESS: double
                (D) TOPOLOGY: linear

15

        (xi) SEQUENCE DESCRIPTION: SEQ ID :809:

AGCAACCCAG CGCTCAATGG TGCTAGTGAA CACAGTTGTG TCAGAAACAA   50
20

CCTCAAACAG ACACCATGGT GCACCTGACT CCTGAGGAGA AGTCTGCCGT   100

TACTGCCCTG TGGGCAAAGG CGAACGCGGA TGAAGTCGGC GGCGAGGCCC   150

25   TGGGCAGGCT GCTGGCGATC TACCCTCGGA CCCAGAGGTT CTTTGAGTCC   200

TTTGGGGATC TGTCCATTAC TGATGCCGTA TGGGCAACCC TAAGGCGAAG   250

ACTAATGGCA AGCAAGTGCT AGACGC   276
30

(2) INFORMATION FOR SEQ ID :810:

        (i) SEQUENCE CHARACTERISTICS:
                (A) LENGTH: 199 base pairs
35   (B) TYPE: nucleic acid
                (C) STRANDEDNESS: double
                (D) TOPOLOGY: linear

40

        (xi) SEQUENCE DESCRIPTION: SEQ ID :810:

407

GACTCCACCT GAACGGGCCC CTTCTGAACC GCCTCTGTGG GAGCAGGCCC   50

CATCTGAGGA GGGTCCATCT GAGCAGATCC CTTCTCAACA GGTTCCTTCT   100

GAGGAGGCTT ACTGCTTTTC TTACTCGATT TATTTTTCAG AGTTTTCTTC   150

TTCGTACTTT TTTTAACGCA AGTATTTTGC TTTTTATTCT CCTCCATTT   199

(2) INFORMATION FOR SEQ ID :811:

         (i) SEQUENCE CHARACTERISTICS:
             (A) LENGTH: 254 base pairs
             (B) TYPE: nucleic acid
             (C) STRANDEDNESS: double
             (D) TOPOLOGY: linear

         (xi) SEQUENCE DESCRIPTION: SEQ ID :811:

AAACAGCACA ACCAATGACA GGATGCAAGA ACTGATAGGG CGCCGCAAAA   50

AAAAAGCGGG CCAAAGATGA AGTAAATAAA CGTAAGGGAG GTACCGAATC   100

TGGGGGGCTT GGCGTAGAGT AAGGGAGAGG AGCTTCAACT ATCTCAATAA   150

GGGCAAGAAA ACACAAACAA CTCCTTCATT CGTCCAAAAT GCTTCTGAAT   200

TGCACCACAA TTGACACACA CACACCTCAA AGCAGAATCC GCACTGACCT   250

AAGT   254

(2) INFORMATION FOR SEQ ID :812:

         (i) SEQUENCE CHARACTERISTICS:
             (A) LENGTH: 284 base pairs
             (B) TYPE: nucleic acid
             (C) STRANDEDNESS: double
             (D) TOPOLOGY: linear

408

(xi) SEQUENCE DESCRIPTION: SEQ ID :812:

TTTTTTTTTT AGCAATGAAA ATAAAAGTTT TTTATCAGGC AGACTCCAGA   50

CGCTCAAGGC CTTTCACAAC ACCCCCCAAT TTAGCAATAG ACTTCAGGGA   100

CCAAAGGACC CTTTAACAGA AATAGAACAA CAAGAAAACA AACTCAAAGA   150

CACTCGAGGG CCAGGGCCTC ACCACACCAA CCCCCACTTC CAAACAGGCA   200

ACCTGCACCG GAGGGGAGAC TTTTTCGCCA AAGCGACGGG CCAGCACACA   250

GACCAACACA TCGCCCAGGA ACCTGAAGTT TTCA   284

(2) INFORMATION FOR SEQ ID :813:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 279 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: double
            (D) TOPOLOGY: linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID :813:

ATACAACAGC AGAAACAGGT ATCCACGCAC AGTCCAGCAA CATTTCTTCT   50

GGTACAACGC AGCTTCAAAG TTCACATCAA ACGTTACTTT GTCATACCAA   100

GGCAAGGATG CTAACTCGAA GTCAATCACG CGAGTGATGT CATTCACAAC   150

CGGTCACGGT GCCGATGTGA CAATCAAGAC TGAAGGCGAT GACGAAGAAG   200

CAGCACTGCC CGCCGATAAC CGCAGCGATG CAAAAAAAAG AGCTAGACGA   250

CTGACGAAAC CTGAGAACCC CGAAGGACT   279

(2) INFORMATION FOR SEQ ID :814:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 208 base pairs

409

```
              (B)  TYPE: nucleic acid
              (C)  STRANDEDNESS: double
              (D)  TOPOLOGY: linear


 5


          (xi) SEQUENCE DESCRIPTION: SEQ ID :814:


      AACGTGCTGG TCTGTGTGCT GGCCCATCAC TTTGGCAAAG AATTCACCCC        50
10

      ACCAGTGCAG GCTGCCTATC AGAAAGTGGC GGCTGGCGTG GCAACAGTGA       100


      CTGAGAAGAC CAAAGAGCAA GTGACAAACG CCGAAGGAGC AGTGGCGACG       150


15    GGCGTGACAG CAGTAGCCCA GAAGACAGCG GAGGGAGCAG GGGGCATCGC       200


      AGCAGCCA                                                     208


      (2) INFORMATION FOR SEQ ID :815:
20

          (i)  SEQUENCE CHARACTERISTICS:
              (A)  LENGTH: 192 base pairs
              (B)  TYPE: nucleic acid
              (C)  STRANDEDNESS: double
25            (D)  TOPOLOGY: linear




          (xi) SEQUENCE DESCRIPTION: SEQ ID :815:
30
      AAACCACGCT CAGTCAGGTT CCGGCAGCAG CTGCAGCATC TCATCTTCTG        50


      CGACTCTCGG TGCCCTCTCC TTCCGATTTC CGGAAACATG GCCTCCGATG       100


35    TGGCTGTCTC TGACGACGTC ATCAAGGTGT TCAACGACAT GAAGGCGCAC       150


      AAGTCTTCAA CGCCAGAGGA GGTGAAGAGG CGCAAGCAGA TA              192


      (2) INFORMATION FOR SEQ ID :816:
40
          (i)  SEQUENCE CHARACTERISTICS:
              (A)  LENGTH: 264 base pairs
```

410

```
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: double
            (D) TOPOLOGY: linear
```

```
        (xi) SEQUENCE DESCRIPTION: SEQ ID :816:
```

```
    GAGAGAACCC ACCATGGAGC TGTCTCCTGC CGACAAGACC AACGTCAAGG          50

    CCGCCTGGGG TAAGGTAGGC GCGCACAATG GCGAGTATGG TCGCAGAGGC         100

    CCTGGAAAGG ATGCTCCTGT CCTTCCCCAC CATGTGAGAC CTACTCCACA         150

    CACTTCGACC TGAGCCACGC CTCTGCCAGG TTAAGGGCCA CGGCAAGAAG         200

    GTGCCCGACG CGCTGACCAA CGCCGTGCGC ACGTGGACGA CATGCCCAAC         250

    GCGCTGTCCC CCTG                                                264
```

```
    (2) INFORMATION FOR SEQ ID :817:
```

```
        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 202 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: double
            (D) TOPOLOGY: linear
```

```
        (xi) SEQUENCE DESCRIPTION: SEQ ID :817:
```

```
    ACCCTACACA CATCCGTTCA ACTGTCCCAT CACCCACTTA CACTCCAAAA          50

    AAAACCACTC AACAAGCAAA CAACCCATCC TGTTTTCATA ACGTTATCGT         100

    AAC  AAAG CCGACCATAA TCAACTTGAA TTTACTTCAC CACAAGGCAA          150

    AGCGATTATT TAGATGAGGC ACTCGCACTA CTGCTTGAAG TGCTACTAGA         200

    TG                                                             202
```

411

(2) INFORMATION FOR SEQ ID :818:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 179 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: double
            (D) TOPOLOGY: linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID :818:

AGTAGAAAAT AAGTTCAAAA TTTTAGAAAT ACTGGCTTTA TACTCGCCCA   50

TGTATTTACA TTCACAGAGA TCTTTATTTA TTTACAAGCG CTTTGAGTTA   100

CTGTATAGTT TTTTTTAACA AAAAAGCGTG GGGGGCTCCC TTTAGCATTC   150

CCCATAGGAT AGGTAATGAA CTTTTTGTT   179

(2) INFORMATION FOR SEQ ID :819:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 260 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: double
            (D) TOPOLOGY: linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID :819:

TGTGCTCTTA TGCTAGATTT ACGGACAGAT TTTCTTCTGC CCTGTAAACT   50

AATAGCATAG GAGCATTTTT TAATACGATT CGATACAAAA AAGAATTTAA   100

GCAATCTCTC GCCGAGACGC ACAATCAAGA CCATTCATAT ACTGATCTAT   150

CCGCTGAATA CGAACCTTCA ATCGACTCAA TCCGTAACTG GATCAAGTTG   200

TACGCGGGTC CACGAAGTGA CAGACGAAAA ATGAACGCAA GCTGATGTAA   250

412

ACGCATCACA   260

(2) INFORMATION FOR SEQ ID :820:

5   (i) SEQUENCE CHARACTERISTICS:
                  (A) LENGTH: 226 base pairs
                  (B) TYPE: nucleic acid
                  (C) STRANDEDNESS: double
                  (D) TOPOLOGY: linear
10

             (xi) SEQUENCE DESCRIPTION: SEQ ID :820:

15   ACTCGGCACT TTCTTAGAAT AGACAATTTG CAAAATGTCC ATCCCAGGTT   50

      CATCCTTGTA GCCTAATGTT TCCGTCACCG TTGCCACTAG TTAACGTGGG   100

      TGAACTTTAT CTGGGAAACG GGTAACATCC GCGACCACAA CTAGACCATC   150
20
      ATTTGACGTA ATGCCATCAG CACTCACCAA AACTTGGCCA ACCAACAGCC   200

      TTTCCGTAAC TGAGTTTGAT TTCTCC   226

25   (2) INFORMATION FOR SEQ ID :821:

             (i) SEQUENCE CHARACTERISTICS:
                  (A) LENGTH: 197 base pairs
                  (B) TYPE: nucleic acid
30   (C) STRANDEDNESS: double
                  (D) TOPOLOGY: linear

35   (xi) SEQUENCE DESCRIPTION: SEQ ID :821:

      CACCTACATA TAGATGCACG AAGTACTTGC TCACTTTTTT TGGTTGTAAA   50

      TTTTCAAAGC GTTGAAGGCA GCATTCTTAG CGGCACGGAT GTCCTTATCA   100
40
      GTGAATGAAT CAGGCTTTTC CATGGCCAAC CAACCAACGA TTCGCATCGC   150

413

GTGATTTCGA ATCATGTCAA GCAAAGCACC GGCTGTATCA TAGTAAC   197

(2) INFORMATION FOR SEQ ID :822:

5   (i) SEQUENCE CHARACTERISTICS:
                   (A) LENGTH: 304 base pairs
                   (B) TYPE: nucleic acid
                   (C) STRANDEDNESS: double
                   (D) TOPOLOGY: linear

10

              (xi) SEQUENCE DESCRIPTION: SEQ ID :822:

15   GGACTGGGTG CAGTGGCTCA CACCTCACGT TACATTTTAT AGCTAGCAGG   50

      GTAATGGGGA GTTATGGCAC TCAGGTCACA TTCTAGGGAA TGTTTATCGG   100

      GCAATCTCAA TGGCACCGCA AGCTAAATGA CTTCCAGTGT TTCTCATCTT   150

20   TGCGCTTTCT TCATCGCAAC CTTTGCCCAA GACATCTGTT TTTTCTGGAT   200

      CACCCTTGCA CAGCCACTGA GGAATGATCT TCTGAAAGTG AATCTTCAGT   250

25   AGACACATCG CCACACCATC TANGTCAGCC ATCACATGCC CAGGTCTNGA   300

      CATG   304

      (2) INFORMATION FOR SEQ ID :823:

30
              (i) SEQUENCE CHARACTERISTICS:
                   (A) LENGTH: 197 base pairs
                   (B) TYPE: nucleic acid
                   (C) STRANDEDNESS: double
35   (D) TOPOLOGY: linear

              (xi) SEQUENCE DESCRIPTION: SEQ ID :823:
40
      GGCCCAGCAG ANGGAGGAAC ACTACCGAGG CTCCAGCTTA ACGGTATTTG   50

414

GAGGTCAGCA CGGTGCTCAC AGAAGCCAGG AACTTGCCCA GGGAGGCGTG   100

CACCAANGGG GCGAACTCNC GGGGAGGCGG GCGACCAGGG TCACCAGCAG   150

GCAGTGCTTA GGAGCTGGGA GCCGACCGAG CCCACCGAAC TCGCGCG   197

(2) INFORMATION FOR SEQ ID :824:

      (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 281 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: double
            (D) TOPOLOGY: linear

      (xi) SEQUENCE DESCRIPTION: SEQ ID :824:

AAAAACAATG TCATTTTGTA CAGACAAAAT TTAGCAGACT CAAGCTTCCA   50

CAGTTAGTGC GAGAGCCTGT GGATGGCATA GTTACATAAG AGTCTGTTGT   100

GGATTCAAAT GTCACCTCTT CCAGGCAGTC TTTCCTGACT TACCCTGGCA   150

GCTTTGTGTT CCCACATTAC TAGTAATGTT TTTTTCCTTA ATAGCAATGA   200

TTTCACTGTA ATAATGTATT TATATGCCTC TCTCCCCCAG ACAGCAAGCG   250

TTTTCCCACA GGTCTCGACA CACAGAAGAT A   281

(2) INFORMATION FOR SEQ ID :825:

      (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 312 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: double
            (D) TOPOLOGY: linear

      (xi) SEQUENCE DESCRIPTION: SEQ ID :825:

415

```
        TATTAAATTT ACTAGAATGT TACAGTTACA AATTTGGTAA TGTTCTTTCT        50

        GAAAAACAGC CTAATTTTGC AGCCTGAAAC TTGACTGAAA ATCTCAATAC        100

5       TTTTATTCAT GATAGAAAAA TAATTCCTGG CTTCATCTCA CAATTAACTA        150

        ATAATTATGT TAATATAAAA TATAACTGTG CCCTTTCTTT TCAGTGATGA         200

        TCAAAGTGAT TCTCCCAGGC CAAAAAATCA AATAAGAAGT TATATTTTAA        250

10      AAAGACATAA CAAGCCATTC TACCCAGTGG GCATCTTCAG TGTACTCCCT        300

        CTACTAATTG GC                                                312
```

15   (2) INFORMATION FOR SEQ ID :826:

            (i) SEQUENCE CHARACTERISTICS:
                (A) LENGTH: 189 base pairs
                (B) TYPE: nucleic acid
20   (C) STRANDEDNESS: double
                (D) TOPOLOGY: linear

25   (xi) SEQUENCE DESCRIPTION: SEQ ID :826:

```
        ACACCAAACA CGGGGAGTGG GGAGTAGAGG CTCTGGAGGT CAGGATGGCA        50

        GGGCAGGGAG GGGAAGGAAG GAGTTGTTGG TCTCACAGTG TGCCTGCCAA        100

30      TCCCAAAGCC CTAGAGACCC CTTCACTGCA GCACCTGCCC CCGGGTCTCA        150

        GGCAGCTTCA GGGCCAGAGA GCTGCCAAGG GCAAGCAAA                    189
```

35   (2) INFORMATION FOR SEQ ID :827:

            (i) SEQUENCE CHARACTERISTICS:
                (A) LENGTH: 232 base pairs
                (B) TYPE: nucleic acid
40   (C) STRANDEDNESS: double
                (D) TOPOLOGY: linear

416

(xi) SEQUENCE DESCRIPTION: SEQ ID :827:

CTCTTAAGGG CTTGAAAATT TCTGTGGGAG TAGGACAGAG TGTAGAACGT   50

ACAGTAAAAG GCAATAAAAC AGTGGGAATA ATTTTACCAG CTATGAGTAA   100

AGGAGTAATG GGTATTTACT GCCTGTCATT AATCCACACA TATATCCATT   150

TTAGAGATTA TTTTGTTGCC TGGAAATCTG TCTCATCACA GAGTGTTAAT   200

ATACACCGGC GGGATATTCA AGAGTGGCTA AG   232

(2) INFORMATION FOR SEQ ID :828:

      (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 282 base pairs
          (B) TYPE: nucleic acid
          (C) STRANDEDNESS: double
          (D) TOPOLOGY: linear

      (xi) SEQUENCE DESCRIPTION: SEQ ID :828:

GGACATTGGA ACACTATACT CTATTATTGC GGTCGTGCCT AGCAGTCTCG   50

CGCATGTCTC CTCAGCGCGC ACAGTCTCTC TCAGAGAGCT CTTCTCTCTT   100

TATATGCGCA GACCCGCAGA CTGGGAGACC CAGACCCAGG GCAAACTCTC   150

TTCTTAGGTA TATCGCACCC ATCATATCTC ACACATCGTG TATGTCGTAT   200

CATCAGACCC CCATAGAGCA TATATGCTAA ATTAATGCTC TCTTTCATCA   250

GTAATTACCC CATATCATAA AATGCGGGCG GG   282

(2) INFORMATION FOR SEQ ID :829:

      (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 230 base pairs
          (B) TYPE: nucleic acid

417

          (C) STRANDEDNESS: double
          (D) TOPOLOGY: linear

5

       (xi) SEQUENCE DESCRIPTION: SEQ ID :829:

CACTACATCC GCAAGTACAA CCGCTTCGAG AAGCGCCACA AGAACATGTC   50

10   TGTACACCTG TCCCCCTGCT TCAGGGACGT CCAGATCGGT GACATCGTCA   100

AGTGGGCGAG TGCCAACCTC TGAGCAAGAC AGTGCGCTTC AACGTGCTCA   150

AGGTCACCAA GGCTGCCGGC ACCAAGAAGC AGTTCCAGAA GTTCTGAGGC   200

15

TGGACATCGG CCCGCTCCCC ACAATGAAAT   230

     (2) INFORMATION FOR SEQ ID :830:

20   (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 226 base pairs
          (B) TYPE: nucleic acid
          (C) STRANDEDNESS: double
          (D) TOPOLOGY: linear

25

       (xi) SEQUENCE DESCRIPTION: SEQ ID :830:

30   TTCCGCAAAT AAAAGAATTC ACTAAGGTAC CAAAACAGAA AATATACAGA   50

GATCAATGAC TTTCATATAC ATTAACAAAC AAAAGTTCAG AGATAAAATG   100

GAAGAGAAAT GCTGTTTTTA ACAGTATAAT TAAGATAAAA TATGAAGGTA   150

35

TAAACTTAAC AAGAAATGTT GCAAAACCAT TATGTGAAAA TTACAACACT   200

CCTGAAGACG CAGACACACC TAACAA   226

40   (2) INFORMATION FOR SEQ ID :831:

       (i) SEQUENCE CHARACTERISTICS:

418

        (A) LENGTH: 247 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

5

        (xi) SEQUENCE DESCRIPTION: SEQ ID :831:

10   AGAAGTCCTT CCAAGAGTCT TGGGTATGCA ACAGCCATGG AGGCTGTGAC   50

        CTTTTTCCTT CTTTTCTACA GCCTGCAGTT CATTTAAGGA TCACCGGAGA   100

        TGACTCGTGC TCTAGTTCTT AAAATCAAAC AAGGATCTGC CAAATCCAAG   150
15
        ACCCTGAATT TGGCCCAAAT TTGTAGAAAC ATTGCTTTTT ACCACCCGGT   200

        GCACCAAAAA TACCTCCCAT TTCAAGGCAA CAACCGCTTT AATTGCT   247

20   (2) INFORMATION FOR SEQ ID :832:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 112 base pairs
            (B) TYPE: nucleic acid
25   (C) STRANDEDNESS: double
            (D) TOPOLOGY: linear

30   (xi) SEQUENCE DESCRIPTION: SEQ ID :832:

        CACCAGGCAG GGGATCCCGG AGGGAAGCCC TCTGCCAGGG ACATGGTGAG   50

        GGCGTGGCCA TCACCCACGA AGGGAGCATA AATAACACTG GCAGGTGGGT   100
35
        GGGCAGCAGG AG   112

        (2) INFORMATION FOR SEQ ID :833:

        (i) SEQUENCE CHARACTERISTICS:
40   (A) LENGTH: 173 base pairs
            (B) TYPE: nucleic acid

419

```
            (C) STRANDEDNESS: double
            (D) TOPOLOGY: linear


5

            (xi) SEQUENCE DESCRIPTION: SEQ ID :833:


   AGCCATTCCC ACTAGAGGCC AAACCGCCTG CCCACAGAGA TTGACAGCCA          50

10  ATGTTCATCT CATAACTCTC CTCCCAGCAG TGCACCAGTA AACTCAGATG          100

   CCTGAGTGCT TGTGGCCACC ACACAACAGA TGCGGCCTTC CTCTTCACTG          150

   GCCCCTCGGC TGCTGCTGGG TCC                                       173
15
   (2) INFORMATION FOR SEQ ID :834:


            (i) SEQUENCE CHARACTERISTICS:
                (A) LENGTH: 288 base pairs
20              (B) TYPE: nucleic acid
                (C) STRANDEDNESS: double
                (D) TOPOLOGY: linear


25

            (xi) SEQUENCE DESCRIPTION: SEQ ID :834:


   TGGCCCATGG GAGCCCTTAT GAGCAAGTTT CCAGGTCCTT ATGACACAAT          50

30  TCCATCATTC TTCGGGTACA TCCTTACTCT CTGGCACAGT AGAGATGTTC          100

   CAGACTTATC TTATATTTTC ACTTCCCCAT ACCTGGAATC AATCACTTCT          150

   CCGAGGATGC TTGATTCCTT TTAGTGAAGA ACAGTCTTTG GAAACCAACC          200
35
   GTCTAGGGAC ATCAAGTATG TTTGCCGCTA TTGGAGTGTC ATTGCTCCTG          250

   AACCTTCTAA GTGGACACAG CTAGGAAATG TATGTGCT                       288

40  (2) INFORMATION FOR SEQ ID :835:


            (i) SEQUENCE CHARACTERISTICS:
```

420

```
             (A) LENGTH: 310 base pairs
             (B) TYPE: nucleic acid
             (C) STRANDEDNESS: double
             (D) TOPOLOGY: linear
```

        (xi) SEQUENCE DESCRIPTION: SEQ ID :835:

```
CTTTTCTATT TTCCTTAAGT GTCTGCCAGT CTGAGAAATA AAGGGACAGA        50

GTACAAAAGA GAGAAATTTT AAAGCTGGGT GTCCGGGGGA GACATCACAT       100

GTCGGCAGGT TCCGTGATGC CCCACAAGCC ACAAAACCAG CAAGTTTTTA       150

TTAGTGATTT TAAAAGGGGA GGGAGTGTAC GAATAGGGTG CGGGTCACAG       200

AGATAACGTG CTTCACAAGA TAATAGAATA TCACAAGGCA AATGGAGGCA       250

GAACGAGATC ACAGGACCAC AGAACTGGGA CCAAATAAAG ATTGCTAAGA       300

ACGTCTAGGG                                                  310
```

        (2) INFORMATION FOR SEQ ID :836:

             (i) SEQUENCE CHARACTERISTICS:
                 (A) LENGTH: 177 base pairs
                 (B) TYPE: nucleic acid
                 (C) STRANDEDNESS: double
                 (D) TOPOLOGY: linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID :836:

```
TCAGTGGAGG AATTAAAACT GGTGGAGAAG GGGAGGTCAG GTTATCAGTT        50

GAAATGCCAA GGTTATCTCT AATCTTAGCT AGATTCTGCC AAAGTTCACA       100

GAGGTAATCA AAAACTTGAG CATGTATTTA AGGATCCATG ATTGAATTTA       150

CATCTCCCAA AATGCCTAGC ATTCTTC                               177
```

421

(2) INFORMATION FOR SEQ ID :837:

    (i) SEQUENCE CHARACTERISTICS:
       (A) LENGTH: 135 base pairs
       (B) TYPE: nucleic acid
       (C) STRANDEDNESS: double
       (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID :837:

CCGTTGCACT TGGTGTTGGC ATTCTGCAGG GCGGCACTCT CCCACTCTTC   50

CCGGCCTCGA GCCAACCTGA CGGCAGCCAG ATGGCAGTCG TAGTGCACAA   100

TGTTGAAGTG GGACACGGTG CTGTAGCCCT GCTGT   135

(2) INFORMATION FOR SEQ ID :838:

    (i) SEQUENCE CHARACTERISTICS:
       (A) LENGTH: 201 base pairs
       (B) TYPE: nucleic acid
       (C) STRANDEDNESS: double
       (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID :838:

TCAGTGGAGG AATTAAAACT GGTGGAGAAG GGGAGGTCAG GTTATCAGTT   50

GAAATGCCAA GGTTATCTCT AATCTTAGCT AGATTCTGCC AAAGTTCACA   100

GAGGTAATCA AAAACTCGAG CATGTATTTC AGGATCCATG ATTGAATTTA   150

CATCTCCCAA AACGCCTAGC ATTCTTCGCC ACATTACAGT AGCAACATCA   200

G   201

(2) INFORMATION FOR SEQ ID :839:

422

      (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 181 base pairs
          (B) TYPE: nucleic acid
          (C) STRANDEDNESS: double

5   (D) TOPOLOGY: linear

      (xi) SEQUENCE DESCRIPTION: SEQ ID :839:

10

TTCTTTGGAG TACATCCTTA CTTTCTGCAC AACAGATGAG AGATGTTCCA   50

GAACTTATAC TGTATCATAT ATTTTACCTC CCCCCCTATA CACCCTGAGA   100

15

TATACATATA CACTATCTCC GCTAGAGAGA TGTCTATGAC ATATCACTTT   150

CTGAGATGTA CACGAACGAG ATCTTTTGAG A   181

(2) INFORMATION FOR SEQ ID :840:

20

      (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 222 base pairs
          (B) TYPE: nucleic acid
          (C) STRANDEDNESS: double

25   (D) TOPOLOGY: linear

      (xi) SEQUENCE DESCRIPTION: SEQ ID :840:

30

CATACAAATG ATTAGAAAGC AATACAGCCT TATTGCTGAT ATGGAGAAGG   50

TTTTAGTGAA CATTCAGAGG AGTTTGGAAG AAAGTCGCTG CACAATCTTC   100

35

ATGGATGACT TTGAGGGATT CAAGACTTCA GTGGAAGAAC TAACTGCATA   150

TGTGAGTAGA AATGGCAGGA GAACTAGAGT TCGAAGTAGG AGCTGGAAGA   200

TAATAACATG GGTTTAAAAA AC   222

40

(2) INFORMATION FOR SEQ ID :841:

423

(i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 293 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
5   (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :841:

10

CGCTCAGCTG GTCTATCCTG CTCTTCCTCT TGTCCTTGCT CTTGCTGCGG   50

CTCCTATCTA CCGGCTACCT GCTGCCCGCT TTGCTCCTGC TACCGGCTCC   100

15   GACTCTGGCG GAGGCTCTTC TCCTGGCTCC TGCCCCTGCT CACAACTCCC   150

TCGCTTCTCC TCCTCCACTC TCCTCTCCCG ACTCCTGCTC CGACTTTTGC   200

TCTTACTTTT ATGCCTGCTA GGACTCCGGC TCTTGGGTTT CCCGAACATT   250
20

GTCATTGTTT TGGAACTTCT CCTTCAGCTT GGTCTTTTGC CGG   293

(2) INFORMATION FOR SEQ ID :842:

25   (i) SEQUENCE CHARACTERISTICS:
                (A) LENGTH: 239 base pairs
                (B) TYPE: nucleic acid
                (C) STRANDEDNESS: double
                (D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :842:

35   ATGAGGAGGT GAGGAAAAGG AGAAGTGCAG CTACCATCGA GTGATTCTTC   50

TGGGATAGGT GTCTCATTTA AATCTCATAA TCATCTTTTT TGGCAGGTCA   100

GTCAACTTCA GGCTCACAGA TGACAGACAG TTGGCCCAAA GACACACAGG   150
40
AAATACATAA GTGACAACGG AATACAAGTC CATGAATTAA AAAACCATGC   200

424

TTTTCTCTCC TTGCCACACA GCTTTAGTTT GAAAAAAAA   239

(2) INFORMATION FOR SEQ ID :843:

5   (i) SEQUENCE CHARACTERISTICS:
                      (A) LENGTH: 154 base pairs
                      (B) TYPE: nucleic acid
                      (C) STRANDEDNESS: double
                      (D) TOPOLOGY: linear
10

                (xi) SEQUENCE DESCRIPTION: SEQ ID :843:

15   TTCCGAATTA TTGAATCTTC TTCTGTAACA TCACAATCTT CCTGGTTTTC   50

        AGAATAAACG CTCTTCTCGC TCGCCTCTCT CTGCACTCAC TCCCACCTCA   100

        CTCACTCACT CTATAATAAA ATGTTTGCAC TCAATTTATA TAGTAGTGTT   150
20
        TGTC   154

        (2) INFORMATION FOR SEQ ID :844:

25   (i) SEQUENCE CHARACTERISTICS:
                      (A) LENGTH: 392 base pairs
                      (B) TYPE: nucleic acid
                      (C) STRANDEDNESS: double
                      (D) TOPOLOGY: linear
30

                (xi) SEQUENCE DESCRIPTION: SEQ ID :844:

35   GTCTTTAATT GAGAAAGCTG GAGTGGAGAC CCGATCCCCT GGGAGCAGTG   50

        CCAGGAGTTG GGTGGAGACT GAGTGGGGTT TGTGTGGGTG AGGGGGCATC   100

        TACTCCTCTT GCAACAAGCC AGAAGTAGAA CAGCCTAAGG AAAAGTGACC   150
40
        TGCCTTGGAG CCTTAGTCCC TCCCTTAGGG CCCCCTCAGC CTACCCTATC   200

425

CAAGTCTGAG GCTATGGAAG TCTCCCTCCT AGTTCACTAG CAGGTTCCCC   250

ATCTTTTCCA GGCTGCCCCT AGCACTCCAC GTTTTTCTGA AAAAATCTAG   300

ACAGGCCCTT TTTGGGTACC TAAAACCCAG CTGAGGTTGT GAGCTGTAAG   350

GTAAAGCAAG TTCTATCCAA TTAGAAGCTG TTGGGGGCGT AT   392

(2) INFORMATION FOR SEQ ID :845:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 200 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: double
            (D) TOPOLOGY: linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID :845:

CAAAGAATAA ATAATTTTTC TATTCCTGAA AGTTAACTAA TTATTTATTA   50

GAAAGTCAGA AATATGTGGA AAGCAAAGGA ATATTTGAGA AAGTGATATG   100

AAATTAATAA GTGGTAAAAA ATTAATAAAA TTAATATTAG AGTTTCCTTT   150

GAGCTAATCC TTTATTTATT TATTTTTTTC CTTGAGACAA TGTCTTGCCA   200

(2) INFORMATION FOR SEQ ID :846:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 311 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: double
            (D) TOPOLOGY: linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID :846:

TTAAAAATAC TCTGGAAAGA GCACTTCCAT CGTTCATTTA CATCATATTA   50

.426

```
GAAATGGATT TCCGAGTCAG CACTGGCTTC CTCCAGAATA GCAGTCCTGG          100

AGGAGCGAGA TCTCCCCAAG CCTCCAGGAT TGCAGTCTGT CTTGTGCCTT          150

CACTCCCTAA TAGGTTTGCC TTATTTAAAG GACCCACCTT CAGAGCTGCC          200

AAGGACTTTC TCAGAGCAGC TCCTTGGTCC CTCCGACAGC CTGGGATGGC          250

ATTTATTCTG GGGCCTGGGT GTGGGGAGGT CCTCACCAGC CTAGGAGTAA          300

GAGGAGGTGG T                                                    311
```

(2) INFORMATION FOR SEQ ID :847:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 287 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: double
            (D) TOPOLOGY: linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID :847:

```
CAGATCAAGA CTGGTGCCCC TTGCCGATCT GAGCGCTTGG CCAAGTACAA           50

CTCAGCTCCT CAGAATTGAA GAGGAGCTGG GCAGCAAGGC TAAGTTTGCC          100

GGCAGGAACT TCAGAAACCC CTTGGCCGGG TAAGCTGTGG GCAGGCAAGC          150

CCTTCGGTCA CCTGTTGGCT ACACAGACCC CTCCCCTCGT GTCAGCTCAG          200

GCAGCTCGAG GCCCCCGACC AACACTTGCA GGGGTCCCTG CTAGTTAGCG          250

CCCCACCGCC GTGGAGTTCG TACCGCTTCC TTAGTCT                        287
```

(2) INFORMATION FOR SEQ ID :848:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 263 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: double

427

· (D) TOPOLOGY: linear

5   (xi) SEQUENCE DESCRIPTION: SEQ ID :848:

GATTACAGGT GTGAGCCACC GTGCCTGGCC TATTAATATG CTCTTAAAAC   50

TCATCCATAC GTTTTCATAG CAAGAAAGCT TATTTCTCCC AACTACCGAA   100
10

TAATATTCTA TCGTATGGCC GCACCTCTGT TTATCCATTT ACCTATCGAG   150

AGGCATCTTG ATTACTTCTA GCTTTGGATT ATTACAAATA AAACTATACA   200

15   AACACGCAAA CAGAGTTTCT CGTGTGAATA TAAACCCGCA AACCGGCTGG   250

AGGCATATNA CCA   263

(2) INFORMATION FOR SEQ ID :849:
20
        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 279 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: double
25   (D) TOPOLOGY: linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID :849:
30
TTGTCAGTCA GAATAGGATG TAAAAGACTA TTTCAAAGAG TTAAATTATT   50

TGTTAATATC AGAGATCAGC CACAGACAAG AAGTTTATGG ATGAGTGCAG   100

35   CAGTGGTCCA TTGGACATGT TAAATACTCG TGGATATCCA CAATTCGAAT   150

TGACATTAAA AACGAATGGA TACCCAACTC TGAATTCCAT ATCGTTTTTT   200

AATATCAAAA ACACAATTTT AACTACTGAT AAACCAGGCA ACCACCGCAA   250
40
GTTTATCGAA ATCCTGCCGC TACTAAACA   279

428

(2) INFORMATION FOR SEQ ID :850:

    (i) SEQUENCE CHARACTERISTICS:
       (A) LENGTH: 173 base pairs

5   (B) TYPE: nucleic acid
       (C) STRANDEDNESS: double
       (D) TOPOLOGY: linear

10

    (xi) SEQUENCE DESCRIPTION: SEQ ID :850:

GCTGAAAGTT GAAGTGGAGA GCTTGAAACG AGAACTCCAG GACAAGAAAC   50

15 AGCATCTGGA TAAAACATGG GCTGATGTGG AGAATCTAAA CAGTCAGAAT   100

GAAGCTGAGC TCCGACGCCA GTTCGAGGAG CGACAGCAGG AGACGGAGCA   150

TGTTTATGAG CTCTCGACAG AAT   173

20

(2) INFORMATION FOR SEQ ID :851:

    (i) SEQUENCE CHARACTERISTICS:
       (A) LENGTH: 240 base pairs

25   (B) TYPE: nucleic acid
       (C) STRANDEDNESS: double
       (D) TOPOLOGY: linear

30

    (xi) SEQUENCE DESCRIPTION: SEQ ID :851:

TCGAGAAAGT TTCAATGTGA TTAGATTAAA ATTAAAAGAA TCCATAAAAA   50

35 TGGAACAAAG AAGAAGAGGA ATGAAATTAC TTTTACTTTA AACAGCATTG   100

TTATCACATA AAACACGTAT CTTACAAATT CATGGGATAG CCCATAAATG   150

GGACTACAGC AACAATGGTA GGAGAGTCCA TCCTTCTTCA AAAGCAACCC   200

40

AGCAGGAATT TTCTGTTAAA AATATTTTTG CCGTAATACT   240

429

(2) INFORMATION FOR SEQ ID :852:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 314 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: double
            (D) TOPOLOGY: linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID :852:

    ACTGGACTGG TCAAGAACAA AGCTCATGGC AATAGTCTTT TGGAATGTTA   50

    AAGGAATTTT TCTAGTTGGC TTTCTGGAGG GCCAAAGAAC AACAACATCT   100

    GCTTATTATG AAAGTGTTTT GAGAAAGCCA AAGCTTTAGC AGAAAAACAC   150

    CTGGGAAAGC TTCATTAGAG AGTCCTTCCC CATCACAACG CTTCTGCTTA   200

    TTCCTCTTAT AAAACAAGGG CAATTTTGTG AGAGCTACTG ACGATTTTCC   250

    CCTCGAAATT TACTATTTCT ACAGCTTATT AATCTCAAAT AGTAAGCATG   300

    TCCTTGCCGT CACT   314

(2) INFORMATION FOR SEQ ID :853:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 267 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: double
            (D) TOPOLOGY: linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID :853:

    TCCTGAAATA CTCTCTACTG TCACTGCTTC AGTTTAATTT ATAGATAGCA   50

    CCAGATATGA GTCCTTATTA GTTCTGATAA CTCTGAAATG GTTATTTGGT   100

430

ATTTCTTCAG TGACAAGCAA ACTATCCCCC CACATGCCTT TAATGGCCAG   150

TGTTTTCGAT TTGTATACCA ATAAGCAATC TAGGTAGAGG TAATCATATA   200

CTGATACGCT AACCTTTGAA ACATAATTTC CAATCTAGTA AGCTAAAATC   250

GCGCCAATAC TGCTTAA   267

(2) INFORMATION FOR SEQ ID :854:

    (i) SEQUENCE CHARACTERISTICS:
       (A) LENGTH: 186 base pairs
       (B) TYPE: nucleic acid
       (C) STRANDEDNESS: double
       (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID :854:

GCAGTGGATC TTTCTTTTTT TCCAAAGGAA ATTTCATATA GAGTCCATTC   50

ATAGGAAACA GATAAAATGT GAACGGCTGC AACTGAGATG GGGGAGAGTG   100

GCTTGGAGCC CCCAGCCTCT TTGCTTTCTC TTATCCCTAT AGGATGGCCA   150

TTAGGTGAAG CAGTTTAGCT TGTTGGTTCA GACCTG   186

(2) INFORMATION FOR SEQ ID :855:

    (i) SEQUENCE CHARACTERISTICS:
       (A) LENGTH: 162 base pairs
       (B) TYPE: nucleic acid
       (C) STRANDEDNESS: double
       (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID :855:

ATTTTGAAAA GAAACCTACA AAAATTGTAT TTCCATATTT CATAGTCAGC   50

431

CAAAAATATT GGTCAACTCA TGCTCTCTGC AAGGTTCTGC AAAAATTGCG   100

GAGTGGTATA GACAAGGCAC CATTGCAATA TATAATACTT TTTGGGTATT   150

GGCCCAAAAA TT   162

(2) INFORMATION FOR SEQ ID :856:

  (i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 286 base pairs
    (B) TYPE: nucleic acid
    (C) STRANDEDNESS: double
    (D) TOPOLOGY: linear

  (xi) SEQUENCE DESCRIPTION: SEQ ID :856:

TCTGTGGCCA CAGATGCATA TTACAAGCCC ATCCAGAGCC ATTATGAAGA   50

GAAAGTGGCA ATTTTATTCT CAGCCTGAGA AATCCACACC AATCTAGTCT   100

GGGTTTCCAA GGATCTGCCG TTTAAGTCAC TTAGCCTCTA TCCTTTCCGG   150

GAACAACCTG CCCCTAGAGA GGGTGAACGA GAATCGTCCC CAGTGCCTCC   200

AACATAACAA ACCCAATCGC CCTGTTAACT TTAAATCTTC AACTCGAGAA   250

AAAGGCTCAT GACTACTTCT AACCATGCCC AAACCC   286

(2) INFORMATION FOR SEQ ID :857:

  (i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 280 base pairs
    (B) TYPE: nucleic acid
    (C) STRANDEDNESS: double
    (D) TOPOLOGY: linear

  (xi) SEQUENCE DESCRIPTION: SEQ ID :857:

432

```
AACTATATGG  TATTATTTCA  CGCTGTACCC  AGTCCATTGC  TTGAACTTAC        50

GGGTACCTAA  TGAAACGTGG  AGGTCCGGAT  GTATGAAAAT  CTCCTCTTTT       100

CCCCTTTACT  TACAGCCTCT  GTAGGCAATA  ATTATAGAGT  AGTATAGATG       150

ATTTTTCTTT  TTTATAAATC  TGCCTATCTC  CAGGAGGATG  GGGCGCGCAC       200

TTTTAGAAAT  GCATATAAAT  GCTCTACGCT  CCTTTTTTCT  GTTACTTAAT       250

CGGCGCCAAG  GCCTTTACAT  GAATACTCAG                              280
```

        (2) INFORMATION FOR SEQ ID :858:

            (i) SEQUENCE CHARACTERISTICS:
                (A) LENGTH: 310 base pairs
                (B) TYPE: nucleic acid
                (C) STRANDEDNESS: double
                (D) TOPOLOGY: linear

            (xi) SEQUENCE DESCRIPTION: SEQ ID :858:

```
CACTGGTTTT  CATGACTGAT  TTCTTTATTT  TTAGTAGTTC  TGACATGTTG        50

GCCAGGCTGG  TCTTGAACTC  CCAGCCAACC  TCAAAGTGCT  GGGATTACAG       100

CTGTGAGCAC  CAGCCCAACC  TCGCCTCTTT  AAAAAGAAAA  AACACAAGTC       150

CACTCTGAAG  TCAGCCTCTG  TAACCTCCCC  ACAAGAAAAC  CGTTTTACAT       200

CAGTCACTAA  CCAAACAACC  AACAGTGCTT  CAACACAGAA  AGTAAAGCAT       250

TATACAGGGC  TTGAACTGTC  TTTTAAGCAA  GCCCCAAATC  CTTTGAAAGG       300

AGGCAGTAAC                                                      310
```

        (2) INFORMATION FOR SEQ ID :859:

            (i) SEQUENCE CHARACTERISTICS:
                (A) LENGTH: 158 base pairs

433

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :859:

TCTGTGTGGA GGGGAGGGAC CCAGTCTGGA CCCAGGTGTC ATCATCTCAG   50

CCACAGCAGG GCCCTCTCAG GCTGGGAAAC TTCTGCCAGA GCTGGCGAGT   100

CCTCTGCAGG TCAAGCCAGG GCTTGGACAC AACTACTTCA TCTATCGCGC   150

AGGAAGAG   158

(2) INFORMATION FOR SEQ ID :860:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 263 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :860:

TTTCTAATAA GAACATAAAA TAAAGGCTAA TTAAAAGAAG GTGACTGAGT   50

CCAGGAAGGC ACTAATCAAA GATGATATAC AGCCAGGTAA AAAAGAACAA   100

TTCACAGGCA CAAGACTATA TAACCATCGT TTTATTTTCA AACGTTATAC   150

AAAATATACT CTACCGAACT ATAATAGATC ATTAATAGTG GCACAATCTT   200

TAGATTCGGA ATAACTTGAA AATAAATCCC AACCACGTAA CTTACTAAAG   250

GAATAATGAG CCA   263

(2) INFORMATION FOR SEQ ID :861:

434

(i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 254 base pairs
    (B) TYPE: nucleic acid
    (C) STRANDEDNESS: double
    (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :861:

ATTTGTCTGA AAAATATATT TCTACACGAT CTGATAAAGT TCAGATAAGG   50

GGCATTCTAT TCCTAAGAAT GTCCTAAAAA TGGAAAACTG ATAAAAGATT   100

ATGCTTAGAA TTATACAGGT AAAAGACCTA CAACAATTGT TCTCTTGTTT   150

TGATCCCATA GGTCATTTGT TATTACTCTT CTTCAACAGA GTGATTTTCT   200

ATTATAAACT TTCTTAGGAG CCAATACAGA GTAGAAAGAA ATATTTTCAG   250

AAAG   254

(2) INFORMATION FOR SEQ ID :862:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 3⁻ base pairs
        (B) TYPE: nuc ⌐c acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID :862:

GTTCCTCCTT TGTAAATTAT GAAATATTTA TAGTTTAGAC TGAGTAATAT   50

GACATGAAAC AACAAACCTG CACATTTCTA ATTTATAACA AATCCGTTTC   100

CTTAATGGGT GGAAGGAAAT CTGAGGACAA TTCTAAGGAG TCTTGTCTGC   150

TTTCAGTGCG ATCTTCTAGT CATACTGAAG ACAATACCTC TCCAGATTGA   200

435

```
TCTTTCCCCT TCTTATACTC TTCCCGATCA ACGTCAATCA CACGCACCAC        250

TCCAGGTTTT AGACTTAGGT CATCCGTCTC TACCTGACTT CTGTTGCCCT        300

TCACCTACAC GTGGCTCGCT TTAGTTTGCT GAGCAGC                     337
```

(2) INFORMATION FOR SEQ ID :863:

    (i) SEQUENCE CHARACTERISTICS:
       (A) LENGTH: 169 base pairs
       (B) TYPE: nucleic acid
       (C) STRANDEDNESS: double
       (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID :863:

```
TGGTGGGTTC GAGCCCAACT TCAGCGCTCT TCGAGAAGTG CGAGGCGAAC         50

GGTGCGGGGG CGCCTCTCCT CTCCACCTTC CTGCGGGAGG CCCTGCAAGC        100

TCTCAGCGAC GACGCCACCA TCTTCTGACC AACTTCAGGC TACTACCCCA        150

ACTTACAATG CCACCGCGA                                         169
```

(2) INFORMATION FOR SEQ ID :864:

    (i) SEQUENCE CHARACTERISTICS:
       (A) LENGTH: 286 base pairs
       (B) TYPE: nucleic acid
       (C) STRANDEDNESS: double
       (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID :864:

```
ATTAAGGTAA AGGAAGACTT TCCATTGTTA AGTAGAAAGA GTGTCCTGCT         50

ATTACTACCA TTCACATCTA GTTTGTGTGA ACTAGGGTTT TCTATCTTAA        100
```

436

CCCTGTTAÀA AACAAAGGAA AGAAATGGGC TGAATGGCGC ACCAGCTATG   150

CGGATAGCAT TATCTTCCTG TGTTCCAGAC TGGAATGAAT TTATGAACAA   200

GGCAAGCACA CCATTATAGT AAATAAAATC TTACCTAGTT TTCGTTTTTG   250

CATTTCTTAC TTCGCAGTAT TTCTCCCGCC AAGAGC   286

(2) INFORMATION FOR SEQ ID :865:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 272 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: double
            (D) TOPOLOGY: linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID :865:

ATATAGTCCG CTAGGGATAG TGAAAAATTT GGGGCTTGGT TTAGATTGGA   50

GAGGTATATG GTGGGGTGTC TTATAAGGCT TAACTTTGGG AGGGCCCAGG   100

GCCTTGATTT CTGTCCCCCT TGCCTTGCGT GGCCTTTGAA TTGAAAGCTT   150

TGAÁTTAGGC CTTCATAGAT TTTAGTGTGC ATACAAATAA CACGATCTTT   200

TTATAAGGCA GATTATGATT CTGAAGGTTT AGTGTGGGAC CCAAGCTTTC   250

GCATTTCTGA TCTATAAGGT GA   272

(2) INFORMATION FOR SEQ ID :866:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 296 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: double
            (D) TOPOLOGY: linear

437

(xi) SEQUENCE DESCRIPTION: SEQ ID :866:

ATGCAGGAGA AGAAGGATGC CAAACTAAGT CAAAAAAACG GAACGCAAAT   50

5   AAAAGGAATG AGCACGGTTA CAAAGTCACA GGATGAGTCC CTGGGATCTG   100

GGGCGGGAGA AGGGGTGAAT CAAGAATGAC TTGAGCTTGT TACTCCCTAG   150

CAGGCTGAGG GCGTGACACA GCAGCTCGAT GACAAAGAGG TCTATTATAG   200

10   TTTCTAACAC TACAACGCTA ACTTTTGGAA CGTATCTACT TCTAGCATGT   250

AGACAGATCT CTAATCGCCT GCCAGACGGT AAGCCGCAGG AATGCG   296

15   (2) INFORMATION FOR SEQ ID :867:

            (i) SEQUENCE CHARACTERISTICS:
                (A) LENGTH: 241 base pairs
                (B) TYPE: nucleic acid
20   (C) STRANDEDNESS: double
                (D) TOPOLOGY: linear

25   (xi) SEQUENCE DESCRIPTION: SEQ ID :867:

TATTTTATCT CAACATAATA AAAACGACTA TAAATCTTCC TAAGAGAATG   50

CTCTACTCCC AAGACTAATT TAAACTCGGG GATCGTCAGA GGGAGTGCCA   100

30   CTGTGACTTC TACGATGAAA GAACAAGGGA GAGAAGATCT TATCGACAAT   150

CATACAAAGC CATATATACG CTATTCCTCA ACTCACAGAG TTAATTAAAT   200

35   GTCACCAGGA TGGAAGAAAC CTTATAAGCC CCTATCTATC A   241

(2) INFORMATION FOR SEQ ID :868:

            (i) SEQUENCE CHARACTERISTICS:
40   (A) LENGTH: 130 base pairs
                (B) TYPE: nucleic acid
                (C) STRANDEDNESS: double

438

(D) TOPOLOGY: linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID :868:

GGACGACTGC AAGCTGGAAC TACACACGCG CACTCGCTCA CACTACACAC   50

ACGCCACTCT CACACACTCT CACACACGCA CCCTCTCGCG CATGCTCTCT   100

CAAAGCCCAA TATAACCAAG GGGAAGGAAT   130

    (2) INFORMATION FOR SEQ ID :869:

            (i) SEQUENCE CHARACTERISTICS:
                (A) LENGTH: 310 base pairs
                (B) TYPE: nucleic acid
                (C) STRANDEDNESS: double
                (D) TOPOLOGY: linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID :869:

TTCAAATATT TATGTATGTT TGAACATTTT CATAATAAAA TGTTGAAAAA   50

CTAATGAGAA TGGCATAAAC AACATTTAAG CAATATATTT TGAAATTTAA   100

TTCAAATGGT CAAATTCCTG GAAAACACAA ACTCCCTTCA CTAACAGAAT   150

TGATAGAAAA TCTGAGTAGT TCACCATTGT TAAAGAAATG GAATGTGCCA   200

TTTAAAACCC TCCAATTGAA AATACTACAT ATAGTTACAA TAGGGAATTT   250

TCCCAAGCAC TTAAACAATA AACAATGCCC TCTTTATACA AACCTTTCCC   300

AGTAATAGAA   310

    (2) INFORMATION FOR SEQ ID :870:

            (i) SEQUENCE CHARACTERISTICS:
                (A) LENGTH: 192 base pairs

439

```
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: double
            (D) TOPOLOGY: linear


        (xi) SEQUENCE DESCRIPTION: SEQ ID :870:

    AAAGAGGCAA GTTCCTGGTG CAAAGGTGGC TCTGCAGCAT AATTTAGGCA        50

    TTGGAGGAGC TGTGTGTTGT AACACTCTAC AAGATGGGTT TTCCGGAAGC       100

    CGCCAGTTCT TTTAGAACTC ATCAAATTGA AGCTGTTCCA ACCAGCTCTG       150

    CAAGTGATGG ATTTAAGGCA AATCTTGTTT TTAAGGAGAT TG              192

    (2) INFORMATION FOR SEQ ID :871:

            (i) SEQUENCE CHARACTERISTICS:
                (A) LENGTH: 250 base pairs
                (B) TYPE: nucleic acid
                (C) STRANDEDNESS: double
                (D) TOPOLOGY: linear



        (xi) SEQUENCE DESCRIPTION: SEQ ID :871:

    ACCATAGATG TGTTCCAGAG GCAAAAGAGA CACATTATCC TAGATGGCAG        50

    AACATGCTTT CAAAACATAT AAAACGTCAA AGTTCCAGAT CTTTCTACAT       100

    TTTAAATCCT GTCTGAGGAT GGCAGCTGAC TTTATGTAGC TGATAGACGA       150

    CTAGAGTTTC ATCCAAATAC CTGACCACGA CTTCATGGAG ATTTGAATAA       200

    TCTATCCGAT GAGATTTATA TNTAAACAAC TCAACTCCTG TCGAAACAAA       250

    (2) INFORMATION FOR SEQ ID :872:

            (i) SEQUENCE CHARACTERISTICS:
                (A) LENGTH: 313 base pairs
```

440

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :872:

10

TCAGCTACGA ATTGCTTCCT TCTCACAGAA CTGTGACATT TATCCAGGGA   50

AGGATTTTGT ACAACCACCT ACCAAGATTT GCGTGGGCTG CCCCAGAGAT   100

ATACCCACCA ACAGCCCAGA GCTGGAGGAG ACACTGACTC ACACCATCAC   150

15 AAAGCTTAAT GCAGAGAATA ACGCAACTTT CTATTTCAAG ATTGACAATG   200

TGAAAAAAGC AAGAGTACAG GTGGTGGCTG GCAAGAAATA TTTTATTGAC   250

TTCGTGGCCA GGGAAACACA TGTTCCAAGG AAAGTAATGA AGAGTTGACC   300

20

GAAAGCTGTG AGA   313

(2) INFORMATION FOR SEQ ID :873:

25   (i) SEQUENCE CHARACTERISTICS:
                (A) LENGTH: 270 base pairs
                (B) TYPE: nucleic acid
                (C) STRANDEDNESS: double
                (D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :873:

35 TAGATGCTGA TGGCAATGAC ACAATTGACT TCCCTGAATT CCTGACAATG   50

ATGGTAAGAA AAATGAAAGA CACAGACAAT GAAGAAGAAA TTAGAGAAGC   100

ATTCCGTGCG TTCGATAAGG ATGACAATGA CTATATTAAC GCTGCAGAAC   150

40 TTAACCATAC AATGACAAAC CCCGAAGAGA AGTTAATAAA TGAAGAAGTT   200

441

GATGAAATGA TCAAAAACGT AGATNATTGA TGACGATGGT AAGGTAAACT   250

ATCCAGCGTT AGCACAAATG   270

(2) INFORMATION FOR SEQ ID :874:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 229 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: double
            (D) TOPOLOGY: linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID :874:

TTGGGCCATG TCCCCATTTT ATCTCCAAAG CCAGCCATGG TGTATTTCTC   50

TCTGCTTTTC TTCCATATTT CCAACCCAGA AATGACTCCT GTTCCCATAT   100

GTGATTATTA TATTGCGCTA ACCCAAGTGA TTAAGGATAA TCTCACTACT   150

TAATGACAGC TGATTATTTC CATCTGCAAA CTTACTCAAG AATGCAATCC   200

AGACTAACAC GACAATAGGA CATCAAGCT   229

(2) INFORMATION FOR SEQ ID :875:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 294 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: double
            (D) TOPOLOGY: linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID :875:

TTTGAACTTT CAGCCGAATA CATCTTTTTC CAAAGGAGTG AATTCAGGCC   50

CTTGTATCAC TGGCAGCAGG ACGTGACCAT GGAGAAGCTG TTGTGTTTCT   100

442

```
TGGTCTTGAC CAGCCTCTCT CATGCTTTTG GCCAGACAGA CATGTCGAGG          150

AAGGCTTTTG TGTTTCCCAA AGAGTCGGAT ACTTCCTATG TATCCCTCAA          200

AGCACCGTTA ACGAAGCCTC TCAAAGCCTT CACTGTGTGC CTCCACTTCT          250

ACACGGAACT GTCCTCGACC CGTGGGTAAC AGTATTTTCT GCGT               294
```

(2) INFORMATION FOR SEQ ID :876:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 173 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID :876:

```
ATTTTTGGTA ACATACATCA AGTGGCACTA ATTACACAGT AACTATAAGG          50

TAACTAACAT GAAACCACAG AACTGTAACT CTGCCACAGC TGCATGAACT          100

CGGGTTGTCC TGACCGAGCC CATCCCCAAA AAACCGCCCA CCCCAGAGCT          150

ACGCCAACAA AAACCGTTAT TAA                                       173
```

(2) INFORMATION FOR SEQ ID :877:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 143 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID :877:

```
TAATCAAAAG AGCTCTAAAT CTGTAATTTC TTTCTCCTTT AAAAAAATGT          50
```

443

CTACTTTGTT TTGGTCCTAG GCATTAGGTA ATATAACTGA TAATATACTG   100

AAACATATAA CGGAAGATGC AGATGATAAA ACTAATTTCG AAC   143

(2) INFORMATION FOR SEQ ID :878:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 213 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID :878:

ACTGAATAAA CTGCTGATGT CCAGGTTCAG TGGTTCCTGC TGTGGGACTT   50

GCGTTTTCAC TAAGTGTGGC GTTAGATCCA TTAGTTCCCG AAGAGCCTCC   100

AGTGCTTCCT AATGCCCCCA AGCCAGGAGT AAACCCTGGA ATGAGGCCCA   150

GGGCTTCTAT TGCTAATGCC TGTAAACCTT GCTGAATCTA TAACAGAGTC   200

TATACCGCTC TCG   213

(2) INFORMATION FOR SEQ ID :879:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 227 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID :879:

AAAGAAGGAA AAGAAAGAAA TAACACTTAA CAGTCCATAA CAAAGTGTTA   50

ACGAGATAGA CACATGCTTA TTCAAACCAC AGATATGATC CAGTTAATTC   100

444

```
CCTTCTTAGA ATGTGCCCAT AGTGCCTTAT TGCCTCATAA TAATGATAAT          150

AATAAGAGCA ACAATAATAA CGGCACAAAC TCCAGTCGAT ACTGACAAAC          200

TACCAGAGTA ACCGTCATCC CCTTGAG                                   227
```

(2) INFORMATION FOR SEQ ID :880:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 221 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :880:

```
ATAGACAAAG TCCTTCCCAC TAGAACTTAC ATTCCAGTGG GAAGAATTAG          50

AAGCCTCAGG AATTCCATTG CTTACTTTTA GTTGTTACTT CAAAAGTACT          100

TACATTTAAT CTGATTATTA ATTATTCGTC ATGAGCTTCA TTTTATTACA          150

TCCAGGGCAC AGTATGTGAA TTGTGTTTCG TTCCTTTAGG AAAAGGAAAA          200

ATAATCACTC TTTACAAGGT A                                         221
```

(2) INFORMATION FOR SEQ ID :881:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 310 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :881:

```
AATTGTGGTA TATTTCATTT AAAATCGATC AAAGACAGCA ACATACATTA          50
```

445

```
ATCAGAGGAA AGCATCAATT AAATGCAGAA ACAAGATTTA AACAAAGATT        100

CATATTAAAA CAATGATAAG TAATACTTAG AAACTGCATC CTAGAGACAC        150

ATCATTCGCA TTTTTAGAAA AACAGAAACA TATTAGTGTG AAAAGATGTT        200

AAAAAATGAA TATTAAACCG TCGAGCACAA CACACTACGC CGATAACAAT        250

ACACCACAAG CGCCGTAATC CTGCCGACAC TGACACACTA CAGGCGTCGT        300

GGCGATCCGA                                                   310
```

(2) INFORMATION FOR SEQ ID :882:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 177 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: double
            (D) TOPOLOGY: linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID :882:

```
GTTCACATCA GTGTGTAGGA TATGCTATCA CGTATGTGCA TGAGAAGAAT         50

GGAGAAAATG GATCTATGCG GATGTCTGTA CACACACACA CACACACATA        100

CACAACAAGC TTGCACATGT ATAGAGGATC CGAAATTCCA CCAATACTGA        150

CGAACTACAA ACGTAACAGC AGCAGGC                                 177
```

(2) INFORMATION FOR SEQ ID :883:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 152 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: double
            (D) TOPOLOGY: linear

446

(xi) SEQUENCE DESCRIPTION: SEQ ID :883:

CAATTCTATT TTCAGAGTTG ACTGTACTCT TTTCCTCTGA AGATACACGT   50

ATAAACGCGA CCAACGAGGT CTCTCGTCCT AATAACAGGT TCAGGCATGA   100

ATCACCGTCT AACAGCTATT TAAACACCGC CTCTTCATAG AAGTAACGCC   150

GA   152

(2) INFORMATION FOR SEQ ID :884:

    (i) SEQUENCE CHARACTERISTICS:
      (A) LENGTH: 177 base pairs
      (B) TYPE: nucleic acid
      (C) STRANDEDNESS: double
      (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :884:

CCATAATATA AGTATTTATC ATGTATTCTG TGTCTGGAAT ACAATTCAAT   50

GACCTATTTC AGAAAAATCT TTTCAAGTAC TGGCTGAAAG AGTGAGGGAT   100

ACATTAGGAG ACTGCAAATA AACTGGCAAT CACAAGAACT TTTTCGGATA   150

AAATGAAATT GTGCCGAAAT GTATACA   177

(2) INFORMATION FOR SEQ ID :885:

    (i) SEQUENCE CHARACTERISTICS:
      (A) LENGTH: 241 base pairs
      (B) TYPE: nucleic acid
      (C) STRANDEDNESS: double
      (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :885:

447

CACAGCTGGA AGAGCGGAGA AATAGAATTG TCTTCAAACA ATATAAAAAT   50

TCATAAAGAA TAGAAAGACT ACTATGTGTG GGTCGGGAAA TTAACTAGAA   100

TTTTTTTATA TCCACACTCT AGTATGAAAT GAGTACTTAT AGAGTAGAGT   150

GTAACATATT TAGACATAGT ATATATATAT ACAAGTGTAA CAAATATATA   200

TATTAAATAT ATATATGTTT TATAGAAACA CAGAGCACAC A   241

(2) INFORMATION FOR SEQ ID :886:

    (i) SEQUENCE CHARACTERISTICS:
       (A) LENGTH: 190 base pairs
       (B) TYPE: nucleic acid
       (C) STRANDEDNESS: double
       (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID :886:

GTAGCAACCG GCGCTCAATA AAATTCAACC AGCAAACTCG ACAAGTAACA   50

ACCATAAAAC CAGCCACACT AAGTCCAGCC ACCACTACTC AATAAAAATA   100

ACACGTATCT TCCACCGTAC AACCAATAGC AACTGCAGGC TACTGCAACG   150

CCATCCATAT ACCAAAAATG CTACTTACAA CACCACAACA   190

(2) INFORMATION FOR SEQ ID :887:

    (i) SEQUENCE CHARACTERISTICS:
       (A) LENGTH: 168 base pairs
       (B) TYPE: nucleic acid
       (C) STRANDEDNESS: double
       (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID :887:

448

CACGCTTTCT CTCACACAGC ACTAGCGCTC TCTCACTATC ACTCTTCTCA   50

CAGAGCTGCG CGCGAGTCTC ACTACTATCA AATATATCTG TCTCTTCTCA   100

CTCTATAGCT CTCTCACAGA TATATATCTA CATATAGCGC TCTCATTATA   150

CTATAATATT ATACTCTC   168

(2) INFORMATION FOR SEQ ID :888:

     (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 174 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

     (xi) SEQUENCE DESCRIPTION: SEQ ID :888:

ACTGGGCGCG CTGGTGCTGA CATCTTCAAG AGCATCTGTC ACTGAATATT   50

GCCGATCTCG CAACCGGTTC CAGTTAGACA GAACATTGTG ATATTCAAAC   100

CACTTTCTCG TAATTTCCAA TGGAGTTGTA AAGTTTAATG AGACCTCGAT   150

AATCATATTC TAGTCCACTG TAGC   174

(2) INFORMATION FOR SEQ ID :889:

     (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 327 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

     (xi) SEQUENCE DESCRIPTION: SEQ ID :889:

ACACCACACT TAAGGAATGG GAGTTATATT TCACTTCCCT GAGGCCAGAA   50

449

```
TATATATATG TATGTATGTA TATGTGTGTG TGTGTCTATA TATATATATA        100

TATAGACACA CACGCACATT ATACACACAT ATATATACAC ACACATATAT        150

ATATGTGTGT GTACAATATA TAAAAAATTA TATGGGAGAA AAGAAAGGCA        200

AATCTCCCAT GGCAGAGAGG TATCCCAAAA AATTTTTTTG TGTGTAACAA        250

AATATGTTGT GTGTATATAT ATATGCACAC ATATTTATGT GTATATATGT        300

ATATATATAT CTGTATATAC AGGTATA                                 327
```

(2) INFORMATION FOR SEQ ID :890:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 181 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: double
            (D) TOPOLOGY: linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID :890:

```
TTTTTTTCTT GTCTCTCCCG CAGCGCGCGC CTCTCGCGGC GCTATCTCTC         50

GCTCTCTCTC GCTCTCTCGA GCTCTCGAGA TATAGCCGAG ACACGAGAGC        100

TCGCTCTCTC CCGCGCGAAG ATCTCACCCC CGCGCGCTCG CGCGATATAT        150

ATCTCCTCGC GCGCGCGCCG AGCGCGCCCC T                            181
```

(2) INFORMATION FOR SEQ ID :891:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 207 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: double
            (D) TOPOLOGY: linear

450

(xi) SEQUENCE DESCRIPTION: SEQ ID :891:

CTCTTTAATA GCAAGCGAAT GGTAATTACA TGGTCGGATG AGGTCCTCAC   50

TCTCAGGGGA GGGAGGAGGG AGCAGAGGTG GACAGGGTGC AGTATAGGAT   100

TTACACTGTT TGAAGCATCT AACGAAGGGC AACAGTTTTT GGCAACCCAA   150

TTCACAGTTT TGTAATTTAC AAGAGATTTC TTTGAAAGGA AATAGGAAGG   200

CAAAGAA   207

(2) INFORMATION FOR SEQ ID :892:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 198 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: double
            (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :892:

CTATCACTTC AGGGAAACAA ACAACTAACA GCCATCAATT CAGAGGGAAG   50

TGATTTTACA GTAGAGTGAA CGAAACTTGG GAAGGAAAAC ATCCAAGAGG   100

CGTCTGTTTG ACGTGGGTAA CGTGGGGAAC GCATACTGTC TGGCAAGAAT   150

TCTACTAGGA CCACGGGAAA CAAAGCAGAT TAAAACACTC TCTACTCT   198

(2) INFORMATION FOR SEQ ID :893:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 96 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: double
            (D) TOPOLOGY: linear

451

(xi) SEQUENCE DESCRIPTION: SEQ ID :893:

CTTTAGAGAA TGCCTTGTGG AAAAAAAAAA AAATGGGCCC CAATACTTTT   50

TACTGCCCTT TATCAAAATT GTTGTGCATG GACCGGGCCA AATAAG   96

(2) INFORMATION FOR SEQ ID :894:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 325 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: double
            (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :894:

AATTGTATAC CAACATATAA ATTAAAAGTG TTATGCAATG AGAAACAATA   50

ATGGAAACAG CATAATACTA CATACTATCG CGCGGGGTTG TCGGCGTGGT   100

GGGCGTGCGT GTAGAGAGAG AGCAAGGGCG TGTGCGTGAG TGGGCGTAAA   150

GAGTGAGCGT GGGAGGGTGT GGTCGGTGGA GGTGTGTGGA GAGGTGAGTG   200

TGCGAGAGGG GCGAGTGTAT GTGTGATAAG TATAGCGCGC AAGAGGCGAG   250

GACAAAATAT ATATATATAT AGATATAATA GATATGAGAG AACACTAAAC   300

AATAACCACT ACTCACATAG AATAT   325

(2) INFORMATION FOR SEQ ID :895:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 266 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: double
            (D) TOPOLOGY: linear

452

(xi) SEQUENCE DESCRIPTION: SEQ ID :895:

ATAGTTGTAC ATTTTTATGG GGTGCATGTG ATATTTTGAT ATGTGCATAC   50

5   AATGTGTAGC AATCAAATCA GGGTAATTGG GATATTCATC ACCTCAAACA   100

TTTATCATTT ATTTGTGTTG GAAACATTCA AACCTTTTCT TCTAGCTATT   150

TATCCATTGT TGGATACTTA TATCAATTCT ATATCTTAGC TGTTGTGAAT   200

10   AGAGCTGCAA TAAATGTAGG AGTGCAGATA TCTCTTTGAT ATACTGATTT   250

TCTTTCTTTT GTTATA   266

15   (2) INFORMATION FOR SEQ ID :896:

              (i) SEQUENCE CHARACTERISTICS:
                   (A) LENGTH: 197 base pairs
                   (B) TYPE: nucleic acid
20   (C) STRANDEDNESS: double
                   (D) TOPOLOGY: linear

25   (xi) SEQUENCE DESCRIPTION: SEQ ID :896:

AAGAAGAGTC TTCTGCACAA ACAAAACCAT AGTGTTGACA AATAGTCATG   50

GCCAATGGCA ATCTGATGGT CCAGCGGCCC TCGGATGACT CCTCTGCAAG   100

30   GAGCATCTTC AGGGTTCTAG GGAAGTCACA GGGGCAACAT ATTGGAAACT   150

AGCAGGCCCA GAAGACCGCC CCGCCCCCCA TGCCCTGGCG CAGGGCC   197

35   (2) INFORMATION FOR SEQ ID :897:

              (i) SEQUENCE CHARACTERISTICS:
                   (A) LENGTH: 192 base pairs
                   (B) TYPE: nucleic acid
40   (C) STRANDEDNESS: double
                   (D) TOPOLOGY: linear

453

(xi) SEQUENCE DESCRIPTION: SEQ ID :897:

GATGGCTGGA GTAGATTAGG GCGTAGGTAG AAGTAGAGGT TAAGGAGGGT   50

GATGGTGGAC TATGATGGTG GGGATGATGA GCGCTATTGT TTTTTGTGAA   100

TATTTTTCTT CCGACTAACT CGCGCCCCAC TCTCTTGCGA GCACAAACAC   150

ACGCGCGCGT GTAAGCGGCG CGAGACACGC GCCCCTTCCC CT   192

(2) INFORMATION FOR SEQ ID :898:

        (i) SEQUENCE CHARACTERISTICS:
                (A) LENGTH: 224 base pairs
                (B) TYPE: nucleic acid
                (C) STRANDEDNESS: double
                (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :898:

TGGATGTTTT CATTCGCAAA TCATGAGAAA CTTAAGTGGG TTTTATGCAC   50

TTGATAGAGT TGGCAAAATT GAACTATGAA GTTAACTATT TAACTCAAGG   100

AATGGGCGGC AAACCCATCC CCTCGATTGA TAAAGAAGGG GAACATTTTT   150

ACATTAGAAC TGACACTGAA AACATAGCTC TTTTTCAGTC CACCCTGGTT   200

GCTCTAGTAG CCCACAGCCC AATC   224

(2) INFORMATION FOR SEQ ID :899:

        (i) SEQUENCE CHARACTERISTICS:
                (A) LENGTH: 362 base pairs
                (B) TYPE: nucleic acid
                (C) STRANDEDNESS: double
                (D) TOPOLOGY: linear

454

(xi) SEQUENCE DESCRIPTION: SEQ ID :899:

GAGGTGATTT CTCAGAGTTT AGAGAATAGG ATGGGGAAAA TTATATTTAG   50

5   TGAGTTATAA CCAGAATTAC ATAAGACAGA TATGGAAATT TTATAAACAA   100

AATGCAAAAT ATTCTAATGT TTCAATGTTC TACATGAACA TATAGGGAAG   150

CATAGACAAT AGCCAAAAAT ATGTTCTGCA TTCATATACT AGTTCAAGTC   200

10   CGAGTCTGGC TACTTTCTAG GTAGTGTGCT TTTTGTCAAA TTATAAAGAT   250

ATATTCCCTT TGTTTTTTGA AAACGAGTGA GATGCTTAAA TAGAGTACAA   300

15   TTATCTCATT CAAAATGTAT GTTGTTTCCT CTCGAGAATT GTGAAGGTTC   350

TGAGATTTGA TT   362

(2) INFORMATION FOR SEQ ID :900:

20
            (i) SEQUENCE CHARACTERISTICS:
                (A) LENGTH: 310 base pairs
                (B) TYPE: nucleic acid
                (C) STRANDEDNESS: double
25   (D) TOPOLOGY: linear

            (xi) SEQUENCE DESCRIPTION: SEQ ID :900:
30
        GTATGTAGCC CAGTGGGTGT CTTCCCACAG GGTAGGTACT CAGTTTGCTC   50

        TGGAGGGTGA CTCATACCTA AACAAGTGCA CATCTCCTTT CTCAGTAAAG   100

35   CCAAAGCAGG TTTCTACATT TGGAACAAAA GAGATCCTGA CCAGAGAGCT   150

        ATCACTGGTG GTCCACTTGG GCCCTCCTTG ATGGGTGTGT TCACTTAGAA   200

        AACCAAATTA CAGATCTGAA GGCTGCTGGG TAGGGACAGG ATTAGAACAA   250

40   AGGGAATGAG ATTGAATGTT ATTTAAGGGA TATTTCTGTC AAGTTTTGGT   300

455

TTCTCGATGA   310

(2) INFORMATION FOR SEQ ID :901:

5   (i) SEQUENCE CHARACTERISTICS:
                 (A) LENGTH: 185 base pairs
                 (B) TYPE: nucleic acid
                 (C) STRANDEDNESS: double
                 (D) TOPOLOGY: linear

10

        (xi) SEQUENCE DESCRIPTION: SEQ ID :901:

15   TTCCCCCATG AGACCGTTAG TCTCTCTTTG CCTGGCTGAC TACCTGCATA   50

       CAGTAGGCAC TCACTGCTGG AGTGAGGCAC TGACTCCTCC AAAGATTGCA   100

       GGGGGCGGAG GAGGGAACCA CGAAGGCCTG GGAGGGGGCA TCTTTGGCCC   150

20

       CCACTAACCA TCTCCCTATT TCTGCATCCT GGTGA   185

(2) INFORMATION FOR SEQ ID :902:

25   (i) SEQUENCE CHARACTERISTICS:
                 (A) LENGTH: 381 base pairs
                 (B) TYPE: nucleic acid
                 (C) STRANDEDNESS: double
                 (D) TOPOLOGY: linear

30

        (xi) SEQUENCE DESCRIPTION: SEQ ID :902:

35   ACAAGCTGCA AGATCCTTCA CTTGAGGCTT TCAGCCTTAT TCTCCTCCTG   50

       TCAAACAACT AAACTACTCC GATGTTTGAT GAAAATTAAA CTGCTACTCA   100

       GGATACTGCA ATTACAAGGA GAGGGAATGA TCAGCCCAGG GAGGCTATTA   150

40

       CGTGTGACCT TTGAGATGGA CCTGATCGCC CCTTTTACTT TTTAGACTAC   200

456

```
AAGTGCAGGG AGGTGGAGCT TATTTGCATT TGAACTCCTG TAAAGAGTAA        250

GAATATGGAA AGGATGAAGC CTCATTCATT CGGGCATATT AAAAAGAAAT        300

TGCCTTCAGA AACACTTTGC CTTTTAATAT GTGTAGCTAC AGTAAGTACC        350

AATGGGCTAA CTAATTGAAG CTAACATTTT A                            381
```

(2) INFORMATION FOR SEQ ID :903:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 240 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID :903:

```
CATCAAGGGT TTTTCCTGCT GCAATTCTTG TCAAAAACTG ACATATGTAT        50

ATCGTTCTCA ACTGGCAAGC TGTTAGACTG GATAGTCCAT GAATAATAGC        100

CTCTGCGCTG TTGCGGGTCC TGCGGAAGTC CTCGGAGCGG CCGTCGCGGA        150

AAGCTCGGCA AAGAGAGAGG CAGAGGAAAT CGAGCATCCA GCCGGCAGCC        200

ACTTTTTTTT TATCGGCACC AGGCCGCGTC CTCCTCCTCC                   240
```

(2) INFORMATION FOR SEQ ID :904:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 280 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID :904:

457

CCCTGGGCAG GCTGCTGGTG GTCTACCCTC GGACCCAGAG GTTCTTTGAG   50

TCCTTTTGGG GATCTGTCCA CTCCTGATGC TGTTATGGGC AACCCTAAGG   100

5   TGAAGGCCTC ATGGCAAGAA AGTGCTCGGT GGCCTTTAGT GATGGCCTGG   150

CTCACCTGGA CAACCTCGAA GGGCACCTTT GCCACACTGA GTGAGCTGCA   200

CTGTGACAAG CTGCACGTGG ATCCTGAGAA CTTCAGGCTC CTGGGCAACG   250

10   TGCTGGTCTG TGTGCTGGCC CATCACTTTG   280

(2) INFORMATION FOR SEQ ID :905:

15   (i) SEQUENCE CHARACTERISTICS:
                    (A) LENGTH: 225 base pairs
                    (B) TYPE: nucleic acid
                    (C) STRANDEDNESS: double
                    (D) TOPOLOGY: linear

20

                (xi) SEQUENCE DESCRIPTION: SEQ ID :905:

25   GTTCTAGTGG TAACTGCTGC TTCTGGAAAA TATTTAGAGA AACCAACGGT   50

        AAAAAAAAAA ATAATAATTA ATACCGTTGG TTTCTACATA CACTCTCAAT   100

        ATTTGCACGA GTAAAGCGTA GCAAGTTTAA CACAACTTAT GTAAACTTGG   150

30   AAAATTTTCC GAAATTTTAT TGACTTTTCT CGGTCTCTCC TATCTTTATA   200

        TACACATCTC TCATGCACAC ACGCG   225

35   (2) INFORMATION FOR SEQ ID :906:

                (i) SEQUENCE CHARACTERISTICS:
                    (A) LENGTH: 161 base pairs
                    (B) TYPE: nucleic acid
40   (C) STRANDEDNESS: double
                    (D) TOPOLOGY: linear

458

(xi) SEQUENCE DESCRIPTION: SEQ ID :906:

GGTGCTGACA TCTTCAAGAG CATCTGTCAC TGAATATTGC CGATCTCGCA   50

ACCGGTTCCA GTTAGACAGA ACATTGTGAT ATTCAAACAC TTTCTCGTAA   100

TTTCCAATGG AGTTGTAAAG TTTAATGAGA CCTCGATAAT CATATTCTAG   150

TCCACTGTAG C   161

(2) INFORMATION FOR SEQ ID :907:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 204 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :907:

AGAGATATAT GCAATCTGGT AGTCCATTAA ATGAGAGTTA CACTTAAAAT   50

ATTTTAGTTC TTTTAAAGAA AAAGTCTCCA TGTGCTATTT GGGAAAACCT   100

TCATTGCCTA AAGACCCACT TGCATAATTA AGGCAGATGA TGATGATCTT   150

TATATATGCG CACACACACA CACACGAC ACGACGACAC ACACACACAC   200

TCTA   204

(2) INFORMATION FOR SEQ ID :908:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 316 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

459

(xi) SEQUENCE DESCRIPTION: SEQ ID :908:

AGTTTCTGCA TTTGGTCTGT GTGACTCTAT GGAGCCCAGG ACTTACAGAA   50

5   AAAGGTGTAA CTGGCTCTTA GGACTTTAAG CCACATTATG GTAGTAGACC   100

TGCCGTTTTA TTTGACATGG TGAAATAAAC TACCACTCCT TTGTGGTACC   150

ATATGGGCAG GACAGAGCTC TTCAACCCTG GCTAACAAGC CTGAAGAAGA   200

10   CCCTGTGAGG CCGCAGCAGC CATGGGAACT TCCCAAAGGA CAGAAATCCA   250

CATTGGAACG TAGCATCCAG ATAGGTGACA GAAATTCCTT CCACCATATC   300

15   CAAATGTGTG TGTTTT   316

(2) INFORMATION FOR SEQ ID :909:

(i) SEQUENCE CHARACTERISTICS:
20   (A) LENGTH: 307 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: double
            (D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :909:

CTAGTAACAT AGAAAATAAA CTTCAGTGGG AATCTCTGCT TCCCGCGTGA   50
30
GGTGTTTAAT TCTTGGCATT TTTGTATTTT AAAGATGTAG CAACTTGTTT   100

CAAGTTAGAG GAGATGGCAG GGTCAAAATT TTAGAAACTG GATCCCACCA   150

CCACTGTGTT ACTTCCTAAA CCTGCATACA AATGTTCTGC AACATGTAA   200
35
TGTGCCAATA GAATTATACG GTGTGAACTG CATATCTCAG TATCTCCACG   250

GGAAAAAACT GTGGTTGGGG CATGGAGGGG GGAAAGGGAA ACTTTTTTAA   300
40
GCTATTT   307

460

(2) INFORMATION FOR SEQ ID :910:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 172 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID :910:

TTTTTTTTTT TTTCCAGGCA CCTAACGATT TGTTTTGCTC AATCAAACGC   50

AGACAGGCGT CTCCGAAGTA CCACCACTGG GATATCCTCG GACCAGCGCT   100

TAAACCGAAT CCCCACAATC TCAAACTCAA CCAGGCCAAA GGGAACACAG   150

TGACACAACA ACAGGGTTCC AA   172

(2) INFORMATION FOR SEQ ID :911:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 255 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID :911:

GCATAGAGAG ATATATACAC AGAGAGGACA TACATATATA TATATAGAGA   50

CACAGAGACA GACATATAGA GATATATATA TACACAGCAT AGAGATACAG   100

AGAGATAGAG AGAGATACAC ATACACACAT TCATCAACGA GAGAGAAGAG   150

AGGAAAGAGA GAGAGAGCGA GCACAGACAG AGATAGAGCA CACAGAGAGA   200

TCGCGCAGAT CTATACAGAG GGATATTCAC CACATTGTAT ATGGAAAGCG   250

461

CATCT   255

(2) INFORMATION FOR SEQ ID :912:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 196 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: double
            (D) TOPOLOGY: linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID :912:

CAAGCGAATG GTAATTACAT GGTCGGATGA GGTCCTCACT CTCAGGGGAG   50

GGAGGAGGGA GCAGAGGTGG ACAGGGCGCA GTATAGGATT TACACTGTTT   100

GAAGCATCTA ACGAAGGGCA ACAGTTTTTG GCAACCCAAT TCACAGTTTT   150

GCAATTTACA AGAGATTTCT TTGAAAGAAA ATAGGAAGGC AAAGAA   196

(2) INFORMATION FOR SEQ ID :913:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 203 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: double
            (D) TOPOLOGY: linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID :913:

ACTATCACTT AAGGGAAACA AACAACTAAC AGCCATCAAT CCAGAGGAAA   50

GCGATTTTAC AGTAGAGTGA ACGAAACTNG AGAAGGAAAA CATCCAAGAG   100

GCATCTGTTT GACGCGAGCA ACGCAAGGAA CACATACCGT CTGGCAAGAA   150

TCCCACTAGG GCCACGAGAA ACAAAGCAAA TTAAAACATT ATCCACTACA   200

462

CGA   203

(2) INFORMATION FOR SEQ ID :914:

5   (i) SEQUENCE CHARACTERISTICS:
                    (A) LENGTH: 262 base pairs
                    (B) TYPE: nucleic acid
                    (C) STRANDEDNESS: double
                    (D) TOPOLOGY: linear
10

              (xi) SEQUENCE DESCRIPTION: SEQ ID :914:

15   CTGCCGAGCC ACCATGCTTG CCTGAAGCTT CGGCCGCGCC ACCCGGGCAA   50

       GGGTCCTCTT TTCCTGGCAG CTGCTGTGGG TGGGGCCCAG ACACCAGCCT   100

       AGCCTGGCTC TGCCCCGCAG AACGGTCTGT GTGCTGTTTG AAAATAAATC   150
20
       TTAGTGTTCA AAACAAAATG AAACAAAAAA AAAATGATAA AAAAATCGGA   200

       TTTCCGGTTA ACACTGTGAC TTCAATTGAA ACACCTTTTT GTAGTATCTG   250

25   GAGGTGGACA TT   262

       (2) INFORMATION FOR SEQ ID :915:

              (i) SEQUENCE CHARACTERISTICS:
30   (A) LENGTH: 191 base pairs
                    (B) TYPE: nucleic acid
                    (C) STRANDEDNESS: double
                    (D) TOPOLOGY: linear

35

              (xi) SEQUENCE DESCRIPTION: SEQ ID :915:

       TGGGTTCTAA TGATGTGCTT GAAGAGGAAG ATTTTGATCG CACCACTGAT   50
40
       ACACGGAGTC TGTATTTTGC ATCCTAGAAT GATTAACCAG AAACAAAGAA   100

463

AGGAAAAAGG TAAAATCAAT AATAAGATCA GCAGCTCTGG GACACAGAAT   150

AAAGAATGAA ATAATTTGAA AAAAAAGGCA GGGCAGGCAA A   191

5   (2) INFORMATION FOR SEQ ID :916:

               (i) SEQUENCE CHARACTERISTICS:
                   (A) LENGTH: 252 base pairs
                   (B) TYPE: nucleic acid
10   (C) STRANDEDNESS: double
                   (D) TOPOLOGY: linear

15   (xi) SEQUENCE DESCRIPTION: SEQ ID :916:

AGACTTGGGG GTTCCTGGTG TGTGAGGGGT CCTGGGATAG CTAGGGGTTT   50

TCCAGGAGTT GTCCTTTGTT GTTTGTCGTG AAGAATTATA CTTTGTGTGT   100

20

GTGTGGGTTG TCCCATGTGT ATGCGTGTAG TGTGACAGTA TATGACCCCC   150

AGTGTGTGCA TATGTTTGTG TGGTTGTCTC TGAGTGATAT CCACCTCTCT   200

25   CTCCCCCTCT GTCTCTCTGC AGAGATATGT GTGGCGTCAC TGTACTCTTG   250

TG   252

           (2) INFORMATION FOR SEQ ID :917:
30
               (i) SEQUENCE CHARACTERISTICS:
                   (A) LENGTH: 247 base pairs
                   (B) TYPE: nucleic acid
                   (C) STRANDEDNESS: double
35   (D) TOPOLOGY: linear

               (xi) SEQUENCE DESCRIPTION: SEQ ID :917:
40
TAGACAGAGT GACAGTGAGA GAAAAAGAGA GGAAGGAAAA GGGAAAAGGA   50

464

GTAGGGAAGG ATGAGGGAGA TAGGAAAGCA CCTAC GAG GCAGAGAGTT   100

TCCTGAAGGT CATGCGATCC TTTACCCTCA GAAACTTTCA GGCTGAAATC   150

ACCATCTCCG TTATCCCAAC AAACGCACTC TCCTACCTCT ACAAGCACTT   200

CAAGTAAAGC AGAAATCACA CCAATACTGA CGNGCTTCAA GCGCAAC   247

(2) INFORMATION FOR SEQ ID :918:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 191 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID :918:

ATTTGGATTC AATTGCCTGT TGCACTTTTA CATTAAGTGT TGCTTAAATA   50

AACAAAAATA GAGCATAAAT TCAATATTCT ACTGTCTAAA CATTTTAAAG   100

CAATGGTTAT GCCATCATAA ACAAGTAAAA TGCACCTAAT TCGAGTCTTT   150

TGACACCTCT TGTTTTAAGT TTCCTGTATG ATAAAGTTCT T   191

(2) INFORMATION FOR SEQ ID :919:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 205 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID :919:

CAAGAGTGAG ACTCCATCTC AACCAAAAAA AAAAAGAAAG AAAAAAAGAA   50

465

```
ACAACCTCCT CATTTTCAGA AGCGAACACA CCCCCGCCCC AAGATAGACG        100

ACAGAGACCG GACTAAGATT TAACCCAGGA ACTTTTCGCT TGGGCACCTT        150

CGAACAACAC ACAACCCGCA AAACCATACA CGCTCCCTTG CCCGAGGCCC        200

AACCC                                                        205
```

(2) INFORMATION FOR SEQ ID :920:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 323 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: double
            (D) TOPOLOGY: linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID :920:

```
GACAAAATTG GGACTCTAAG TATTGCGCTT TTTTTTCCTC TCCAACGACT         50

CGTTCCCTTT CAACAAATAG CACTTCAGTC CACTGTGTAC AGAAGTAATA        100

CATCTCCTAT CGTTAGTTGA ATAAATTCAC ACACCGCGTT TAAGAGATGA        150

AACCACGACT TCGTCAAGCC ACATTCGATT GCCATAAGAT TCCAAAGAAT        200

TCTATCCTCT TAAAGCGAAC CACATGTAAC CCGAAGGTCC CCACCTATCA        250

AGGTTAGAAC TGATATTCAA ATTATAGACT CATTCCACTA AGCAAGTAAG        300

CTCTAAGCTA CAGGTTGATC ATA                                    323
```

(2) INFORMATION FOR SEQ ID :921:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 230 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: double
            (D) TOPOLOGY: linear

466

(xi) SEQUENCE DESCRIPTION: SEQ ID :921:

AACATTGACG ACGCTAAGGA TGCCATGATG CCATGAATGG GAAGTCTGCA   50

GATGGACGGC AGATCCGAGT AGACCAGGCA GGCAAGTCGT CAGACAACCG   100

ATCCCGTGGG TACCGTGGCG ACTCTGCTGG GGGTCGGGGC TTCTTCCGTG   150

GGGACCGAGG CCACGGCCGT GGACTCTCTA GAGGCGGCGG GGATCAAAAC   200

TATAGAAACA ACAAGTTAGA GTACAGACGT   230

(2) INFORMATION FOR SEQ ID :922:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 239 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :922:

TATTTTTCCT GATGTTCTCC CTTCCTCCAG TCCCCGACCT CCCACAGGCC   50

CCAGTGTGTG TTGTTCCCGT TCCTCGTGTC CGTGAGTTCT CATTGTTCAG   100

TGCCCATTCT GAGGGAAAAC ATGCCAGTGC TTTCGCGTTC TTCCTCGCTC   150

TCACCCACCT CTCAGCTTAT CGCGTCGCGC GCGCAGTATA TTCGTCTCTC   200

TCTCCAGTCT CTCTCGCGAC ACACATCTCT CTTTTGTAA   239

(2) INFORMATION FOR SEQ ID :923:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 178 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

467

(xi) SEQUENCE DESCRIPTION: SEQ ID :923:

5   GTCAGTTCAG TTGTGAACAA AGCCCTTTGT GTACGTTTTT AAATTTTAGT   50

        TCACACGATA ACAATGCTTT GCAAGTAGGT GTAATTATTT TACTCCCATT   100

        TTATGGATGA GAAAACAACA GAGAGGTTGA TTGGCCCCAC CTTCAAATCC   150
10
        TGAAACCCGT CCACTCAATA AATTTTTG   178

        (2) INFORMATION FOR SEQ ID :924:

15   (i) SEQUENCE CHARACTERISTICS:
                (A) LENGTH: 325 base pairs
                (B) TYPE: nucleic acid
                (C) STRANDEDNESS: double
                (D) TOPOLOGY: linear
20

        (xi) SEQUENCE DESCRIPTION: SEQ ID :924:

25   CAGCTGGTCC CCCACTAAAA GAAGGGGCAG ACCACCACTA GCCAAAAGAG   50

        ATAGCAAGAC TAACATCTGG AAGAAGCGAG AGGAACGCCC ACTGATTCCC   100

        AAAAAAAAAC TCCAATGGGG ATTGTGTGTC TGCTGTCTCG TGCTGTTTAT   150
30
        TCTTGCTTCT TGTTGTAAAT TGCAGTACGA ACTTAAGAAA ATGAGACTGA   200

        GCAATCTCAT GGTTCTTGGA CATGTCTCAA GCAGAGTAAA TGGTAATTCA   250

35   GTAATCAGAG AGAAAGATAC CAAGGAATGC TTTTTCTGGC CTATTCATTT   300

        ATTTTTGGGG GATGAATTTA CAGTA   325

        (2) INFORMATION FOR SEQ ID :925:
40
            (i) SEQUENCE CHARACTERISTICS:
                (A) LENGTH: 261 base pairs

468

```
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: double
            (D) TOPOLOGY: linear


        (xi) SEQUENCE DESCRIPTION: SEQ ID :925:

    ATGGCTATGA CCTGGGACAT GGAAACAGTG ACCTCCGCGT TCTGGTCCCG        50

    AGATCCTCGC ATCAGCGTCA TCGTGTGCAC CGGCTTGGGG GGCTGGAGTT        100

    CCGGTTTTCT TTGTTTTTTC TCTTTATTCG TCCTTTCTCA AAGATGGGAT        150

    ACTGATCAGA ATCGTTCTGT ATATGCTTGG GACTGGATGG AAAGACTTTG        200

    AAGCAGCTGT GGGGGGCGGG AGGACACCGA CAACCAAACA GACGTGTTGG        250

    TTCCAGTCCT G                                                 261

    (2) INFORMATION FOR SEQ ID :926:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 173 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: double
            (D) TOPOLOGY: linear



        (xi) SEQUENCE DESCRIPTION: SEQ ID :926:

    GTCAGCCTGG GCAATCACAA CGACAACAAA AGGTACAGTC TCAAGAGTCC        50

    AACTGGGTTC AAATCCTGGC TCTGTCACAT ACTAGCTGTG TGACCTTGGC        100

    CAAGTTTCTT AACCTCTCTG TGTGTATAGT CCTTATCTGA AAATGGGGAT        150

    AACCAACCAA GAGAGCTGAG AGA                                    173

    (2) INFORMATION FOR SEQ ID :927:
```

    (i) SEQUENCE CHARACTERISTICS:
       (A) LENGTH: 223 base pairs
       (B) TYPE: nucleic acid
       (C) STRANDEDNESS: double
       (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID :927:

```
AACACTCAGA CCGGACGGGA CGAGGGATTC CCCTGCCTTC GCTTCCCTCC     50

CTCGCTTGCT TTGTAGTTTT CCCGCACCAG CCCGCTGCCC TGCGCCATCC     100

TAGGGCCTCG AAGCCCGGGG AATCTGTCCC ATCCTGTAAC GGGCCGCCCC     150

CTTNGATTTT TCTGCCCGTG CCACCGGAGG TTGCTGCGAC GCGCACCGAC     200

TCAGATCATT ACTACTGAAC TCG                                 223
```

(2) INFORMATION FOR SEQ ID :928:

    (i) SEQUENCE CHARACTERISTICS:
       (A) LENGTH: 212 base pairs
       (B) TYPE: nucleic acid
       (C) STRANDEDNESS: double
       (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID :928:

```
GTTATAATTA TTTACATGCT GCAACACGTC ACAACATAAA TTTACCAAAT     50

ATTTCATGGT GGGATGCTGT AGGTTTCAGA TAATAGTTTT AAGATAAAAA     100

CCACAGATTA AGTGAAGACA CCCACAACTT TAATGACTCT ACGACTCTCG     150

GTTGCTAAAT GCTAGAAGTC AAAAGGCAGT GTTTTTTCAG TCCTACCTGT     200

CATAACTTGC AT                                             212
```

470

(2) INFORMATION FOR SEQ ID :929:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 233 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: double
            (D) TOPOLOGY: linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID :929:

        TTAACATAAT ATTTTGAATA TATAGGGCTC ATAAGATATA TTATTAAATT   50

        ATAAACAAAA TAATCAGGAA CTTAGTGTGG TGCCTAGTTT GATATATGAT   100

        TACTTTTTGA AATGCACTAA ATTCCACAAA TAATGAAAGT ATTCTTTGTG   150

        TATAATGTTA TGTTTGGTTA TTATGTATGG TCTTCGTATC CAAAGGTATG   200

        ACATAACTTG AGTTTGTTTG CTTGGTATTT ATT   233

(2) INFORMATION FOR SEQ ID :930:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 235 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: double
            (D) TOPOLOGY: linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID :930:

        AGTCTGTAAC GATACACCCA TAGATGTGAA TTATGTATAT TCGAGAAGGA   50

        GATCAGATGG CATCCAGAAG ATAGTTTAGA TTTCAGCACA TTCATGGTTC   100

        AGATGCAAAA TCAGATCATC AAATAGATCC AGCAATTCAC AATCATCATA   150

        GCCATATCGC GTCACGTCCG CCGCACAAAG ATCCGCACCA ATTATCTATC   200

471

```
TCCCACCCCC CCCAGGCATT CAGCACCCGC AAAAG                         235
```

(2) INFORMATION FOR SEQ ID :931:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 221 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: double
            (D) TOPOLOGY: linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID :931:

```
CTATCTAGAA TTACTTATTT CACTTGAAAT GTATGGTTTC AGGAAAATTT          50

TCAATTTAAC TTGAAGGGAT TATCTCTTAT TTTGCTTGGA ATAATGGCAT         100

CTCAGAAACA TGGGTTTACC TGTGATTTTT TTGTTTGGGT GAATGCTTAA         150

AAACAAAAAA AAAATTTACA TATGCATTTT ATGGATACAC ACACACACAC        200

ACACACACAC ACAAAAAACA C                                       221
```

(2) INFORMATION FOR SEQ ID :932:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 333 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: double
            (D) TOPOLOGY: linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID :932:

```
TGCTCTATTG CTATCTCCTG ATATAGGTTA TATATATATT ATGTCTTGAG          50

CGTCATGTCT TGTGCTACTA CACCGTGTTA ATCCCAGCTA CTCAGGAGGC         100

TGGAGGATCG CTTGAGCCCA GGAGTTCTGG GCTGTAGTGC GCTATGCCGA         150
```

472

TCGGGTGTCC GCACTAAGTT CGGCATCAAT ATGGTGACCT CCCGGGAGCG   200

GGGGACCACC AGGTCTGCCT AAGGAGGGGG TGAACCGGCC CAGGTCGGAA   250

ACGGAGCAGG TCAAAACTCC CGTGCTGATC ATGTAGTGGG ATCGCAGCCT   300

GTGAATTAGC CACTGCACTC CAGCCCTGAG CAA   333

(2) INFORMATION FOR SEQ ID :933:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 281 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID :933:

AGATTTATGG CTGCTTTCAC TTGGCTCCAT GTTCTGCTGA TAATTAAACA   50

GTTTGTGTGT CCTGTCTTTC CTCAAAGGAA CTTGTCAACC TTTGGAATTT   100

TGTTCATCTC AGAGGGACGT CTTAAGTACT CAGCTTTCTG AATGTTTAAG   150

AAAAAAATAA TACTTTTCAG AATTACCTAC CTCTTTCTCA TTTTTAGCCT   200

GGGATCAATT ATTCCCTTTC ACACTTTTTT ACATCCTAAG TAGAAATAAA   250

ACTCTTTATT CTATTTTTTT TCAGTTATTG G   281

(2) INFORMATION FOR SEQ ID :934:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 266 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

473

(xi) SEQUENCE DESCRIPTION: SEQ ID :934:

AATCTTGTAT TATGTTAATA TTAAAATCTA ATAATAAGAT ACTGTAGAAG   50

TATTTTACAT TTTTGGGGTA TAGGCACAAA TATATACATT TAAATATTAG   100

TAATAGAATT GAACAATTAA CTATAAAATA TTATATCATA ATAAACTGTT   150

GTTTTATCCC AAGGGTAGAG GGACTCTAAG TAAAACTGTA ACAGAATCAA   200

AAGGTTACTG ATAGTTAGAA TGGGTTGAGA ACTATTTTAA CTTGGGAACT   250

TTAAATAAGT AAATCT   266

(2) INFORMATION FOR SEQ ID :935:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 178 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :935:

GGAAAACAAA TGTAAGGAGG GAATTCAAAT ACCTAGTTAA TCTATTAACT   50

ACTAATAACT CATTAAATAA ATTAATAATA TTAAATGATC TGTGTGTTCC   100

ATGCAAATAA CAGAATGATT TCCACTGAAT AGTCATGATG GTTTAAAATA   150

TTACTCTAAC ACCAATAACA ACACGTAA   178

(2) INFORMATION FOR SEQ ID :936:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 224 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :936:

ACTCAGCTCC GTGCGACCCA CATGGCCCCA GGCGGGGGGA CACCAGAGGC   50

TCCTCCATGA GCAGCAGGAG TGAGCGGAGG AATGTGCCCC ACAGCAACTT   100

TCCCAGCCAA TGCCACGATG GAGATGACAA CCCCAGATCT GGGGANACAG   150

AAACCACTCA GAACGGCACA GGGTAACTGG CCCCAAACGC TGAAAGTTAG   200

ACTTCACCCG AATTACATTT ACCA   224

(2) INFORMATION FOR SEQ ID :937:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 270 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: double
            (D) TOPOLOGY: linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID :937:

ATTTTTTTTC CCAAGAATCC CCAACTCAAT AAAACCGTGA AACAATTGCT   50

GGGGATGGGT AGAGAAAACC CATTTATAGT ACTTTTCTGC CTTCTTGTGG   100

TTTTCGGCTT TGCGATCAGG GACTGAAGAT AGAAGGAAAA AAAAAAAAAA   150

AAAACAAACA CAAAAACATT TCAAAAGAGA AAGGAAAAAA CTTTTTCCAA   200

CCAAAACTCC TAAAAAACCC AAAAACAGAA CAACCAATTA AACCCGACCC   250

GACACAACTA CCAATGACTG   270

(2) INFORMATION FOR SEQ ID :938:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 215 base pairs
            (B) TYPE: nucleic acid

475

```
            (C) STRANDEDNESS: double
            (D) TOPOLOGY: linear


       (xi) SEQUENCE DESCRIPTION: SEQ ID :938:

  AGCCTTCTCC CTATTCGATA AAGATGGCGA TGGCACCATC ACAACAAAGG         50

  AACTTGGAAC TGTCATGAGG TCACTGGGTC AGAACCCAAC AGAAGCTGAA         100

  TTGCAGGATA TGATCAATGA AGTGAATGCT GACGACAATG GCACCATTGA         150

  CTTCCACAAA TCTTCAACTA TGATGCCTAG AAAAAAGAAA GATACAGATA         200

  CTAGAACTAA AGTCA                                               215


  (2) INFORMATION FOR SEQ ID :939:

          (i) SEQUENCE CHARACTERISTICS:
               (A) LENGTH: 303 base pairs
               (B) TYPE: nucleic acid
               (C) STRANDEDNESS: double
               (D) TOPOLOGY: linear


       (xi) SEQUENCE DESCRIPTION: SEQ ID :939:

  TGTCGTCCTT AATATTTCTN AGCCTTTTGT CATAGAGGTG GTCGGTTGGA         50

  CCTCAAAGCC TCCATCTAAT TTTTTTTGTC TATGTTTCTA TATCTCTCTC        100

  TTTTACGCTT CTTTCCCGGA CCGTCCCCTC CCTCTACAAT TATATTTACT        150

  ACCTTCATGA TTGCTTTTTA TTATTTCTTT CACTCATCAT TATTGTTCAT        200

  TTTTTAATTA ACAATTTTTT TCATTATTCT TTTTCTTAAT TTGTAACCCG        250

  TTTCTAATTT TCTCAATTAT TGCGCTTTCT CAACCCCCCT CCTTCCTCAT        300

  TAC                                                           303
```

476

(2) INFORMATION FOR SEQ ID :940:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 330 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID :940:

ACACTATTTT CAAAAATCCA AATAAAAGTG CAGTTTCAGA CTTTTTAAAA   50

AAACACCGTT GACCTGTCTT AGTTGTACAT TCAGAAAATG TAGCCTCGAG   100

CGTTTGCATG CAACACTGCA TATTTTTTCT AATCAGATTA ATATGAGTTT   150

TAATGTTTAG CATGAACTAC AGCTAAGGAT AAAAATTTTA AAGTAGCTTT   200

CATAGTCTAG ATTCCTGGTT TCATAATGCT TTATGTAGTA CATTTCAGTT   250

TGCTTTGCTT TGTGGAGACT TGCGCGTATT TTCTTTTGCT TGTTTGTTTA   300

TCGCCAGGCA GCGCTGTTCG AACTGTGAGA   330

(2) INFORMATION FOR SEQ ID :941:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 107 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID :941:

TTTATTTCAG ATAATTTTAT GTAAACAAAT TAAGAGTTAT TCATTCAAAT   50

TTTTGGCAGT GTTAATCTGT AAATGATGAC TTGATGTACA GAAAATGCAT   100

TTTTGCT   107

(2) INFORMATION FOR SEQ ID :942:

      (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 126 base pairs
          (B) TYPE: nucleic acid
          (C) STRANDEDNESS: double
          (D) TOPOLOGY: linear

      (xi) SEQUENCE DESCRIPTION: SEQ ID :942:

CCACAGCATA CACACCTTGG AAACCAAGAA GACTCTTTGT GTGTGTATGT   50

GTGCGAGACT GACGCGTCTC TACGCGCTCT ATGGGGGGAG ATTTGGTTAT   100

TTCGGCGTTA CACCTCCGGT GTTCTC   126

(2) INFORMATION FOR SEQ ID :943:

      (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 155 base pairs
          (B) TYPE: nucleic acid
          (C) STRANDEDNESS: double
          (D) TOPOLOGY: linear

      (xi) SEQUENCE DESCRIPTION: SEQ ID :943:

ACTGAACAGC CGCTGGTTCC AGAACAGGCA CAGAAGGCTC CAGCGCTAGA   50

AACAACTGGC ACAGGAATGG TAACAATAGT CTGGCTCAGC CACAACAGGA   100

GGCTCCGGGA CAGTCACAAC CGAGAGCTTC CAGGACAGTT ACAGTCTGTA   150

AGCTC   155

(2) INFORMATION FOR SEQ ID :944:

478

(i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 287 base pairs
    (B) TYPE: nucleic acid
    (C) STRANDEDNESS: double
5   (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :944:

10

CGTGAGGAGC AGGTACCATT TTTAGTAGTC ACACAATTCC ACCTCCTGTT   50

TTTACTACTG GCAACTTCTA CTTGAGAATA ATGTTCTGAA AATGGAGGTG   100

15

GGGGGGGGTT TGGAAGCAAA CACATTTGGG GTTTTTAACC AATTGTTAGG   150

TTCTTTTTAT TTAGGGTTGT GCAGGGAACT GTTGGGAGGT TTCTTTAGGT   200

GGGATGGGGG GACTGGGTGT TGGTTTTTGG GGGGTTTTTG GGACGGGTTT   250

20

TATTTTGTCC CTTAACTTGG TTTGTTGGGC AGGTGGG   287

(2) INFORMATION FOR SEQ ID :945:

25   (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 149 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: double
            (D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :945:

35 ATCATTGATC AATGATATGG TTTGGATTAC TGCCCCGCCC AAATCTCTTG   50

TCCAATTATA ATCCCCAGCA TTGGAGGAGG GGCCCGGTGG GAGGTGATTG   100

GATCATGGGC ATGGACTTCC CCCTTGCTGT TTTCGTGATA ATGAATTCT   149

40

(2) INFORMATION FOR SEQ ID :946:

479

```
            (i) SEQUENCE CHARACTERISTICS:
                (A) LENGTH: 261 base pairs
                (B) TYPE: nucleic acid
                (C) STRANDEDNESS: double
5               (D) TOPOLOGY: linear



            (xi) SEQUENCE DESCRIPTION: SEQ ID :946:
10
        TTTAAACTGC AAATAGTCGT TACAAAAAGT TTTNNNNNTT CTTTTAAATA          50

        AATTTCACAC AAAGAAAGAG AAATAGAAAG CGACGGTAGT GACCAGCAAG         100

15      AGGAATAATA ATTACATTCA TCTTAATGTG TGTGTGCCAG TTCTGTTTAC         150

        ATTAACATTG GAAAACTCCA GACCTGGACA CCAGAACCTC AAATCTGTGA         200

        GTGGAATGTC TTGAGATGGG CACGCTGGAA GTCAAAGGGT TTCTCTTTTT         250
20
        TTTTTTTCCC C                                                  261


        (2) INFORMATION FOR SEQ ID :947:

25          (i) SEQUENCE CHARACTERISTICS:
                (A) LENGTH: 264 base pairs
                (B) TYPE: nucleic acid
                (C) STRANDEDNESS: double
                (D) TOPOLOGY: linear
30


            (xi) SEQUENCE DESCRIPTION: SEQ ID :947:

35      CTTTAGGAAC TGTCAGCATG TTGTTGTTGA AGTGTGGAGT TGTAACTCTG          50

        CGTGGACTAT GGACAGTCAA CAATATGTAC TTAAAAGTTG CACTATTGCA         100

        AAACGGGTGT ATTATCCAGG TACTCGTACA CTATTTTTTT GTACTGCTGG         150
40
        TCCTGTACCA GAAACATTTT CTTTTATTGT TACTTGCTTT TTACACTTTG         200
```

480

TTTAGCCACT TAAAATCTGC TTATGGCACA ATTTGCCTCA AAATCCATTC   250

CAAGTTGTAT ATTT   264

(2) INFORMATION FOR SEQ ID :948:

     (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 149 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

     (xi) SEQUENCE DESCRIPTION: SEQ ID :948:

CCTCGACTTA CCACGGGTGA TCCCAGAATG GACTATCAGC GGTGTTTTGA   50

GCCAGGTTGA TTGAGCACTG GGCTCCAACT TATTGTTAAT GAGAAACGGC   100

CCAACTTGGA CCATGACTTT CCCATTTGCA GGTCTTAGAA TAATTTTTT   149

(2) INFORMATION FOR SEQ ID :949:

     (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 242 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

     (xi) SEQUENCE DESCRIPTION: SEQ ID :949:

CGCTCAGGGT GGAAGTGGCC GGGCGCGTCG AATGTGCCGA GCTGGTGCGA   50

GTGGGCGAGC AGAGCGCCTT GAGGGTTGAG CATCTTCTGG ATCCAGCAGA   100

GGCCTCCCAG GAGGGGAGCC AGGTGGCTGA AGGCAAGCAC TTTNNNNAGG   150

TTCTAGTCCC CTTTTTAGAT CCTAGGGGAC TGGAGATTTG GCACCTTCCC   200

481

CCAAGGCTTG GCCTCGTGCC CTATAGGGTG CCCCCCTCTC TT   242

(2) INFORMATION FOR SEQ ID :950:

        (i) SEQUENCE CHARACTERISTICS:
             (A) LENGTH: 153 base pairs
             (B) TYPE: nucleic acid
             (C) STRANDEDNESS: double
             (D) TOPOLOGY: linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID :950:

ACTCTGCCTG CACTATAAAA TGAACCAAGG AGGATCCAGT TTGCTGTCTG   50

CACTGACAGA TTTACAGACA GGAAAACAAA GCCTTACTTA CCAGGAATCC   100

AAAGTTTATA CATGAAAATT TAAAAAGGGA GTCTATGCAA AGCGGAGTTC   150

AGG   153

(2) INFORMATION FOR SEQ ID :951:

        (i) SEQUENCE CHARACTERISTICS:
             (A) LENGTH: 128 base pairs
             (B) TYPE: nucleic acid
             (C) STRANDEDNESS: double
             (D) TOPOLOGY: linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID :951:

TGCGGGAGTC TCACTGGGGG GGGGACACCT GTGCAAACGC GTAACGCAGG   50

TTGTTCCTAA GGCGAGCTCA GGGAGGATAC AGAAAACTCT CCTGTGGTGC   100

TATGAAATGT GGCGTAAAAA GCATTCTG   128

(2) INFORMATION FOR SEQ ID :952:

482

(i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 213 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :952:

GTTGGAAATT TCCC AAAT CACCTACCGA TTACCCTTGA TTTCCCTTTG   50

TTTTCAGTTT CTCAAAACGA ATGAAATAGA ATATAGCAGA ATGTTAACCC   100

ATATAAAAAT AAAGTGTACC CAAATATTGT AATGTATATT GCTGCTCTTC   150

TTCAAATTAA ATAAGGGTTT AAAACCACTT AATTGGTAAT ACAACATCTC   200

AATTGATACA AAT   213

(2) INFORMATION FOR SEQ ID :953:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 236 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID :953:

GCAGCAGTTT CTTTGAAAAT TTGGACCAGA AGGTGCATAA CAAGTTGTTC   50

TGCAGAAGTT CTTATCTGAT ATTCTTAGGG AGCTATCCTG CATGTAATCT   100

TCATTATTTT TTTTCTCTAC CATCATGTAG GCATACTCAG TGTAGACTAC   150

CACAATCCTG GATACCTCTC TGCTTAGATT TACAATCTCT GCTAAGATTT   200

GCCACTGCAG AAAGTGTAGT ATTTTCACTA CATTAT   236

483

(2) INFORMATION FOR SEQ ID :954:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 217 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID :954:

GCAGCAGTTT CTTTGAAAAT TTGGACCAGA AGGTGCATAA CAAGTTGTTC   50

TGCAGAAGTT CTTATCTGAT ATTCTTAGGG AGCTATCCTG CATGTAATCT   100

TCATTTTTTT TTTCTCTACC ATCATGTGAG GCATACCCAG TGTAGACAAC   150

CACAATCCTG GAAACCTCTC TGCTTAGATT TACAATCTCT GCAAAGATTT   200

GCCACTGCAG AAAGTGT   217

(2) INFORMATION FOR SEQ ID :955:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 256 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID :955:

AGCAGCGACC GCGCTCACTG GCTTTTTGTT TCTGCTTGGG CCTTTTCTGT   50

TCAGTCCATG CTTGAACTAC TCCACCCCCT TAAATCCAAC GTAAAAACCA   100

GTCTTTTCTG TGCTTGTTCT CTGTGCGTTA ATGCTTTTTC TTATGCTTGC   150

TTATTGAAAT ACTGTATTTT CATTGTCCCC TGGCCAAAAC ATCTGAGTCG   200

484

TGAAACCATT TTAGATACTC TACTTTCTTA CTGTGTTACG TGGCATTTTA   250

TGCTTG   256

(2) INFORMATION FOR SEQ ID :956:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 194 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: double
            (D) TOPOLOGY: linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID :956:

CAAGCAATTG AGAGACTTTT TTCCTGTTAT TTTTCTACCA TTTATTTCTC   50

ATTTCATTAT ATTATGGTCA GAGAATATAT TTTGAATGAT TTCATTTATT   100

AATTTTTAAA AATAACATTA AAAAATTTTT TAAAATGTGA ATATACCACA   150

ATACAGTATA AAGATTGTAC ATTCTGTTTT TGGACAGTTT TCTA   194

(2) INFORMATION FOR SEQ ID :957:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 196 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: double
            (D) TOPOLOGY: linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID :957:

ATCTATTTTT CTTGGTCTCA TACTCAGTTT TTTATGTAGT CACTTAGTAA   50

ATAACCTAAA AAAACATGTT TTCTCCACAC TAATTTTAGG GTGAATTCCT   100

CATTTCGCTT TTCAGATCAT GGGGTGAGGG GGATGGTTCG TGTGTGTGAG   150

485

GAACTGAGGA ATCAGATGGA AAACAATGCC TCTGCTCCTT TGAGTA   196

(2) INFORMATION FOR SEQ ID :958:

5   (i) SEQUENCE CHARACTERISTICS:
                   (A) LENGTH: 105 base pairs
                   (B) TYPE: nucleic acid
                   (C) STRANDEDNESS: double
                   (D) TOPOLOGY: linear

10

          (xi) SEQUENCE DESCRIPTION: SEQ ID :958:

15   GCGCTCAGCT GGAACTTCCG ATCTATTTTT TCTTGGTCTC ATACTCAGTT   50

        TTTTTATGTA GTCACTTAGT AAAATAAACC TAAAAAAAAA CATTGATTTT   100

        TTCTG   105

20
        (2) INFORMATION FOR SEQ ID :959:

              (i) SEQUENCE CHARACTERISTICS:
                   (A) LENGTH: 261 base pairs
25   (B) TYPE: nucleic acid
                   (C) STRANDEDNESS: double
                   (D) TOPOLOGY: linear

30
          (xi) SEQUENCE DESCRIPTION: SEQ ID :959:

        GACAGCGACC GACACTCAAT GGAATCCCGA TTCCATGGAA ATGGAAAATA   50

35   GCTCTATTTA TACAGCAAAT TCAAATACAG TAGCTTGCTA AGCAACTTCA   100

        TAATTCATTA ACACTCGATG GCAGAGCAGA TAGTCACAAT TACTAACGAT   150

        TATCATGATC TGCATTCTTG ACAAGTATAC TATGGCGAGA TAAATCAAAC   200

40   TCAGACGATG ATAAGCAAAC TCAAAAATGA AAATGATGAT GCCAACTAAG   250

486

CTTTTGTTAA A   261

(2) INFORMATION FOR SEQ ID :960:

5   (i) SEQUENCE CHARACTERISTICS:
               (A) LENGTH: 188 base pairs
               (B) TYPE: nucleic acid
               (C) STRANDEDNESS: double
               (D) TOPOLOGY: linear
10

          (xi) SEQUENCE DESCRIPTION: SEQ ID :960:

15   CACAGTTTTG TTGACTAAAC TCTACAGAAG TCAGGTATTG GGAAGGAGAA   50

      TCGTTTCTTC TTTAGAGGAG TAGGTTTTAA CCATGTTAAA TTTCCAAGAA   100

      TAAATTTATT TATCACCTCT ACACAGCGCA GACCATTTCA GGAAAATAAA   150
20
      TAATTTTCGA TTCAAGTACT ATACAAACTT AACGATGG   188

      (2) INFORMATION FOR SEQ ID :961:

25   (i) SEQUENCE CHARACTERISTICS:
               (A) LENGTH: 191 base pairs
               (B) TYPE: nucleic acid
               (C) STRANDEDNESS: double
               (D) TOPOLOGY: linear
30

          (xi) SEQUENCE DESCRIPTION: SEQ ID :961:

35   ACTTTCGCCT ACCCGGAGAG GCCCAGAAAA TTGACCAGAT GATGGAGGCC   50

      TTCACCCAGC AATACTGCCT ATGCAACCCT GGAGCTTTTC AATCCACAGA   100

      CACACGCTAT GCACTGTCCT TCGCCATCAT AACGCTCAAC ACCAATTTCT   150
40
      ACAACCAAAA AGCCAGAGAC AAACCTGACC TAAAGCGCTC C   191

487

(2) INFORMATION FOR SEQ ID :962:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 191 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID :962:

CCAAGGCAGA GTTTATTAGG TTTATGCTTT ATATTTATAT ATAAGGTTTT   50

ATTCATGTTA AAAACTTAAA ACCAACGGAT TATGCAAAGT GATAAGTGTA   100

TCAATGAATA TACAACTGAC TGGATTTTAA ATATACACAA ACCAGTATAC   150

CCCCAGTACT TAAATGAAGG CACTCAGTAT ACACCAAAAT T   191

(2) INFORMATION FOR SEQ ID :963:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 178 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID :963:

AGCAGGCCAA AAGCCCAGGT GAGGCCCAGC AGGAACAGCA GCCCAATGCC   50

TCCTAGCACT CAAGATCCAC CATAGTCCAA GCAACTGCAG TTACACTTGA   100

GTACAAATAC GCTCCCGACA GCCTCATGCA GCGACACCCT AAAGGACACC   150

CGAACACCAT CAATAACCGA ATAGACTA   178

(2) INFORMATION FOR SEQ ID :964:

488

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 199 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: double
            (D) TOPOLOGY: linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID :964:

        ACTTTGCAGT CCTCACATCA CAAATAGAGT AAAAGATTCC CAAAAGGAAG   50

        GGGATCCTTT TGACTGCCAG ACGCGGGAAG GAAAGAATGA AATTAAAGAA   100

        TATCCTTTTA AACACACACC TCGACACAAT TTTCCACTCT GCTAAGGGAT   150

        CACAAAGACT AAGACGCGGG CAGACTCCCC ATAAGCCACG CTTATAACC   199

    (2) INFORMATION FOR SEQ ID :965:

            (i) SEQUENCE CHARACTERISTICS:
                (A) LENGTH: 217 base pairs
                (B) TYPE: nucleic acid
                (C) STRANDEDNESS: double
                (D) TOPOLOGY: linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID :965:

        ATGGAGCAGG ACCTGCGATG TTCTGATGGA TTATACCCAC AGTGTATTTT   50

        GGCACATCTG CCAAAAGCTA CAAACAACCC CTAATAATTA CACACTACAG   100

        ATAGTGAGAA GCGTCCTACC CAGGAGTCCT GAATGTGATC TGAGTATGCT   150

        CTAAGGCAGC CCCAGGAAAA GCAATCCAAT CCCTTTCTCC TCGCCTTTAA   200

        ACCTGCAGGT TGGGGCT   217

    (2) INFORMATION FOR SEQ ID :966:

489

    (i) SEQUENCE CHARACTERISTICS:

        (A) LENGTH: 175 base pairs

        (B) TYPE: nucleic acid

        (C) STRANDEDNESS: double

5   (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID :966:

10

ATTTGCGACC AAAATCATCT GGGTTTATAT TTGAAAAAAC CTTGTTTTCC   50

AATTTAAAAA TGCCAAGAAA GTTGTGAATA CCGTTCATTA TCACTAGGAT   100

15 CAAGAAAAAG CAAATGGTTT AAGTTTTTAC ATAGGAAATC TAAGAACTAC   150

TCATCAATAA AACGCAACAC TATCA   175

(2) INFORMATION FOR SEQ ID :967:

20

    (i) SEQUENCE CHARACTERISTICS:

        (A) LENGTH: 92 base pairs

        (B) TYPE: nucleic acid

        (C) STRANDEDNESS: double

25   (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID :967:

30

AGGGGTTCAG GCCTGGAGTC AGGGAAGAAG GGGAAAGGGG CAGATAGCTG   50

GGGGACAAGG AAAACCTGGC GCCCCCCACC GCGAAAAACA CA   92

35 (2) INFORMATION FOR SEQ ID :968:

    (i) SEQUENCE CHARACTERISTICS:

        (A) LENGTH: 208 base pairs

        (B) TYPE: nucleic acid

40   (C) STRANDEDNESS: double

        (D) TOPOLOGY: linear

490

(xi) SEQUENCE DESCRIPTION: SEQ ID :968:

GTAATATTAG GGACATGAAT GTTAGTACAG TAATTACCAC ACATGGAAAA   50

TATTGTTCAG CAGGAAAAGT AAAACTTTCA AAAAATTCCC TAAAGATCCT   100

ATTCAATAAA CAATTTTAGA TTTAAGGAAC CACTTACGCA AAACTCGAAC   150

AAATAACCGA AAACTCCACC TACCGCGCAA TACTCAAAAA CACAAAAATA   200

CTACTAAC   208

(2) INFORMATION FOR SEQ ID :969:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 256 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :969:

AGTGGTTGGT GTTTACTGGA ATCTTGTTTT TTTTTTTTCG GTTTTTTTGA   50

CTACTCGGGG GGTTTTCCTT TTTTACAGGA ACTAAATCAA CAAACTTTTT   100

CGATTCCTCA ACTTTAGATT TTTATTTTTT TTGATTACCA TTTACTTTTC   150

TTCATTTAAA ACTTTTAACG CCTCAGCCTT TTTCTTAGGC CAAGGCCTTC   200

CACCAAGGAT TTACTCCGGG ACGGATCTAA CTGGATTTTC CGAGGTGGGT   250

TTAAGA   256

(2) INFORMATION FOR SEQ ID :970:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 240 base pairs
        (B) TYPE: nucleic acid

491

```
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear



    (xi) SEQUENCE DESCRIPTION: SEQ ID :970:


AATCTATTTT CCTTGGTCTC ATACTAAGTT TTTTATGTAG TCACTTAGTA        50

AATAACCTAA CCCGCTTGTT TTTTCCACAC TAATACTAGG GCGAATTCCT       100

CATTTTATTT TTAAGATCAT GGGGCGAGGG AGATGATCGC GAGCACGAGG       150

ACCTAAGACA TCAGATGAAA AACAATGCCT CTATTCCTTC AAGTATAATA       200

AATGATACCC GAGAGTAAAG AGCTACACTT CGCACCTCTA                  240


(2) INFORMATION FOR SEQ ID :971:


    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 184 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear



    (xi) SEQUENCE DESCRIPTION: SEQ ID :971:


ATCTATTTTT CTTGGTCTCA TACTCAGTTT TTTATGTAGT CACTTAGTAA        50

ATAACCTAAT CCGCTTGTTT TCTCCACACT AATCCGAGGG TGAATTCCTA       100

ATCTAGCTTT TCAGATCATG GGACGAGGGA AATGACCGCG TGCGCGAGGC       150

CCTAAGGAAT AACATAGAAA ACACCGCCTC TGCT                        184


(2) INFORMATION FOR SEQ ID :972:


    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 234 base pairs
        (B) TYPE: nucleic acid
```

492

        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID :972:

GTGTTCTCTA AGGTGATACC TTTTAATTTT GAAAGACTAA ATAATTTTAA   50

TCGAGAATTT CCAGTCTTTC AGTCTGATCT ATTTAATTCA CTACTTGTTA   100

CATAATCCAG TGAAAACTCT ACTTGTTGAA ATTATGACAT AAAGATCTTG   150

CAGCTTTATT TGAGTATTTG TTCTTTTGTG TAGTTTCCAT CTTTTAAAAT   200

ATTTAAAATA TTTTCAAGGA TAAAAGTATT ATCT   234

    (2) INFORMATION FOR SEQ ID :973:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 197 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: double
            (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID :973:

TTTTCATCTA AAGGAGAGAG GCAGGCTCAG CTCCTGAAGG TCGCAGAGCC   50

TCAGTAGTCC TCCTGAGTGC GTCTAACTAA CTACCATCAA AAAACAAACA   100

AAAAAAACAT CACAAAACTG AACTGCCGCC ATCACCACTA CACCAAGTAT   150

GTGATTGAAT TATTCAATGA TCTGTTTTCG CGGTAGTGAC CAACANC   197

    (2) INFORMATION FOR SEQ ID :974:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 244 base pairs
            (B) TYPE: nucleic acid

493

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :974:

AGCAGGAGAT TTTTTTAATA ATAAACANCA ATGGAGAGGT GGAAATAGAG   50

ATGGAAAAAC AGGATCAAAG GAGCAACATA TCCAGTGACT TAAAAAAATA   100

ATCACACGTG GCAAGAAGTT TTCTAAAGTA AACTGTATGT GGGGAGAAGC   150

ATACAGAAAA AAACGAAATA CATACACCCC CAGGTTTGAA AGAAAATAAT   200

TTTGAGTTGT ATCAATCTAT CGATATCAAA GAATGAATGA CCGC   244

(2) INFORMATION FOR SEQ ID :975:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 330 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: double
            (D) TOPOLOGY: linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID :975:

TTTTTTTTTC TGAACACTTT GCTTCACACC TTCTCATATT CACGGTTATG   50

AATTCTCCTG ACTATATCTA TTGTAACCCA AAACAGCAGA CTGTATTTAG   100

AGACCCATTA GAGATTTCAT GTCTATATGC CCAGAGCCTG ATATAATGCC   150

ACCTTACTAT ACACATAATA TAGAATCTGA GGACTACGTT AACTGATACA   200

TGTTAAGTAT CCTGCAGAGA GCTGGCACAT TGAATGTGCT CAATAATCGT   250

TAGCTTTAAG TATCTACCTC AAAGGGCTAC TGTGTGACTC CAATGAGATA   300

ATGTGCAATG AAGGGTTTCG TGTAATATTG   330

(2) INFORMATION FOR SEQ ID :976:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 200 base pairs
5   (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

10

    (xi) SEQUENCE DESCRIPTION: SEQ ID :976:

TGGTGAAAGG AATAAGCAAC TCAAGGTAAA TAAAGAAGAA AGATGAAGAT   50

15 TCTTAGAATC GTAGAAAGAC TGCAGGGGGA AATAATTAAA GCAGCTTTAT   100

TCCTTACGGC ATTCATCATT CGTCGAGCTG GAAAGCACTG ACAACTTTGT   150

AATGAGTTTT TTGCGCTTAA CTCTGTCAGG TGATTTATAT GAATNACTTA   200

20 (2) INFORMATION FOR SEQ ID :977:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 296 base pairs
25   (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

30

    (xi) SEQUENCE DESCRIPTION: SEQ ID :977:

AAAGGACAAT TTAATATAAA TCTATGTTTG TGCATTTCTG ACAGGCCATT   50

35 ATTATCTGCT TTGACAAAGC CTTTCTGAAA CGCAGTGTAC AATGAATCTT   100

AATGATGTTA TGAAACGAGC TTTGCT. G GCTCTTGATT GGAGCTTCCG   150

GTATGTGATG ACGGTATGTC ATGTATGCAT GGATGTAC.C AACTGTGTTT   200

40

AATACTCTGA ATTTTAATTA GAAAAAAATA CAATAGCAGC AAGGCCCTGG   250

495

TTTCTAAGCT GCATACTTTT ACTAACGCGG GACATGAGCA AATGCC   296

(2) INFORMATION FOR SEQ ID :978:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 228 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: double
            (D) TOPOLOGY: linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID :978:

GAATCNCGCC TGACACATAG AATGCATAAA CGAGGGGGGT CCTTCTGCAG   50

ATACTCTAAT CACTACACAG CTTTCTCTAT AAAACTACCC ATAAGCCTTT   100

AACCTTTAGA GAAAAATGAA AAAGGTTAAT GCTTGGAAGC CGGGGGAGGA   150

CTGACCACTT CATAAGCCAG TACGTCTGAG CTGAGTATGC CCCCAGAATC   200

CAGCCACTAC TGATAATTCA CAACGGTA   228

(2) INFORMATION FOR SEQ ID :979:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 171 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: double
            (D) TOPOLOGY: linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID :979:

CGTACAAAAG CGCTTTGGAG ATGCCAGAAA AAACCCTACG GGAGGGTTAT   50

CCCCCTGACG CTAGGCCATG ACACAACTAA ACTTCAATAC ACCAGGACTA   100

AGGCAAGTAT GAAGAAGCAA AATATCGTAA CGACGCACCC TCGAGATCTA   150

496

CCAGGCAAAA CCAGAACCTG A   171

(2) INFORMATION FOR SEQ ID :980:

(i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 241 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :980:

TGATTCCCCA TTTCCCTGGA CAGGGCAGAG TCAAGCCGAG AAGGAGGAGC   50

CACAGGCCAG CTGTTAATGA GACACTAAAT AAAACGTTCA GTATTCATAC   100

CTGTGGAACA TGGGTGAACC TTTCTGGTAA CTCGATTTTT CACACCAATG   150

ACAGCAAATG AGAAAGTGAG AGAAGCTAGA TAAATGTTTT TAAAGCATTA   200

CTGCAGTGGA AAATAACTGC ACTCTCAGGA CACAGCACTG T   241

(2) INFORMATION FOR SEQ ID :981:

(i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 227 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :981:

TCACTGCAAT CACGGTAGCT TCGCCCATTG CCTCTTCAAC CAGGCACATA   50

CATCGAGAAG TTGAACCTGC ACTTTATTTC ACACTGAACA GACTTACCCC   100

GACAACAACA CCTCCCCAGT GGGACAAACC TACCCCACCT CCCCACACTC   150

497

TACTCCCAGC TAACGTTCCC TATAATCATC ATGACCCATT AAACATTTGC   200

AAAACCACAC TTCAACCCAC AGGAAGA   227

(2) INFORMATION FOR SEQ ID :982:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 205 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: double
            (D) TOPOLOGY: linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID :982:

CGTTGTCGCC ATGGTAATAC CGCTCAGTAC GGGAGGACCC ACAGGCTAAG   50

ACACTCGGAG CACGAGCTCG CCTGAGGGAC CAACGAGGCG AAGCCACAAT   100

CCGCGAACTC ATGACTGACC CCTTCTAAGT AAGAATCCCA CCCAGGCAAA   150

CCAATCCGAC AACCGAAATA GCGCAGGCAC CGCCAAATTC AAGGCGCCCC   200

AAAAG   205

(2) INFORMATION FOR SEQ ID :983:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 204 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: double
            (D) TOPOLOGY: linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID :983:

AGCAACCGGC ACTCAAGTGG AATCCCGAAA AAGTGATTTA AAAATGATCT   50

TACCTGTACC AGAAAAGCAA AATTAAAGGA AACAAAATAA GAACCATAGT   100

498

CCCAAATGAC ATTTAACCGT ACATACAGCG ATAACATGTT CAAAATCCAA   150

CAAATAACGC AACTTCCAGA CGTAAATATC CGCCACTCGA TTCCCTCCCC   200

CCCT   204

(2) INFORMATION FOR SEQ ID :984:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 168 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID :984:

ATTTGTATTA GAAAAGTAAA GTTGAAGGAA ATAAAATTTG CATTCTTGTT   50

TTAAGTGATC TTTAATTGTA TATATCGCGG TAGTATGTTC AAAATCCACT   100

AAGTACTGTG ACTTTTAGCT GCAAATCTTT GCTCTTTGCT TTTTTTTTTC   150

TTTCTCCCCC CTCCCCAG   168

(2) INFORMATION FOR SEQ ID :985:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 350 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID :9£

CTCAGCTGGA ATGTCCGGTG CCTGCTAGGT GCATGGCCA: AGAAGCATGG   50

GCTGGGCCTG GGCACAGGAG GAGCAGCTGC TTTGGTCGGG GTGGAGACTT   100

499

```
TTTTTTTTTT TCTACCCACA GCCTATTCCA CTCCTCCCCA TCTCCAGGCG          150

CTGGGAGGGG GGCCCTCACC CCGTCACGCC TCGCTCCCTC CTGGCCCTCT          200

GGTCCAGCCC CTTACGCCTC CTCTCAGTCT ACTCAATTGT GACTGTCCCT          250

CCTGATGTAT TTTTTTTTCC TCCAACTCAA AAGGCAAAAA TAATCCTATT          300

TTTATTATCT TGCTACAACT GCAACTTTCT GCCCTATAAA TTTACATTCC          350
```

(2) INFORMATION FOR SEQ ID :986:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 289 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: double
            (D) TOPOLOGY: linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID :986:

```
AGCGACCGCC ACTCACTGTG AGTTCCACTT AATTCAGGTG AGCCGCTCTT           50

CTGCACCTCC TCCTCACACC TCTCTACCTA TACTAACCAT TTTTGAAGGT          100

TCAACAATGC TCTGCAAATC TTTTTAAGAC CCGTTACTTC AACAACTCCC          150

AATACCTTCC TCCTCAACGG AACAACTTAA CCGTTACCTT TTAAACCCGA          200

CGAGCTACAA AGCAAGAGAT ACTTCGCGAG CCAAATTCTA CAAAGGACCA          250

AAAAAGAAAC CCATTACCTT ATAGTACTCA TGCAAAAAA                      289
```

(2) INFORMATION FOR SEQ ID :987:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 134 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: double
            (D) TOPOLOGY: linear

500

(xi) SEQUENCE DESCRIPTION: SEQ ID :987:

CACAATCATA GCATTTATTA CACGATTTAC ATCTGATCCT CACGCAATTT   50

TCTTCCTCAC CAATAAAGAA CTAATAGGAC AGCATATTAG AAGCAACATA   100

CATTCTTTTA TTCTTGCATC GCTATAAAGA AGTA   134

(2) INFORMATION FOR SEQ ID :988:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 287 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: double
            (D) TOPOLOGY: linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID :988:

TTCTGAAATG AAGGTTTCGT CTTTAGCTAT TGACTGTAGG ATTTGTAATT   50

CAAATCATCA CAGCATCCTA AAGAAATACT GTGTGAATGG AATGCACACA   100

ATTCCTACAG AACACACAAA CTGATGTCCA AAAGGCACAG AGTAATGCTG   150

GTGGCTCTTT CTAGTCAGTT AAGAAACAAT AAAAAGTCTG CATTATTCTT   200

TCATAATTTA AATACTTAAG TAATCTCCAC TTTATTATTT TATAACAATG   250

ACTTCAAATT TACATTATTT TAAGTACCAT TGTAATC   287

(2) INFORMATION FOR SEQ ID :989:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 177 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: double
            (D) TOPOLOGY: linear

501

(xi) SEQUENCE DESCRIPTION: SEQ ID :989:

AGCAACCAAC ACTCACTGGA ATCCCGCAAT CAAGAGCTAA AAGGACTTCT   50

TCCATCTCTC AGGGACACAC ATCCACCGAT AAGAATAAAA GAAATGCCTG   100

AATGACTCTC ACTGGCACTT TTAAACACAG CAAGCCCAAC ATATTTTCTC   150

CTTTTCATAA AGAAGCCTAT ACACCAT   177

(2) INFORMATION FOR SEQ ID :990:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 158 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :990:

TTCCTATACT ATGTCGGTTA AAAGCCTTCA TAGAATATAG GCACCAAAAA   50

TAAACTAACC CCACACCCTC ACCAACCAAA GGAGGCACAA TCCAACGAAA   100

CTGATGAAAA GTCGAGGTAA CGACTCTGCA GACCGTACTC ATTTCTAAAC   150

CAAAAGTC   158

(2) INFORMATION FOR SEQ ID :991:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 267 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :991:

502

```
TAATCCCTTT TAAGCAGAGA TACACATTCA CAGAGAGAGA ATGTTTTAAA        50

AAGACCCACA AGGGGAAGGG ACCAAGTAAG CACTTTTAAT TCATTTTGAT       100

TACACAAAAA TAAGGCAAAC TAAATGATTC AGAACAATTC AATTTAACTG       150

AAGCCTTCTA GAAAAATACT CAACAGGCTT CAACAAAAAG ACTTAGCGCA       200

CATAAAACAA TCACGAAGAT CACAATTTCA GCACAAATAT CTGAAGGAAT       250

ACACGCAAAA CATCATA                                          267
```

(2) INFORMATION FOR SEQ ID :992:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 199 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: double
            (D) TOPOLOGY: linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID :992:

```
AGGATGTGTT CATGCTGGCT TTCAGGATGT CCCAAGGCAC GGCACAGTGA        50

TTGTCAAATT CCACTTTGCA TGGAAGACAG CACAGAACCC TGCTCTGCGT       100

CAGCTGGAGA GCTCCGGCCA GCACGGCCAC CAGCAGCATG ATCAGTGTGA       150

TGCAATACCA GAAGCCGTCC CACCATGATT TTAAGATGTG ATAAGATGA        199
```

(2) INFORMATION FOR SEQ ID :993:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 198 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: double
            (D) TOPOLOGY: linear

503

(xi) SEQUENCE DESCRIPTION: SEQ ID :993:

TTTAAGGTGC TAAACTTGCA CCTCATGTCC ACTCAGTAAC AAGTATTGGG   50

ACGTAGAGCA CAGCCTCACT CAGCTCTGAA AGGTAATACA GCTTGCGAGG   100

AAGTGAGCCA GCAGTGGCCT TTGCAATTGT GGATCTTGAG CTTTGCTCTT   150

AGCAGATCTC AGGCGTAACC ATTCGCTAAC TGTACTGAAG ATGCGTCC   198

(2) INFORMATION FOR SEQ ID :994:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 183 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: double
            (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :994:

GCTATCTGCG GGGCCATTCG TAGGATGGGT GAGTCAGATG ATTCCATTCT   50

CCGATTGACC AAGGCCGATG GCATCGTCTC AAAGAACTTT TGACTGGAGA   100

GAATAACAGA CGTGGAATAT TTGTCATAAA TAAATAACGA AAACCTAAAA   150

AAAAAAAAAA ACAACAAACC CCAACAAACT CAA   183

(2) INFORMATION FOR SEQ ID :995:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 199 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: double
            (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :995:

504

```
ACCTCTGCAT TAACACTCCA GCACCTTTGG TTAGCCAATT TGGCCTTATT          50

TGTGTCTCCA CCATTGGATT ATCTGTCCAT CAAGGTCAGG AATGTTTTCG         100
```

5
```
GGTTACCCCA CTGTCCCCAA CTTCGAATAT GCTCACTGCC TGGAAAATGT         150

TTATCTGAAT ATAAGGCATC AAGCCAGAAC TTGCCCAAAA CTAAATCTA          199
```

(2) INFORMATION FOR SEQ ID :996:

10
    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 177 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
15
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID :996:

20
```
GGTCTTGGCT GGTGGTTTAT GGCCCGGGCC TTCTTTCTAC GGGGGCCAGG          50

GTCCAATTTT CCACCTGGGG TTTAAAAGTT AAGGAGGACC AGCCTGGGAA         100
```

25
```
CCCCTCGAGT GGGGACGCCA TTTCTATTAC CAGGGCCCCC TTATATTTTA         150

AGGGGACACC ATATGGAGAT TTTATGC                                 177
```

(2) INFORMATION FOR SEQ ID :997:

30
    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 229 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
35
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID :997:
40
```
GAGTTTCCTG TGCTGTTACA AATGTAACAT TCTCATATAC AACATTCATT          50
```

505

GAAGAGGCAC AATTCTTATT TTGAGGTGGC ACAGATTAGA CAAATTTTTC   100

AGTGAATAAT TCCTCTTTCA TTAGGAAATT TAACCACAAG CTGTATTTTC   150

GTAGAAAGTT GCTTGAAATT CTTTTCCTAA AAAAATTTAA TTTTTCTATC   200

TCAAAATGAC CGTATGCAAA CGAACATTA   229

(2) INFORMATION FOR SEQ ID :998:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 233 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: double
            (D) TOPOLOGY: linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID :998:

TTGCAGTGTT TATGCCCGCC TTCTTTCACG GGCAGGTTCA ATTTCACTGG   50

TTTAAAAGTA AGAGACAGGC TGAACCCTTC GTGGAGCCAT TTCATTACAG   100

GTCCCTTAAT TTAAGGAACA AGTTGATTTA TGCTACCTTT TTGCACGGTT   150

TAGGGTACCG CGGCCGTTAA ACATGTGTTC ACTGGGCCAG GCGGTGCCTC   200

TTAATATCCG GGGATGTCCA GAAGGGGAGT TTT   233

(2) INFORMATION FOR SEQ ID :999:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 216 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: double
            (D) TOPOLOGY: linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID :999:

506

TCAAAAACTC AATATAATAT GTAAATCAGG GGTGTCCAAT CTTTTGGCTT   50

CCCTAGGCCA TACTGGTGTT AGGCCACATT CAAAGCTATC CTAGGCCACA   100

TGTGGCTGGT GGGCCATGGG TTGGACAAGC TTGATGTAAA TAAAACCACC   150

AGTGGAAAGA GTTTGTTGTG AGTTACATTC AAATACAACA GGAGTAATAC   200

TATCATGATA TTAGTT   216

(2) INFORMATION FOR SEQ ID :1000:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 280 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: double
            (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID :1000:

GACAAGACCT AGAAGCAACA ATGCCCAGTA GAAACAAACA CACCTACTGC   50

CTGGATCTTA GTTTTTAATT ATATTCCCCA ATAAAGAGAC CCAGGGCTCC   100

TTGTTGAAAT GGCTGATTCT AGGACTGGGG CAGGAAATAT GCAAGATGAA   150

CCTAGAATAT CTAATACTGC CAAAAATTAA GAAAGTGTTC TAAAAAAAAT.   200

CCCCACGGAT AGGGTGTCAA AAGAGACATA GAAGCCATCT GAAGGAGTTC   250

CCAATGGCCA AAGATCAAAT AATTTTTCAA   280

(2) INFORMATION FOR SEQ ID :1001:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 324 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: double
            (D) TOPOLOGY: linear

507

(xi) SEQUENCE DESCRIPTION: SEQ ID :1001:

TGCATGATAG GAGCGTCCTT TGTTCTCATG AGGTGACTCT TGGTGGGCTC   50

CTTATTTGGG GACTGGTCAC CAAAAATACC TAACTATGGT TGGAAGCTTA   100

GTGCTTTCAG CCCCATTCCC CATCCTCTGG AAAGGGGAGC AGAGCTGGAG   150

CTCGATCATG CCTGCGTGAC AAAGCCTCCA GAAAAATCCT TGAAAGACAG   200

GACATGGAGA GGCTGCTGGG TTGGCGAACA CAGCCATGTG CCGGGAGGAT   250

GGTGCACCCC AACTCCACAA GGACCCTTCC AGACCTCACC TGTGTATCTC   300

TTCATCTGGC TGTTCATTTG TATC   324

(2) INFORMATION FOR SEQ ID :1002:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 254 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: double
            (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :1002:

ATTTCCATTC ATAAGTCCTC ACAAACCCAC TTTTCCTCTT GCCTGAGTGC   50

CTCACATACC CTACTGCCTG AGATGGTTCC AGAGGCGGTC TCCTCTCTCC   100

CCCAACGAAA CACCAGGCAC ACACCTGCCC CCAGTCTTGC CTGCACTCTC   150

CTTTCCTCCC GCAGAGAGGC ATTCCTTTCT CCTCCTCTCA TCCTACACAC   200

ACTATAAGAG ACAACTGAAA TCTTGCCTCC TCCAGCAAGC TTCTTAATTC   250

ATTT   254

(2) INFORMATION FOR SEQ ID :1003:

508

(i) SEQUENCE CHARACTERISTICS:
      (A) LENGTH: 265 base pairs
      (B) TYPE: nucleic acid
      (C) STRANDEDNESS: double
5   (D) TOPOLOGY: linear

      (xi) SEQUENCE DESCRIPTION: SEQ ID :1003:

10

AAGGTTGCGC TGCCCATCCT CTCGCCCTTC GGAATTTACC CCTGGCCGCT   50

CAGGGTCTCG CTTCTAGAAG AAGATGATGG ATACTAGGGC GATCCTCCTA   100

15 TTGCCTTTAT ATTTAACAGG CCCGCCGAGG AGGGGCTCCC GCTGGTGCCC   150

ACATAACTCT ATTAGACCAT CTGAGGCGAC TTCCCCCACC CCCTCCAACG   200

CGCCTCACGC ACGACTCTAG CAAAAGACAG GTTCCGCGGT GGTCACGTCG   250

20

TTTGAGACTA TACTG   265

(2) INFORMATION FOR SEQ ID :1004:

25   (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 263 base pairs
          (B) TYPE: nucleic acid
          (C) STRANDEDNESS: double
          (D) TOPOLOGY: linear

30

      (xi) SEQUENCE DESCRIPTION: SEQ ID :1004:

35 AAATATGCCC TGAGGATTAT CTGATGTCGA TGGTGTGGAA AAGAACTCCA   50

GCAGGCGACT TCG ATTCAA TCAATGTCCC CTGAATGCCA CAGAACCACT   100

AGCAGACGCT GCTCTCTCAG TCTTAATGGA GTGGCCTTCT GGGAACAGCC   15C

40

GAGCTTTGAA AGATGCATAT CAAATGAGTA CAGACACTTG TAGCATTTAA   200

509

TCAAAGAGCA CCTTGCTAAG AGGCAGCGAA TGCTGGCAGG TGATGGAATG   250

CCCCAGGTGA CCA   263

5   (2) INFORMATION FOR SEQ ID :1005:

            (i) SEQUENCE CHARACTERISTICS:
                (A) LENGTH: 317 base pairs
                (B) TYPE: nucleic acid
10   (C) STRANDEDNESS: double
                (D) TOPOLOGY: linear

15   (xi) SEQUENCE DESCRIPTION: SEQ ID :1005:

        CGAGACTGCA GTACTTCTAG AAAGTTGTGA ACTTCTAAGA AAGAGCCAGG   50

        CTTCCATCTC ACTATTCCTT GATCATTATC TCTGAAGTCC CTACCTGCAC   100
20
        TTCCCTGATT GTCCTGTAGC AACACCAGCA TGGTGGGAAT TGCAGGCAAA   150

        GATTGTGAAA AATCCCTAAA GGGTCATTGC TCATGACGTT ATTTCGAATT   200

25   GTAAAATCGT GAGCCACTCA TATTCAAACT AAAAAAAGAA CAGAACTTTT   250

        ATTCACGTTG TGAAGCTTAC TCCCTCGCCA TTTTACGGAT CAATGTCAAA   300

        CGCTTGCATT CATAAAG   317
30
        (2) INFORMATION FOR SEQ ID :1006:

            (i) SEQUENCE CHARACTERISTICS:
                (A) LENGTH: 287 base pairs
35   (B) TYPE: nucleic acid
                (C) STRANDEDNESS: double
                (D) TOPOLOGY: linear

40

            (xi) SEQUENCE DESCRIPTION: SEQ ID :1006:

510

```
CGGAAGCATT ATCCTGTCAT CAGAAGATGG ACCTTTCCCT GGAATGCCTT        50

TTCCCTATCA TGTCTGTGTG GTAAATACCT ATTCATCCTT AACAACCTAG        100

CTGAGGTCTT ACCTCATCAG GATTTGATCC CCCAAAAAGA TTTGTCCCTC        150

TCTGAGCTAT CTTTATAACT AGTACATACT CCTACCAGCG GACTATGTTA        200

TAATAATGTG GCTATATGCC TGTGATCTCA GCGTGAGCTC TTTGAGGACA        250

GAGTCTTTGT CTAAATACTC AAAACCCTGT TTACCAT                     287
```

(2) INFORMATION FOR SEQ ID :1007:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 273 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID :1007:

```
GGGCACCAAA ATACACATCA GAGGAGACTG GCTTCCATGA GACGCTTCGA        50

CTGTCTCATC GGGGCACTTG TAATAAGCAT CTTGATGCCA CTGAATGCAA        100

TGCTGTATTC AAATAATAGC TTTCATCTTC ACTATAAAAC AATACAAACG        150

TAAACTTTGA AGCCCTTTGA AGGACCTAAC CAAACAACAC AAGGATGAAA        200

ATAGATCAGT ACAACTTTGA GACACATTAT TAGGTCAAAT CTGCAAAGCA        250

TATTCGGATT TTACCGTAAG GAA                                    273
```

(2) INFORMATION FOR SEQ ID :1008:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 308 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double

511

(D) TOPOLOGY: linear

5   (xi) SEQUENCE DESCRIPTION: SEQ ID :1008:

TAGAGTGGGG GGCCAAAACC TCTGCAGTCC CCGGCAGTGA GCTATGGACT   50

TTCTTCCCCC TCACAAGGCT GGGGGCCTCC TGCTCTCGTC CCTGGCCCTC   100
10
CCTGCACAGG GCAAAGCCAG TCTGGGCTAT GGCACACAGA GTTCATGTTT   150

GCGCCCTCTC CCTGCCCCTC ACCCCAGAGG GTGAGGAGGA ATGAGGGGCA   200

15   TTGATGGTTA GGCCGGTTGT TGCCTCGAAC AGCTGGAGGG AAGCTGCAGG   250

GGTGATAAAA TCAAAGCGAT ATTGACACAC TACAAACATT ATAGAACCTG   300

CAAAAAAA   308
20
(2) INFORMATION FOR SEQ ID :1009:

       (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 187 base pairs
25   (B) TYPE: nucleic acid
            (C) STRANDEDNESS: double
            (D) TOPOLOGY: linear

30
       (xi) SEQUENCE DESCRIPTION: SEQ ID :1009:

GAACCGCCTC TGTTTCCAGA GCAACTGGTC AAAACCTCTC CAAATACCGA   50

35   GCAGTTTTGA AAACTGGATT AGGAACCACT AATGAAAAAG AACAGACTCA   100

GGGACAAGTG TTTGGCGGGA ATGTGTGAAG AGGTAACTAA TGAGTGTCAC   150

TGAATCACAC TATTACACAG ATGAAACAAA GCCTTTA   187
40
(2) INFORMATION FOR SEQ ID :1010:

512

(i) SEQUENCE CHARACTERISTICS:

    (A) LENGTH: 175 base pairs

    (B) TYPE: nucleic acid

    (C) STRANDEDNESS: double

5   (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID :1010:

10

AAGAAAAAGA TATTAAGATG GGCAAGTCCT GGTGGCAAGA CAAGCAGATG   50

ACATTACAGA CAATGGACAT CAAACTGCTG CCAAGCTAAT TTAGATTGTA   100

15 AAAACAGCTC CATAGTCAAT ACCCATGAGT GATCTTAAAT ACGCACAATT   150

AAGCTACTTC TCCTTGATAT TACCT   175

(2) INFORMATION FOR SEQ ID :1011:

20

    (i) SEQUENCE CHARACTERISTICS:

        (A) LENGTH: 208 base pairs

        (B) TYPE: nucleic acid

        (C) STRANDEDNESS: double

25   (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID :1011:

30

TGAAAAATAT TTGGAACTCT TTAGTACAGA ACAGTTTCAA TATGAGTTAA   50

GAATCATGCG ATGACTACCA AAAAGCTAAT GCGATCCCAG GCTGCGGTAA   100

35 CAGAAGCAGA GCAGCTCAGC TGGGGAACGT GATAGTGATA ACTACTTCGT   150

ACTAGGTTAG ACTGTACCGA GAGACCTATG TTCAGTTCTG GGAGTGAAAG   200

TATTTTAT   208

40

(2) INFORMATION FOR SEQ ID :1012:

513

(i) SEQUENCE CHARACTERISTICS:

    (A) LENGTH: 184 base pairs

    (B) TYPE: nucleic acid

    (C) STRANDEDNESS: double

5   (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :1012:

10

ATGATATCTA GACTACCAGT ATTTTTTGAA TGAGGCTTTC TTAGGAGTAT   50

GTTGATGCAC TCTCATCCTT TCCTCCCCGG ACTCCTACCA CAACCCTCTG   100

15   ACTGTGGAAT AGCATGGTTG TGTGTAAGGC TGGAGCACAG GCACAGTGAG   150

ATGAGGATGA GGGATTGAGG GATGCTATAA GCCA   184

(2) INFORMATION FOR SEQ ID :1013:

20

    (i) SEQUENCE CHARACTERISTICS:

        (A) LENGTH: 263 base pairs

        (B) TYPE: nucleic acid

        (C) STRANDEDNESS: double

25   (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :1013:

30

CTTTGACATT TGATCAGACC AAACAGTGCT GTTTCCCGGG GAGGAAACAC   50

ATTTTAATAA ACACATCATC CCGCAGGCTC CCACCTTTAC CTCATGTTTC   100

35   ATACCTTGTT TATCAAATGA GCGACTCAAA ATGATTAAAA ATAATGCTGT   150

TCTTTAGTAG CAACTAAAAT GTGTCTTACC GTCATTTATA TCTTTGTCAC   200

CGGAAAGAAG CATTTTTGAT ACTTTACTGC GAGTCAAAAA TCAATACGCA   250

40

GAATGGCATT TGA   263

514

(2) INFORMATION FOR SEQ ID :1014:

     (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 229 base pairs
5
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

10

     (xi) SEQUENCE DESCRIPTION: SEQ ID :1014:

CAAATTAAGT GCCAGAATGA TGCAGCCCGC TCTCACCAGG AAGAACGACA   50

15   TGTGAGAAAA CTTATAGCAG ATGCAAAAAT GTCAACCCAC CATGTTATTT   100

AAAAAAAAAT ATGACCAGGA TACAAGGACA CTTCACCGTT TTTAACCCAC   150

ACAAGGTCAG GTAATGTTTA CCTTGAAACA CAATCGCATA TGACCCTTTA   200
20
TGCCACTCAC CTAGGCCTTT AATAATGAG   229

(2) INFORMATION FOR SEQ ID :1015:

25   (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 246 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

30

     (xi) SEQUENCE DESCRIPTION: SEQ ID :1015:

35   GAAAATAATG ATTCATATTA CCGGGTATTT CTTATCCAGT CTTTCATTCT   50

ATGTAAATTG TGTGTGTGTC TATATATGCG TGCATGTCTC TCTCTACATG   100

TATATGTGCA TATGTATGTA TATATATGCA TATGCACATA CATGCCACAC   150
40
ATGCACATAT ACACACACTC ATAGAGAACA AAATTATTCC GAATATTTCA   200

515

TGAGGTTTCT TATTATAAGG AGACAATATT GATGCAATCT AATTAA   246

(2) INFORMATION FOR SEQ ID :1016:

5   (i) SEQUENCE CHARACTERISTICS:
             (A) LENGTH: 287 base pairs
             (B) TYPE: nucleic acid
             (C) STRANDEDNESS: double
             (D) TOPOLOGY: linear

10

         (xi) SEQUENCE DESCRIPTION: SEQ ID :1016:

15   TTCATAATCG CTGGCACTGA ACAAAGTTGC AGAATTCTTT GCCAGGTACT   50

     TTAGGAAATC GTGAAGATAA TTGAGTAATA AAGCAAGGCT CTTCTCATCC   100

     AGAGGTGTAT AAGCCAACAT CGCTCCAATT CGTACAAATA ATCTCAGGAG   150
20
     ATGTGGCGCT CCATACACCT GGGACATGGG TGCATCGGGA TGATCTGCAA   200

     GAATTTCAGC ATACTGTGGT CTCTCAAATT TATAGAGTAG CTGGGTACCC   250

25   AACATTACGT TGAAGTATTC TTTTATACTC GCCACAA   287

     (2) INFORMATION FOR SEQ ID :1017:

         (i) SEQUENCE CHARACTERISTICS:
30   (A) LENGTH: 299 base pairs
             (B) TYPE: nucleic acid
             (C) STRANDEDNESS: double
             (D) TOPOLOGY: linear

35

         (xi) SEQUENCE DESCRIPTION: SEQ ID :1017:

     ATATGAGAAA GCAGAGCAAA ACAGATGATG CTCTAAATGC AACTGACACA   50
40
     CTTGCTAAAG ACGTTAGGTG CTCCATAAAT GCTTGTTGAA ATGCTGTTTG   100

516

TCAACATTTG TTGTGAAAAA TTCATCTCTC CATCTAAGAA TCCTCATGAG   150

TTAACCACAA TCAGTTCTAC ATAATTTAAC AGAAAACATC TGGTGGCACT   200

TTTAAATGTT TAAGGACAGC ATTTCACAAA CTAAGCCCGC CCCCAGTCCC   250

ACTGCAGCAG GAGAAAATAA GGCTATGGAG AAAAGCAAGA TGAGTTATA   299

(2) INFORMATION FOR SEQ ID :1018:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 274 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID :1018:

ATTACTCCTT CTCTCGAATG CTTCCAGAAG AGTAGCACTC ACCACCTCAT   50

GAGGAAAGGC ACTGCAACTT TGGTCAATGA TATCTGTTAG AAAGATCTTT   100

TCCTATATTT AGAAGAGTGA TTCTCATACC TGAGCATGTA TGAGAATCAG   150

TGGGTTTGAG GTGGGCCCAA GAATTTCCCT TTTTAACAAG TTCCCAGAAG   200

ATGCTGATGT GGCAGCTTCT AGCACAGTGC TTGAAAATCC ATGAGTTTTC   250

AAGAGGACAA TCTAAAGTGC TCCC   274

(2) INFORMATION FOR SEQ ID :1019:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 232 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

517

(xi) SEQUENCE DESCRIPTION: SEQ ID :1019:

TTTCTTTGTC CTTGACAAAT ATTTATGGAA TGCCGGAAAT TATGGAAAAA   50

5   CAATTCCAAT GTTACGAAGT CCAAAGAACT GGAATGAGAA AACTCCTCAC   100

GGCACATTAT GCTGCATGGA ATGACAATCA TCCTCGGGGA ATTAGGGCAG   150

CATCTTCTAC CACTTTTAAA GGCTACCACG AGACGGGGTG GAAATGCCAA   200

10   AAATGGCACC TCATCTTTGA TCAAAGATTC AG   232

(2) INFORMATION FOR SEQ ID :1020:

15   (i) SEQUENCE CHARACTERISTICS:
                 (A) LENGTH: 133 base pairs
                 (B) TYPE: nucleic acid
                 (C) STRANDEDNESS: double
                 (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :1020:

25   AACAGTCCAT GCTGATCTTA GTAACTATGA TGAAGATGGT GCTTGGCCTG   50

TTCTTCTTGA TGAATTTGTT GAGTGGCAAA AAGTCCGTCA GACATCATAG   100

CAAGAACTAT GTGAAGAAAA TGCAAACCTT TAC   133

30   (2) INFORMATION FOR SEQ ID :1021:

            (i) SEQUENCE CHARACTERISTICS:
                 (A) LENGTH: 280 base pairs
35   (B) TYPE: nucleic acid
                 (C) STRANDEDNESS: double
                 (D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID :1021:

518

TCCTAGAACT CTGCTTGGAC CAGAAGATGT GAATAAACTT AAGCTTATTT   ()

ATTTAAAATC ACAAATGAGT TGCTCTAGAT TCTAAAAGGG TGAAACTTTG   100

ACTGTTGAAA GTTTAAGTAT TAGTAAACTT GAGTTACTTT TTCTTTCAAA   150

TTTCACTCCG CTTCCCTGCA TTTCGAAGCT GCTCTTTCTG GTCCTACCCA   200

CCACCCCACC AACAAGACTT GTGTTTGTTA ATAGAAATAA TTTATCAAGG   250

TATTGGGGAT CCATTGTCTA TATTTAAAAC   280

(2) INFORMATION FOR SEQ ID :1022:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 304 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID :1022:

AAAATAAATA ACTTCTTAGA TTTTTGACTG AAAAGATCTG AGAATGTTCT   50

GCCAAACAGC CGACCAACTG GTGCAAAAGG TTAAGGCTGA CTTGACTTAG   100

CAACCTGCAG CACAACCAAA AACACTGATG CAGTTCAGAG CTCTTCAAAT   150

GCATACTTCA GTGTTACACA CACATCAATT AAATTAGGTT AAATTAGTTA   200

ATCCTCTAGA CAGTTTTCTT TTTGTTTTGC ATGCATCCCG TTCCATTTTC   250

ATTACGGGCA TCTATTCCTT GATCAATTAT GTGCTTTGCT TTTTAATCGG   300

TTTT   304

(2) INFORMATION FOR SEQ ID :1023:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 237 base pairs

519

        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

     (xi) SEQUENCE DESCRIPTION: SEQ ID :1023:

TTTCTTTGTC CTTGACAAAT ATTTATGGAA TGCCGGAAAT TATGGAAAAA   50

CAATTCCAAT GTTACGAAGT CCAAAGAACT GGAATGAGAA AACTCCTCAC   100

GGCACATTAT GCTGCATGGA ATGACAATCA TCCTCGGGGA ATTAGGGCAG   150

CATCTTCTAC CACTTTTAAA GGCTACCACG AGACGGGGTG GAAATGCCAA   200

AAATGGCACC TCATCTCTGA TCAAAGATTC AGAGCAT   237

(2) INFORMATION FOR SEQ ID :1024:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 320 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: double
            (D) TOPOLOGY: linear

     (xi) SEQUENCE DESCRIPTION: SEQ ID :1024:

GGCATGATTA TTAGAAACTA TTTAAGCTTT TTTCTTTGAA AAACAAGCTC   50

CTTTTACAGA ATATAAACAA CAGTAGTGCC TGTGGTTTAG CCCACCAATC   100

TTGATGACTA AAAGTAGCTG ATGCATTGTG CATATGATGC TTGAGATGGT   150

TTTTGCAAAA GCAGAAATCG CTGCAAGGTA ATCACAATAG ATAAAAGTGG   200

TATTTTAAAC CTTTGAAATA AATGGATGTA ACTGTACCTT GGTACAGCTT   250

TTCACTTGTT TAGTTTTTAA ACGTTAGTAT AAGATTAGGT AATTGAGGGT   300

520

TAGAGCCAAC AGGAATCTGC   320

(2) INFORMATION FOR SEQ ID :1025:

5   (i) SEQUENCE CHARACTERISTICS:
                (A) LENGTH: 202 base pairs
                (B) TYPE: nucleic acid
                (C) STRANDEDNESS: double
                (D) TOPOLOGY: linear
10

        (xi) SEQUENCE DESCRIPTION: SEQ ID :1025:

15   TTCTGGCACC ACATTCAATA CTGATTCACA GGGATCTAAA ACATTCTAGT   50

      TATTCAGTCA CTCTGTCCTG TGTGGCAGAT AGGACTTATG TATCTTCAGA   100

      ATATTTGAGG AGTCATTCTC AGAGTCTCTC ATGAGTGCTC AACTTAACTG   150
20
      TTCCACAAGT CTGTCTTCAT AGCTGCATGT TGCATCTTCC AGTCTCTGTT   200

      CT   202

25   (2) INFORMATION FOR SEQ ID :1026:

           (i) SEQUENCE CHARACTERISTICS:
                (A) LENGTH: 243 base pairs
                (B) TYPE: nucleic acid
30   (C) STRANDEDNESS: double
                (D) TOPOLOGY: linear

35   (xi) SEQUENCE DESCRIPTION: SEQ ID :1026:

      ATTGGTAGAC AATATCATAA GAGTTTTCTG ATAAAAGATG CTTTTTAACC   50

      CTGACTCCCA GTCACAATTT TGGCATCTCA TCCATGGGAA AAAAATAGGA   100
40
      AACTTATACA TTTCATAAAC TAAAGGTCAT CCAAACACTG CCAAAAACGT   150

521

| TTTTATAAAT TGAGACCTAC TTACATCACA TCGGTTTTCC AAAGAGAATA | 200 |
| CACAGCGAAA GATGAGGCTC CACCCGGCCG GCACAGTCAT GAA | 243 |

(2) INFORMATION FOR SEQ ID :1027:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 185 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID :1027:

TATTTGCATT GAGGAAATAT TAATTTTCCA ATGCACAGTT GCCACATTTA	50
GTCCTGACTG TAGGAAACAC TGATTTTGTA AAGTTGCCTT TATTTGCTGT	100
TAACTGTTAA CTATGACAGA TATATTTAAG CCTTATAAAC CAATCTTAAA	150
CATAATAAAT CACACATTCA GTTTTAAAAA AAAAA	185

(2) INFORMATION FOR SEQ ID :1028:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 312 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID :1028:

GCTTCTCTAT TCCTCCTGCC CGGGAGGAGT AGAGGAATTC TGGAGCCACC	50
TTAGTGGGCA ATGGGGGAGC TCCTGATGGT TCAGGAGCAG GAAATTTATG	100
AGCAGAGTGG GGTCCCAGGC CACAGGGAGA TGTCTATCCA CAAGGGATGG	150

522

TGGCCAAGGG TTGAATGGAA AGAGGCAGGC AGGGGGAGAG GGGCAGAGGG   200

TGTGGGTATT CCCAGGGCCT TGAGAGTGGA CATGGCCCCT TCTCCTCAGC   250

CTTCCATTAG CAAGGATGTC ACTGCTGCTC TTGCCTGATG ACAGCCAGAT   300

CTGTTCACAG TT   312

(2) INFORMATION FOR SEQ ID :1029:

   (i) SEQUENCE CHARACTERISTICS:
       (A) LENGTH: 218 base pairs
       (B) TYPE: nucleic acid
       (C) STRANDEDNESS: double
       (D) TOPOLOGY: linear

   (xi) SEQUENCE DESCRIPTION: SEQ ID :1029:

ATTATTTATA AATTTTAGTG AGCACCACCA AAGTTAGGAT TCAATTGAGT   50

TTGAATTCAA ATTCATTCAA AAGTTGCACA AATTTATTTC TTTTTTCCTG   100

AACATTCCTT TACTTCAGAT TGACAATTCA TTCTATTTAG AGCGCTATTT   150

TAAGAAACCT TGATGAATCG CCCTTGACTA AAGGAAACAA AGTAGAATTT   200

TATACAGATG GAAAAAGA   218

(2) INFORMATION FOR SEQ ID :1030:

   (i) SEQUENCE CHARACTERISTICS:
       (A) LENGTH: 124 base pairs
       (B) TYPE: nucleic acid
       (C) STRANDEDNESS: double
       (D) TOPOLOGY: linear

   (xi) SEQUENCE DESCRIPTION: SEQ ID :1030:

TTATTAGGGG GTTTAGAAAA TAAATTCGTA GGGTTTAAAC ATTGAATAAA   50

ACTACAAAAA AAGACACACA TTCAGGTAGC GAGGCTCTGG GGGTAACTCT   100

5   TTCTTAGTTC TTTGGACACA TCCG   124

        (2) INFORMATION FOR SEQ ID :1031:

            (i) SEQUENCE CHARACTERISTICS:
10   (A) LENGTH: 237 base pairs
                 (B) TYPE: nucleic acid
                 (C) STRANDEDNESS: double
                 (D) TOPOLOGY: linear

15

        (xi) SEQUENCE DESCRIPTION: SEQ ID :1031:

        TTTTGCCAAG TATATGTAGT GCAAATATTT TCTTTCAGTC TGTAGCTTGC   50
20
        CTTTTTATTT NTTAATGGGT ATCTTTAAAA AAATGGAAGT TTTAAGTTTG   100

        AATGGAATTC AGTTTGTTTT TAAAGCTTGT GCTTTTTGTG TTCAACTAAG   150

        GGATATTAGC TTACCATTTT TCTCGGTTGA ATATTATGTG TTTATAGACA   200
25
        AGAAATGGTC ACTAAAGCAA AATAACTGAA AATTATC   237

        (2) INFORMATION FOR SEQ ID :1032:
30
            (i) SEQUENCE CHARACTERISTICS:
                 (A) LENGTH: 147 base pairs
                 (B) TYPE: nucleic acid
                 (C) STRANDEDNESS: double
35   (D) TOPOLOGY: linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID :1032:
40
        ACAGCAACCG GCACTCACTT GGAATCCCAG TGTTCCGAGT TCTAAGGCCA   50

524

CTGAAAACCA TCAAGCGCTT GCCAAGCTCA AGGCCATCTT CGACTGCGCA   100

GCGACTTCCT TGAAGACTGT TTTTAACATA CCAAAGGAGG ACAAGCT   147

(2) INFORMATION FOR SEQ ID :1033:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 238 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: double.
            (D) TOPOLOGY: linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID :1033:

AGGCCTGCCT ACCGTAGGTC TCTCAGAGCC TTTACTCTAG TCACTCTTTA   50

GAGGGGGGCA CTAGAAGCAA TATCTCCGAA ACTTCTTCGA CTGTCGAGAC   100

TTTTTACTCA TAATTCGCTT CAAGCCAACT ACGGAGGCGC ATTTACAAAA   150

CTGAAATACG AGCGACACCC CAGGAACGCA CGGAGACATG ACGCCCTTAA   200

TCCTCTGTCC CTACTCCCTC TCCTAGGACA CCGCATTA   238

(2) INFORMATION FOR SEQ ID :1034:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 63 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: double
            (D) TOPOLOGY: linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID :1034:

TCCATGNCTC NTGGTCTCTG TGCNCTTGNC AGGGGCATGC CAGGGCCCTT   50

GGACTGTGCA GGG   63

525

(2) INFORMATION FOR SEQ ID :1035:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 180 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID :1035:

CGACCGGCGC TCAATGGCGA AATTCCGAGC CAGAGCTATT GGTTGAATGA   50

GTAGCGCTGA TGGTTTAGAT AATAACTAGT ATGGGGATAA GGGTGAGCAG   100

GCGCGCCTTG AGGCAAGAAG CGGGTTAGAG CATCTCTACT TTAAAAGCCA   150

AAGCCTATAA CGGTAGCGTC TACATCACGA   180

(2) INFORMATION FOR SEQ ID :1036:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 142 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID :1036:

CCAAATACGA TGACATCAAG GAGTCGATCC GTCAGCGTGA CTTGAATACA   50

CCACCGCCGA CGACCCGAAA GCCTGATGAG GAGAAGTCCA GAATCAGGAA   100

CAACGGCGAC ACTCGACTAA CCATTTTAAA CCAATTGGAA CC   142

(2) INFORMATION FOR SEQ ID :1037:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 95 base pairs

526

        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID :1037:

CCACATGGAG TGACCTGGGC CTCTGCAAGA AGCGCCCGAA GCCTGGAGGC   50

TGATTGTCAA AGCAGGGGGC AGGACCCGGG GGCAGGAGAA ACCAG   95

(2) INFORMATION FOR SEQ ID :1038:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 195 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: double
            (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID :1038:

ATTTTATTGT AGTAAGAATA ATACATAGAA ATAACATTAA ATAAATATGT   50

TTGACAAAAA CATACACACA TAGTACAGGT AGAACATATA ACTGGTTGAT   100

GCTAAATAAC AGATCCAGAT AATTTTCAAT TTGAATTAGC AGCAGGGAGT   150

CATTGAATGC TATGCCCTTA GAATGGCTTG CAGGCTTTCA CGAGT   195

(2) INFORMATION FOR SEQ ID :1039:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 218 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: double
            (D) TOPOLOGY: linear

527

(xi) SEQUENCE DESCRIPTION: SEQ ID :1039:

GGTTGTCAAG AAAATGAAAG GTAAAGCTCA GAAGGGATAA GGGAAGACAT   50

5   TACAGAATTT ATCATCAAGC AGGAGGTTTT TTCCAGGTTC TAAGATGAGG   100

TTAAGTTTCT TAACAAAAGA ATAAACAACT GTGACTCTAT CTGTCGGGGG   150

AGGGTCTAGA CAGAAAAAAT GAATATACCC CAAAAGGCTG AAAAAAAAAA   200

10   CGAGACTTTG ATGGAGAC   218

(2) INFORMATION FOR SEQ ID :1040:

15   (i) SEQUENCE CHARACTERISTICS:
                         (A) LENGTH: 318 base pairs
                         (B) TYPE: nucleic acid
                         (C) STRANDEDNESS: double
                         (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :1040:

25   TTTATTATTT TGAATGATTT AATGGTTTTC TACACAATTT ACATCACAAC   50

ATGTAAATTT TAGCAGTAAC ATCTGATTCT AACAGCACAT CATGCTATTC   100

CTTTCATAGA GCCTTCAGAG ATTCAATGCT AAACAAATTT CCTTAGTTGG   150

30   CATCAAGGCA CTGATCACTT TAGAGGCTTT TAAGAAATTA TTTAAAGATG   200

CAAATGCCTC TGAGTGAAGT GTACTATCCC ATCACTGAAG CCCACAGGAA   250

35   CAAGTCCTAC AATTTTAAAA AGGCTCGATG GAAAAATTTC TCAATCCTGA   300

AATCCCCTAG GGAAGGGG   318

(2) INFORMATION FOR SEQ ID :1041:

40   (i) SEQUENCE CHARACTERISTICS:
                         (A) LENGTH: 199 base pairs

528

```
                    (B)  TYPE: nucleic acid
                    (C)  STRANDEDNESS: double
                    (D)  TOPOLOGY: linear
```

5


```
            (xi) SEQUENCE DESCRIPTION: SEQ ID :1041:

      ACGTACCGAG CCGTCGTCGC GGTGCTTGAG CTTGAAGGCG AGATAGCCGA          50
10
      TGCCGCCGAG GCGGTGGACC GCATCACGGT GGCGCTGACG AACGCGAGAT         100

      TCAGCAGCAG CGATGCCATC AATAGCAGCC TGATCGGACG CATGACCGAC         150
15
      TCTCCCTGTG AGCGGAGGTT GGGGGGCCGA TCTCCCGCCG GTGCCGGGC          199
```

      (2) INFORMATION FOR SEQ ID :1042:

```
            (i) SEQUENCE CHARACTERISTICS:
20                  (A) LENGTH: 300 base pairs
                    (B) TYPE: nucleic acid
                    (C) STRANDEDNESS: double
                    (D) TOPOLOGY: linear
```

25


```
          (xi) SEQUENCE DESCRIPTION: SEQ ID :1042:

      GCCTCTAACA AAACTAGGCT GTCCCGGACC ATGGTAATAG AATTGTTTAC          50
30
      CTTTATACCA AGAAGGTTGG GAAAGCACCA AAATCTGCAT GTGGTGTGTG         100

      CCCAGGCAGA CTTCGAGGGG TTCGTGCTGT AAGACCTAAA GTTCTTATAG         150
35
      ATTGTCCAAA ACAAAGAAAC ATGTCAGCAG GGCCTATGGT GGTTCCATGT         200

      GTGCTAAATG TGTTCGTGAC AGGATCAAGC GTGCTTTCCT TATCGAGGAG         250

      CAGAAAATTC GTTGTGAAAG TGTTGAAGGC ACAAGGCACA ATGTCTGGAA         300
40
      (2) INFORMATION FOR SEQ ID :1043:
```

529

(i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 170 base pairs
    (B) TYPE: nucleic acid
    (C) STRANDEDNESS: double
    (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :1043:

GAGACCAGTC TCAAGTGGGA GGGGCTGATG GTGGGAAGCC CTAGAAGAGA   50

GTCTGGGATG AAGCGGCCTC CTCCCTGTCT TGCCCTCCAA AATTGAGTCT   100

GGCCTGATTC CTTTGAGGAG CAAATTTTAC AATCATCCCT CACCCTAACA   150

CACGGTGAAA CTGGAAAACC   170

(2) INFORMATION FOR SEQ ID :1044:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 260 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :1044:

GGCCCCCCCT GGGGACTGCT GGTTTCCAGG GGCCACCCCC CCTCATCCAA   50

AAGAAGAATC AAGTTTTGTT TTCCTGTGGT TCCCTTGCTC TCCCCGGCCT   100

CACCTCGAGC TTCCACTTGG GCCCTTTCCC ATGCTTCTAC TTGAGCCCCG   150

CCTGCCTCAC CGTCTGCCTC ACCGCCACCT CCTGCTCAGA GTGAGTGCAT   200

GCATGCCAGA CAGATACACA TATACATACA CACACACACA CACACCCTAT   250

TTTTTTTTTT   260

530

(2) INFORMATION FOR SEQ ID :1045:

        (i) SEQUENCE CHARACTERISTICS:
                (A) LENGTH: 164 base pairs
                (B) TYPE: nucleic acid
                (C) STRANDEDNESS: double
                (D) TOPOLOGY: linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID :1045:

AAATCTATAA TTTTAAGGGC TTAACCTGTG ACTTTAATAA GCTGGAACAG   50

TCCACTGAAT GGGTATAATG AATTGCAGTA TATACGTATG ATCGCTTTTT   100

AAGTGATTAT CTTTTCTTTC GTTAAGTCAT GTAAATTCAT AAATTTTTTG   150

GCACTGATGT GTTG   164

(2) INFORMATION FOR SEQ ID :1046:

        (i) SEQUENCE CHARACTERISTICS:
                (A) LENGTH: 130 base pairs
                (B) TYPE: nucleic acid
                (C) STRANDEDNESS: double
                (D) TOPOLOGY: linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID :1046:

TCCCTCCTTT CCGAACTGGA GCCCCATCCT CTCCAGAGTA TCCAGGGCTT   50

CTTCACTCCC GGGTACCTGC CCTTCGGCCC CTTTTCACCA CAGCTGTGCT   100

ACTGTCAACC AGTCTTTGCT GCATAGGCAT   130

(2) INFORMATION FOR SEQ ID :1047:

        (i) SEQUENCE CHARACTERISTICS:
                (A) LENGTH: 285 base pairs

531

```
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: double
            (D) TOPOLOGY: linear


        (xi) SEQUENCE DESCRIPTION: SEQ ID :1047:

    GCTTAACTGG AAATTGGAAG GGAAAAGAAG AAGAAACAAT GTAATGTAGC          50

    AGTGGAAGCA AAATTCTCAC AATGAATAGC AGTCTTTCCA GCTTCTTTGA         100

    CACGGATTTT CTCATTAGAA AAGACGACTC TCCTGAACTA GGGATGAGTG         150

    TGAATCTCCA TTCGAGGAAG GGGAAGAAGA GCTCGGAGGG TGACAGCCTC         200

    CCCCTGAGAG AGCCAGTTGC GTTCATGATT TTGATTCCTT CTTCCTCCTG         250

    ATGAAGTATC TGCCCAGGAG CCCAGGAGCA GAATA                         285

    (2) INFORMATION FOR SEQ ID :1048:

            (i) SEQUENCE CHARACTERISTICS:
                (A) LENGTH: 233 base pairs
                (B) TYPE: nucleic acid
                (C) STRANDEDNESS: double
                (D) TOPOLOGY: linear



        (xi) SEQUENCE DESCRIPTION: SEQ ID :1048:

    TAAAACTGAC CTAGAAGCTA TCAGCAACCA CAAAGAGACA GAAGAAAAGA          50

    CTGCTTCTGA GGCTCTCTCA TGGAACCTAC TGATGATGGT AATACCACGC         100

    CCAGAAATAA CGGAGTCGAT GATGATGGCA ATGATGACGG CGATGATGAC         150

    GGCACTGATG ACCCCAGGCA CAGCGCGAGT GATGACTACT CAACACGAGC         200

    CAGGTCTTTC TGAAGGCCGA GAGAGCTAAA TAA                           233
```

532

(2) INFORMATION FOR SEQ ID :1049:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 293 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID :1049:

ACTTTAATTT ATTTCGGATG CCGGAATTGT GCCCAGAGTT TCTCCTGAGC   50

TTGATTCCAT AGCTAGCAGC TTCAATCCTT CGCAGCTGCG GTGCGTTCTG   100

AACTCTGAGC TGTCCTTTCC TGACAGGCAC TTTCCATAGC ATCTGCCTGC   150

TTAATTCCTC ACGACTCAGA AATGTTAACG GCACTGTCGA GTGCTGTGAT   200

CATTTTGCTT TAACTATGTA AAGCTTTATG CCCTTCGAGA AGCTTATTTC   250

GAGATAGAGC TAGAGAAGAA AAGCAGCAAA ATTCGGTCGA TAC   293

(2) INFORMATION FOR SEQ ID :1050:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 219 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID :1050:

AAAACTATAC TTTCATTCAA AAGAAGAGCT GAATTGATGC TTGAGTTACA   50

GCACAAATCT ATTATTAGTG AATGAAGTAT ATTCTTGGCA GATAAATACC   100

AGATCAAAAG TCCTGTTTCA GTAATTTGAT TAAACTGTAG AATACTAAAA   150

533

AATAAGTTAT TTCTACAGAA ATCTTTGAAG GGAGCAAAAA ATCAAATCAC   200

AGTATATACC TAATGGCTA   219

(2) INFORMATION FOR SEQ ID :1051:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 70 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID :1051:

AGCGACCGGC GCTCAAGTGG AATTCCGTGC AGTGTTTGAT TTTTCGTTTT   50

TGCGATAGTT TACTGAGAAC   70

(2) INFORMATION FOR SEQ ID :1052:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 204 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID :1052:

ATTCCTGACC TGTGATATCG GCCATTAGAG CCTTTCAAGA ATGGTACCTC   50

CTGCCGATGA TTTTTTTTAA AGCCTTAATG AAGAGAGTGT CCTCTGACTC   100

CTTCCAGAGA AGATAGGATG TGAGTGAGTA AGTTATGTAT AATAATTTTA   150

TCTCAAAATA ACCACGTCCT TGATACCATT CCCTGTATAC CAAGGAAGGG   200

TATT   204

534

(2) INFORMATION FOR SEQ ID :1053:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 252 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID :1053:

```
ACTAAACACA GCACTGAGAA TTCTCCTCTT TTTACAAAAA TGACAGACTT        50

AAGAGAGGGC ATGGAACAGA TTAAGAGAAT TAACACGGAG AGGAGAGCAG       100

AGGTATAAAA GGTATCCAAG AAAAGTAAAA CATACAAAGG CAATTCAAAT       150

CAAAGTGAGC ACTGCCTATA TACAGACAGA AAGCGAGTCC TCTATGAAAC       200

CATACCCGAC AGAAAGTACC GGAATACCAC CGACACTGAT GTCTTCCAAA       250

CG                                                          252
```

(2) INFORMATION FOR SEQ ID :1054:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 212 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID :1054:

```
AAATCAGGAA ATTGTACATG TTAACAAAAT AGTATAACCA TGCATACATA        50

CATCTGCTTA TTAAACACTG AAGTAAAAGA ACTAATCCAG TTTGCAGTCT       100

TTAGAGGTGT TTAGTATTTC ACTCCGTTCT GATGGAAGCA CTTTGAATGC       150
```

535

TTGCATGGAG ACATAAAACT GAATATTTAA TTGACAATAG ATCATGCGCC   200

TGTATTTATA AA   212

5   (2) INFORMATION FOR SEQ ID :1055:

              (i) SEQUENCE CHARACTERISTICS:
                   (A) LENGTH: 152 base pairs
                   (B) TYPE: nucleic acid
10   (C) STRANDEDNESS: double.
                   (D) TOPOLOGY: linear

15   (xi) SEQUENCE DESCRIPTION: SEQ ID :1055:

         ATAAACTGTG CTAACTAAAG TTTTTATTTC ATCAATATAA AAGCTGTAAA   50

         AAAACTGAGG AGAAAGCAGT TGCCAAAAAG ATGAAAGAAA AACAACATAG   100
20
         AAAACCTTTA AAACAGGCAA AAGTCAGTTC ATAATAAAGT AACTCATCTC   150

         AC   152

25   (2) INFORMATION FOR SEQ ID :1056:

              (i) SEQUENCE CHARACTERISTICS:
                   (A) LENGTH: 205 base pairs
                   (B) TYPE: nucleic acid
30   (C) STRANDEDNESS: double
                   (D) TOPOLOGY: linear

35   (xi) SEQUENCE DESCRIPTION: SEQ ID :1056:

         AACAGATCCT CAGTTTCTCT GGAGACACCC CCAATTCTCG GGTGAGTGTT   50

         GAAACCTGAC AACTGACTGT TAGCCTTGTC ATCATCCTCA TTGGAGATGG   100
40
         AGATGTTGTA GTCGGAGCCT CATTCCTTCC GGGGCACTGT TTCTTCTAAT   150

536

GGCAACCATC AGAGCCTGTC TGGAAACAGC CTGCTGCCTT TGCTAGGGGG   200

GCAAA   205

(2) INFORMATION FOR SEQ ID :1057:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 174 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: double
            (D) TOPOLOGY: linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID :1057:

GAGAGAAGAG CGCTTTTCTG GGCTCTTGGT TACTCCGTCA GAGACTTTGC   50

CCTTTGTCTG TTTAAATACA CTGGGAGCCA GAGCTGATTC CCCACCTGCT   100

GCTGTGGTTT TCCGCTTAAC ACAGGAGAGA TGAGTTGGTC TGGTATATTT   150

GATAGCAGGT TTTAAAATGA ATCC   174

(2) INFORMATION FOR SEQ ID :1058:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 125 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: double
            (D) TOPOLOGY: linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID :1058:

TATTTGATGG TCCATAAGAC TTTGTCAAAT GTAAACCTAC AGTTTGATAA   50

GCTTTAAAAT ACCATGTTGA CAGCATTTTG AATTGTTTCA TAGACGTACT   100

TATTTAACTG ATGCGAACAT TCACA   125

(2) INFORMATION FOR SEQ ID :1059:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 205 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID :1059:

TTATCTTACA ATTCTACTTC CCAGCATCCT GAAATTTTCA AATACTGTCT   50

TAGTATATTA AACTCTTTTG AAATAGATAA CAAAAGCACC ATGGGAGTCC   100

GTTGAAAACT TAGGTTTGTT CCTTCTAAAA TTTCTAAGTC CTTCATTATG   150

ACTATAAAGA AAAAGGTTC ATCAATTCAA AAAAAAATCC TGATTCTTCA   200

AAATA   205

(2) INFORMATION FOR SEQ ID :1060:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 249 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID :1060:

ATCTCACAGA TTCTTTTTCA CAGATTCATT CATGTTGAGT GAAAGAAGCC   50

AGATGCAAGA GTCCACACCA CATGATTCTG TTTCTATACA ACTTAATTTG   100

AAAACTAAGC AATACTTACA GAAGTGAGAA TAGTAGTTGT CTCAGGGTAG   150

GTGAGTGTCA TGAAGGGAAT CTTATACGTT TGCTAAAAAT GTTTTATAAT   200

538

ACTTGGATTT TGGGTCTA⁻   ᴳCTGGCAGG GGAAGGᴳ⁻TA CATTGCAAA   249

(2) INFORMATION FOR SEQ ID :1061:

(i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 200 base pairs
    (B) TYPE: nucleic acid
    (C) STRANDEDNESS: double
    (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :1061:

TAGCACATTG CATCCCAAGA GCTGTAGTCA AAATCCTCAA AATCTGATGA   50

AAATGGCATA CTACACTAAG GAGGATTTTT TGGGCATTTT CCATTCATAT   100

GCAGAATCAG TGGTTGAAAA AGGAGAAAGA GAGATTTTCT TTACAAAAGC   150

TCCTGACCCC ATTAACATCT TATCTATAAA TCTGATATGT TCCTGACTCC   200

(2) INFORMATION FOR SEQ ID :1062:

(i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 200 base pairs
    (B) TYPE: nucleic acid
    (C) STRANDEDNESS: double
    (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :1062:

GCGCACAGCT GAGAATCTCC GGTCTTGTCT CACTTTGGAC TGGGACAGTG   50

GATGCCCATC TAAAAGTTAA GTGTCATTTC TTTTTAGATG TTTTACCTTT   100

ACAGCCATAG CTTGATTGCT CAGAGAAATA TGCAGAAGGC AGGATCAAAG   150

ACACACAGGA GTCCTTTCTT TTGAAATGGC CACGTGCCAT TGTCTTTCCT   200

539

(2) INFORMATION FOR SEQ ID :1063:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 246 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID :1063:

TATCAAATCA TGAGTTGAAA GATTTTGACT ATTGAAAACC AAATTCTAGA   50

ACTTACTATC AGTATTCTTA TTTTCAAAGG AAATAATTTT CTAAATATTT   100

GATTTTCAGA ATCAGTTTTT TAATAGTAAA GTTAACATAC CATATAGATT   150

TTTTTTTACT TTTATATTCT ACTCTGAAGT TATTTTATGC TTTTCTTATC   200

AAATTCAAAT CTCAAAATCA CAGCTCTGAA TCTTAGAGTA TCATAA   246

(2) INFORMATION FOR SEQ ID :1064:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 170 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID :1064:

CCCTCATGTG CCAGTTCGGT CTGCCTGCAG AGGCTGTGGA GGCCGCCAAC   50

AAGGGCGAGT GGGAAGCGTT TGCAAAGCCA TGCAGAACAA CGCGCAAGTT   100

TGAGCAGAAA GAGGGCGACA CGAAGGACAA GAAGGACGAA GAGGAGGACA   150

TGGAGCCTGG ACTGAGCCAC   170

540

(2) INFORMATION FO͗ ͗EQ ID :1065:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 171 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: double
            (D) TOPOLOGY: linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID :1065:

    CTCTCCCCCA CAGGTTCTCA GCAGTTACTA AGATGTCCCC TGATTTCATT   50

    GACCTCTGTG TGTCTTCAGT CCTTGACCCT TTAAGGCTCC CTGGTGCCAG   100

    AATGTCTGCA GCTGTAGGAT CAAAGACCCT TGGGGGAAAA ATCCATTCTC   150

    AAAAGAGAGG AAGATGGGGT G   171

    (2) INFORMATION FOR SEQ ID :1066:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 201 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: double
            (D) TOPOLOGY: linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID :1066:

    GAGTCTATAT CCCTTACTCA GTGCAGTTCT CAAAGTCCTT TGTATGTCGT   50

    ACAGGATCAC ATCTGTACAT ATCACACTCT TGTGGGGTAA GCCCAGAAGC   100

    TCATACACAG CTTCATGGGT TTACTTTCCC AAGCACTTCC TCCCTCCCTG   150

    CAATATCTCC CCAGCACTTT CTGCTTCCTA TCAGCTTTCC CCTTTTTCAA   200

    C   201

541

(2) INFORMATION FOR SEQ ID :1067:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 151 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID :1067:

ATCAACCGGA GGTGAAATGA AATACCGTCA ACCTGTGCAT GAGTTTGTGT   50

GAACTGAATG TGTGTGCATA CACATAAGCA TGTGTGCGAG CGCAAATGTG   100

GCGTCTCCAC AGCATGCGCA ATCCATGAGT CTGTTTCTAA CGCGCGCGCG   150

C   151

(2) INFORMATION FOR SEQ ID :1068:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 273 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID :1068:

ACTGTGTCAT GTCAGGTTAG ATCTGAATCT CTAGGAGAAT AGCTTTTTTG   50

ATCTGTTTGC TCCTTTGAGT CTCCCTTTTA CTTTACAACT AGAAAACCAA   100

TCGCATACTT CACTTCTATC GCTTCCAGAT ATGGCATATT TTTCTTAGGC   150

TACCGTTGAA ATTTAGCATA ATATTTCTCC CTTACCTTTA CGTCCTTTTA   200

AAAAAATAGG ACTATAGTAA GTCCTCCGTG TCGGTGGCAT GTTTTTGGAA   250

542

ACTGACTTTA AAGAAAACAT ACA   273

(2) INFORMATION FOR SEQ ID :1069:

5   (i) SEQUENCE CHARACTERISTICS:
                (A) LENGTH: 189 base pairs
                (B) TYPE: nucleic acid
                (C) STRANDEDNESS: double
                (D) TOPOLOGY: linear
10

        (xi) SEQUENCE DESCRIPTION: SEQ ID :1069:

15   CAATCTTGCT TATAAAATAA GAACACCTTT CAATTAAGTG AGTGGGTCAT   50

        TCCTGGTGCA ATTGTGATTT TTTTTTAGCC AAAATGAATG GCAAACTCTA   100

        TTTAGAGCAA AGTAAGTATT AGAAAACCCT AGGAACTCTT AATCAACGTT   150
20
        TATTACACTT TTATAAAGGC AAACTACGCG AAAGAGCCC   189

        (2) INFORMATION FOR SEQ ID :1070:

25   (i) SEQUENCE CHARACTERISTICS:
                (A) LENGTH: 280 base pairs
                (B) TYPE: nucleic acid
                (C) STRANDEDNESS: double
                (D) TOPOLOGY: linear
30

        (xi) SEQUENCE DESCRIPTION: SEQ ID :1070:

35   TTTATTCCAC TGGAGAAAGG GGATTGAAAA TCAGTTAGAA CCAATGTATT   50

        TCTTGCCCCA CGGAACACTA TTCCTATAAG ACAGCTGAAA GAAGCTGCCG   100

        TGAGGAGCTC AGCTCCAAAC ACAGGATCAG CACCTCGCAT AGGAATTCCC   150
40
        ATGAATCACG ACTTCTCATC CCGTTTTATC AGAGTGCATA TACGTCCTAC   200

543

TTAAGGAAAA GTAAAACAGT CATTTACGAA AGAAAGTCAA TCTGTATCCT   250

AAGCATTTTA ATAAAAAGTC AGAAGGAATT   280

(2) INFORMATION FOR SEQ ID :1071:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 193 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID :1071:

AGAACCGAAG CCTGCAGAGA GGCCATTCTG ACAGGCTGGG AAATGTAGCC   50

TACCGCCAGA AGCTAGAAGC AAGCACTTCC TCCTAACCGA GTTTTTGAAA   100

GACTAAGGGA AAGAGAATAG AGAAGGGATA TTCCCATCTA CCGGGGAAAA   150

GATGCGCAGT AACAAACCAT CTAGGGAGAC AGCCTTCTAA CAG   193

(2) INFORMATION FOR SEQ ID :1072:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 175 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID :1072:

AAAGCACCTT CCCCTCGCTG AGCTCCAGGG GGCCCAGATA GGCCACGCGC   50

AGCTCCAGCA TCTTGGAGAG CTGCACGTCA TCTGCCGCGT CGTAATCCTC   100

CACTCTGCAG CCATAGGCCC CACTCTGGCC CCGGGTCACT CCCTCCAGGG   150

544

TCAAGTTCCC CTCGAGATTC ACATC   175

(2) INFORMATION FOR SEQ ID :1073:

5   (i) SEQUENCE CHARACTERISTICS:
                  (A) LENGTH: 339 base pairs
                  (B) TYPE: nucleic acid
                  (C) STRANDEDNESS: double
                  (D) TOPOLOGY: linear

10

           (xi) SEQUENCE DESCRIPTION: SEQ ID :1073:

15   AGTGCCCTAC TCTTTTCCCA AGAAGGGTCA AAGCCTACAA TATCATCAGG   50

       GGGCATGAAG CACATTAATT TGCAGTGGCT GCTTCATATG AGGAGGTATG   100

       GTGGACAGGC TAATTTTTCC TTGAAAATGT GGCTTCTTCA ACTCCTTTCA   150
20
       AATTTAGGAT GGAATACTTC CTGAAATAAA AACTGGGCTT TATGCAGGAT   200

       TCTCTTTGAA AATTCTTGTA TGTCCAGAAC AAAAGATAAA ACTAATTGTA   250

25   TTCCTCACAT TCACAATCCC CATTGGTCTG AAGTCACGTG ACACAGAGCA   300

       TCTATATAGC ACATAGTGTT TAAAGACTAA TGAATGCAA   339

       (2) INFORMATION FOR SEQ ID :1074:
30
           (i) SEQUENCE CHARACTERISTICS:
                  (A) LENGTH: 172 base pairs
                  (B) TYPE: nucleic acid
                  (C) STRANDEDNESS: double
35   (D) TOPOLOGY: linear

           (xi) SEQUENCE DESCRIPTION: SEQ ID :1074:
40
       ATTAATTATG CGGTCCTCCT CCTGGCAGCT GGACACCAGT TTGAATCTTC   50

545

CTTTGAGCTC CGGAAAGTTG GTAATTACAA CTTGATATTT CTACATGGAA   100

ATCAAGAAAC TCGGACCCAA CTTGGTGCAA AGACGGATCT CCGCCGATTC   150

TGACGGCTCT CCAGGTTTTG TC   172

(2) INFORMATION FOR SEQ ID :1075:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 299 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID :1075:

AGAGTAGGAA GAGGGAGGGG AACAGGCATC TAAGATAGAC TTTCTCCATC   50

TGTTGGGAGC CTGGGCAAGT AGGAAAGAAG CCTTTTTCAT ACACTTCAGT   100

CGTATGACTG AGCTGCTTGG CAGGGCACTG GAAACGACGA ACTCGCGCAG   150

CCTGCAAATG AGACCACTCT CATTTCTCAG TTTCGATTTG ATTCACTCAC   200

TAGTAGTTAG GTAAATACGA GCTCTATGTG ACTCAAGGAA TGTCAGGCTG   250

GGGCAGGTGG CAAAAGCTAC AGTGATCGAA ATTCACGTTG CTACTGATG   299

(2) INFORMATION FOR SEQ ID :1076:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 283 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID :1076:

546

GCCCTCATCG GCGATACTGG AGGTTCGCTT TCTCAACCCT GTGGGCTTCA   50

CCCCAGACAC GCCCTGAATC GTTTCATGTT CCAGCATGCC TGAGACAATC   100

ATCGACTGAA GGATGTTCTC TAACACCCGC ACGAGCTGCC GGCAGATCTG   150

AATGCCCAAG TCACTCAGCA CCTGCCGATA CTCAGCCAGG TCAAAATCGG   200

CGAGGTAGTG CTCATGCCTG GCGAGACGTG TTGTGCTTAA TGAAGCCCTA   250

TCATTCGAAG TATTGCTATG AGCAGTGCGA AAA   283

(2) INFORMATION FOR SEQ ID :1077:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 297 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID :1077:

ACCAATCAAG TACACTAAAT TAGAATATTT TTAAAGTATG TAACATTCCC   50

AGTTTCAGCC ACAATTTAGC CAAGAATAAG ATAAAAACTC GAATAAGAAG   100

TAAGTAGCAT AAATCAGTAT TTAACCTAAA ATGACATATT AGAAACAGAA   150

GATATTACGT TATGCTCAGT AAATAATCAA GAGATGGCAT CGCGTAAGAA   200

GGAGCCCTAG ACTGAAAGTC AAGACATCTG AATTTCAGGC TGGAAAACTA   250

TCAGTATGAT CTAAGCCTCA GTTCTCTNGT CTGCAAAATG AAAGCAC   297

(2) INFORMATION FOR SEQ ID :1078:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 291 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double

547

(D) TOPOLOGY: linear

5   (xi) SEQUENCE DESCRIPTION: SEQ ID :1078:

AATCTTTTAA TCAATCGAAA CCTTAATAAT TAGGACTGAT AATAGTGATC   50

AGTGATTGAA CCTTTATTAT TTACCAGCTA ATATAGTAGG CCCATAAATA   100
10
GGTTATATCA TTCGTAGTCA CAATAACCAC ATACATCACA CACCATGACG   150

TAGCGCTACT. ACCCATACCT GCTAGCAGTC AAGGTTCAGA TAATCATAAC   200

15   ACGCCCAACA TCTCATTGAT AGTGAGTTAT CCAAACAGGA ACAATCTCAA   250

GTTTATATCT AAAGCCCATG TTCTTTTGCT TAATATTAGA G   291

(2) INFORMATION FOR SEQ ID :1079:
20
        (i) SEQUENCE CHARACTERISTICS:
             (A) LENGTH: 136 base pairs
             (B) TYPE: nucleic acid
             (C) STRANDEDNESS: double
25   (D) TOPOLOGY: linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID :1079:
30
AGTCACAGCC CCTATACTCC CTCTACACAT TAACCACAAC ATAAGCGGGG   50

CTCACTCACC CACCACATTA ACACCACGAA ACGGGTAATC TAACACGAGA   100

35   AAACACCCTA ACGTTCATAC ACCCCATACA CCATTA   136

(2) INFORMATION FOR SEQ ID :1080:

        (i) SEQUENCE CHARACTERISTICS:
40   (A) LENGTH: 300 base pairs
             (B) TYPE: nucleic acid
             (C) STRANDEDNESS: double

548

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :1080:

CCAAGGTCGC CTGTGTGCTA GTCACGACCA TTAGGATCCG AAGAAGAGAT   50

GATGACTACC CTAAAAGTAA GGTCTGTGAA CAGCCTGTAA TGGGACGTGA   100

GCTGCGGTAT TAAAAAAATC AAGAATGGAA GCGTTCCTCA ATTGTCGTTG   150

AGAATCATAC CAACACGGCA GATGCAACCA TGAAAAACGC AGCTGCGTAT   200

CGCGCGTTTT TCATGGTTCG CATCTGCCGT GTATGCAATG ATTCTCAACA   250

CACATTGGAG TCACGCGGCC TGCGTAAGAG TATGAAGGTC TTCCTGTAAA   300

(2) INFORMATION FOR SEQ ID :1081:

      (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 219 base pairs
          (B) TYPE: nucleic acid
          (C) STRANDEDNESS: double
          (D) TOPOLOGY: linear

      (xi) SEQUENCE DESCRIPTION: SEQ ID :1081:

GTTAATGGTT TTTTCATACA TATGAGACTG AGCGGTCAAA GTTTTACTAA   50

AGTCTTTATG ATCTTTAATT AATACTCCAA GACATCCGAG TTTGGCAGAT   100

ATTGGATGAG ATTTGTTTTG CTCCTTACTT TCTTTGTATA CAGCCAAGCC   150

TGAAAATCTC TAGACATTTG CTGAAATTGA TGAGAGCATG CACAGGACGA   200

CTGAAGGTGC TGGACATGA   219

(2) INFORMATION FOR SEQ ID :1082:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 360 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID :1082:

```
ATTTTGGGAA AGTGAGCATG AAGAAGGGAC TCAGAGCTGC CAGGTACCCG          50

AGTCTCAGGC TCTGACATCT CTTGGGGCCC CCTTCTGCCA CAACTTCTTG         100

CCACTTCACG GACTTGAATT ATGTCCCGCG CCTAAAAAAA AGATTGGCCT         150

GCAGCACAGG CGTGTATCCT CTCCAAAAAG CTGCTGCTCA TTTCTGGCCC         200

CATCTGCTGC TATCTTTGCC AGTCAGCCAT CACAGTTTGG CATCATCAGA         250

GTCTCAGCTA GAGGGAGCGT GTCATTTCTG CCTTAGTGGT TTGCCTGCGA         300

CCTGACCAGG GCAAGACCAG CTGGGATGTC AAGTGACATT TTGGGAACTT         350

GTCGGAAGTT                                                    360
```

(2) INFORMATION FOR SEQ ID :1083:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 250 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID :1083:

```
CATACATATG AGACTGAGCG GATCAAAGTT TTACTACAAG TCTTTATGAT          50

CTTTCAATTA AATACACTCC AAGACATCGA GTTTGGCAGA TATTGCGCCC         100
```

550

GCCGTTTTGC TCTTCTTATC TTTGTATCCA GCCAAGCCTG AAAAGTCTCT   150

AGACATTTGC TTGAAATTTG ATGAGAGCTT GCACAGGCCG ACTGAAGGAT   200

GCCGGACATG ATTCTCTGCT TTCTGGTTCA ACAAAAAAAA AAAGTTCCAG   250

(2) INFORMATION FOR SEQ ID :1084:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 261 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: double
            (D) TOPOLOGY: linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID :1084:

TNCTAGATAC NTCCCTCTGT CTCACATTCA TAGTGTGTTC TTGTCTAGTG   50

TATGAAGTCT CACNCAAGGA AAGTGTNCAG GCAGAGTTTG GGGAGAGTGA   100

AAAAAGTGAA TGGCCTATAT NTGCTCTNTT GGGTGNTCCA NCCATTATTG   150

GGGTGAACCC TTTCAGCTTT TTCCTAAAAA TTTGAAAGA NTTTTTTAAA   200

AAATTAAAAA GAGGATTTTT AAAAGGAATA TCTTGTTCAA AATTTNTTAA   250

GTTTTAATAG G   261

(2) INFORMATION FOR SEQ ID :1085:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 260 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: double
            (D) TOPOLOGY: linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID :1085:

551

```
GCAATCCATA AGTGTCCTTA TCTACAAAGT GAAAAGTTGG ACAAGATATT          50

CTTCATGATC TTTTTCGATT TTAAAATGTC ATGCAATTTT AGAGAAAAGC         100

TGAAGGGTCA CCCAATATGG CGCGACACCA AAAGACAAAT ACGAGGACAA         150

TCACTTTTTC ACTTTCCGCA AACTATGCCT GGACACTTCC TTGGCGAGAC        200

TTAATACACC AGACAAGAAC ACACTATGAA TGCGAGACAG AGGGAGACAG         250

AGGCGAAATA                                                     260
```

(2) INFORMATION FOR SEQ ID :1086:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 213 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: double
            (D) TOPOLOGY: linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID :1086:

```
AAGACGTGGA TTTGCTGGAA GACACGGATT TCCTGGAAGA CCTGGATTTT          50

TCGGAAGCTA TGGATTTGAG GGAAGACAAG GATTTTCTGG AAGACATGGA         100

TAATCTGGAA GACATGACTT TGTCGGAAGA CGTGGACTTG CCGGAAGACA         150

CGAATTTCCT GGAAGACCCG GATTTTTCGG AAGCTATAGA TTTAAGGGAA         200

GACAAGACGG ACT                                                 213
```

(2) INFORMATION FOR SEQ ID :1087:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 256 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: double
            (D) TOPOLOGY: linear

552

(xi) SEQUENCE DESCRIPTION: SEQ ID.:1087:

```
TCCCAGGCAC CCGCTGAATT TCTGAGGCCT TGCTTAAAGC TCAGAAGTGG          50

TTTAGGCATT TGGAAAATCT GGTTCACATC ATAAAGAACT TGATTTGAAA          100

TGTTTTCTAT AGAAACAAGT GCTAAGTGTA CCATATTATA CTCGACGTCG          150

ATCATTTCTC AGTCCTATTT CTCAGTTCTA TTATTTGAGA ACCTAGTCAG          200

TTCTTTAAGA TTATAACTGG TCCTACATCA AAATAATAGA AATTACGTTT          250

TTTTTT                                                         256
```

(2) INFORMATION FOR SEQ ID :1088:

       (i) SEQUENCE CHARACTERISTICS:
           (A) LENGTH: 264 base pairs
           (B) TYPE: nucleic acid
           (C) STRANDEDNESS: double
           (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :1088:

```
TTGCTTAGAA CGGAGCTAGC AAGACAAAAA TACTTCAGTT GGCATCTCCC          50

TTAAAGCACA TCCCCAAACG CGGGTCCTGG CCCCAGACAG GGAGACCAGG          100

GCTCTGACAG TGACAGGTTC TTCCCTCTGA AAAAAGAATA GAAGAGGAGC          150

TCCTCCCTAA CCCACAGATT CCCAGGGCAG ACCCTGGGAG GAGGTGCTGA          200

AACACAGAAG AGAGTGTGTC TTCCCCAACC TCTACCAGAC AGTAGAGAAA          250

CTGAGGCGAG AGGC                                                264
```

(2) INFORMATION FOR SEQ ID :1089:

       (i) SEQUENCE CHARACTERISTICS:

553

```
                  (A) LENGTH: 157 base pairs
                  (B) TYPE: nucleic acid
                  (C) STRANDEDNESS: double
                  (D) TOPOLOGY: linear
```

```
            (xi) SEQUENCE DESCRIPTION: SEQ ID :1089:
```

```
GACCTGGAAT TTGTTTTCGT CTGTTCAGTA GACTCCGATT TCAGAATATG          50

TCGGAATTTC AGACTCCGGA ACTTTTGAGA ATGTCATTAC AGGAACTTTG          100

TTTACATACC GAGCTGTTAG CCCCAGTCAC TGGGTCCGAA ATTACGCCGA          150

TACCGAC                                                         157
```

```
      (2) INFORMATION FOR SEQ ID :1090:

            (i) SEQUENCE CHARACTERISTICS:
                  (A) LENGTH: 366 base pairs
                  (B) TYPE: nucleic acid
                  (C) STRANDEDNESS: double
                  (D) TOPOLOGY: linear
```

```
            (xi) SEQUENCE DESCRIPTION: SEQ ID :1090:
```

```
GCATATACCA AAAAAGGACA AACAGATAGA AGAGTCATCT CAGTGTGTAA          50

CGAGGAAAAG ATTTATCTCC CATCCTCTGA TCCTCCATAT GATATCTGAT          100

AGCGAAGATG ACAATAACCC CTTGACTCTT CACGAAAACT CGATGAGAGA          150

GAAACTTGAA AAGTCAGAAA ATAAGTTCAT ACCGCAATTA ACCTTTTGGT          200

CAAGTAATGG AAACTTTTGA CTACTAGTGT AAGTCAAAAG ACAAAGGACT          250

CCAGCAAGAT GAGAGATTTC TCTATTTTGT AACGAGTAGT CCACCGATCG          300

TCATCAAAGA GAGAGAATGA ACAACTACGA AAGTTTAAGG GAAAAAAAAA          350
```

554

AAAAAACATA GATGTT   366

(2) INFORMATION FOR SEQ ID :1091:

5   (i) SEQUENCE CHARACTERISTICS:
                        (A) LENGTH: 305 base pairs
                        (B) TYPE: nucleic acid
                        (C) STRANDEDNESS: double
                        (D) TOPOLOGY: linear
10

                   (xi) SEQUENCE DESCRIPTION: SEQ ID :1091:

15   GGTCTGAATC ATGAAAAAGC CCATAAGAGA GATACAGTGA CTCCAGTTTC   50

       AATCATATTA CAGGAGATGA ATCTGTTGCT CTCCCATTTT GCTCTTGTCA   100

       CACCATATGA AGACATCAAA AAACACTTAA GGATTCGAGA AAGAGAACAT   150
20
       CTTTTGTTAA AGAAGAGAAT AAGATTTTGG AAGAAAAAGT AATAGCAAAT   200

       TTGAAGAAGA AACAAGTTAC GTAGGGACGA GAACAAGTAA ATAAGGCCTA   250

25   TCATGCATAT CGAGAGGTTT ACATTGATAG AGATAATTTG AAGAGCAAAT   300

       GGACA   305

       (2) INFORMATION FOR SEQ ID :1092:
30
                   (i) SEQUENCE CHARACTERISTICS:
                        (A) LENGTH: 237 base pairs
                        (B) TYPE: nucleic acid
                        (C) STRANDEDNESS: double
35   (D) TOPOLOGY: linear

                   (xi) SEQUENCE DESCRIPTION: SEQ ID :1092:
40
       AAATGGAAGT TGAACTGAGT GTGGTTTCCA GTACAGGGCA TCTGGCCACC   50

555

```
TTCACCTCAG TAAATACTGC TGATCGACTC TCTCTGGCTC TGGCTGTCCT        100

GCCAGAGACA GCCAAACACA GGAGACATGA CAAATTACTA TCATCTTTTG        150

CTTCTTTATT TTTATTATTA TTATTTTTCT TTTTGTGGAG AACAGCGTCT        200

TGCTGTATTG CCCAGCCTGA TCTCAAACTC CTGGGCG                      237
```

(2) INFORMATION FOR SEQ ID :1093:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 420 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: double
            (D) TOPOLOGY: linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID :1093:

```
AGAAATTTAT TGCCTCACAG TTCTGGAGCC TGGAAGTGCA ATATCAAGGT         50

GGAGACAGGG TTGGTTTCCT CTGGAGGCCA TAATGAAAGC ATCTGTTCCA        100

GGTCTCTGTC CTTGGCTTGT AGAAACACGC ATTCTTCTGG TGGATCCACA        150

CAGTCTTCTC CATGTGTATC CTTCCTTCAG TTTCCCTTAT AGGACACCAG        200

TGATGTCAGA TTAGGGATCG AACCCAACAA CCTCATTTGA AGTTACTCAC        250

CTGTTTGAAA ACCCTATGTC CAAATACAGT TATAGTGTAA GGAACTAGGA        300

CTTAGGGCTT ACAAATATGG AGTGGGGCAT CATCCAGACC ATACCATTTA        350

AATTGCAGGG TTTCTCTCCA ATGTGAGTTA CATACACACA TTAAGGTTTG        400

TGGGATTCAG AAAGGTATAC                                         420
```

(2) INFORMATION FOR SEQ ID :1094:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 192 base pairs

556

```
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: double
            (D) TOPOLOGY: linear
```

```
          (xi) SEQUENCE DESCRIPTION: SEQ ID :1094:

    GTTTCTTGGG TAACCTCCCC TCCTTAATCC TTCTGGCATA GGCAGACTCA        50

    CAGCAGGTAC CCAGTAGAAG GTAAGGTGGC TGATCATTTT TCCATAGGAG       100

   .GTCTCCATGG CACACAGGGT AGAAAGTGCA TTCTGTGAAT TAGAGGCAGC       150

    AGAGCATGGC AGCTAATGGA AACTGGCTCT GGGAGGTCAA AT               192


      (2) INFORMATION FOR SEQ ID :1095:

            (i) SEQUENCE CHARACTERISTICS:
                (A) LENGTH: 228 base pairs
                (B) TYPE: nucleic acid
                (C) STRANDEDNESS: double
                (D) TOPOLOGY: linear



          (xi) SEQUENCE DESCRIPTION: SEQ ID :1095:

    AGAGAGCTTA ATAAGACCTA ACTACAGGCA AACCTGACTG GAACGTGAGT        50

    ATCTGTGGTC TGGTGTGGAA ATAGCTCTCT AGCCCCATCT CCCTCCTCCC       100

    ATTGTCCACC CCCATCCTCC TTACCACGAA ACACATTTTT CACCAGCATT       150

    GCCAAACCAC TTGGGATTCC TGCGCATGGC TTTGCTTAGT TTGCTCTTCT       200

    GCTTCTTGGA TACCTCCTTC AGGAAATC                               228

      (2) INFORMATION FOR SEQ ID :1096:

            (i) SEQUENCE CHARACTERISTICS:
                (A) LENGTH: 198 base pairs
```

557

```
                    (B) TYPE: nucleic acid
                    (C) STRANDEDNESS: double
                    (D) TOPOLOGY: linear


  5


            (xi) SEQUENCE DESCRIPTION: SEQ ID :1096:


     ATTTTTTATG GAAAAAGGGG GATAATGCAA AATAGCAAAA ATTGTAAACA        50
 10
     AAGTTAAAGA TTATCTTCAT CTAAACCTTA AGCTGACAAT TTAAAACACC        100

     TTGTGCATAA TGCAGAAAAA AACTGTCCGT TTGACTTCAC TTTCATTCAC        150

 15  ACTGCTCCCT ACGCATGAGA AAGACCAGAT GTCTGGTTTC AGAGTATT          198


        (2) INFORMATION FOR SEQ ID :1097:


            (i) SEQUENCE CHARACTERISTICS:
 20             (A) LENGTH: 118 base pairs
                (B) TYPE: nucleic acid
                (C) STRANDEDNESS: double
                (D) TOPOLOGY: linear


 25


            (xi) SEQUENCE DESCRIPTION: SEQ ID :1097:


     TAGAGAGAAG TTGATATATG AAGATAGGGT GGACAGGACT GTGAAGGAGG        50
 30
     CTGAAGAAAA ACTGACTGAA GTGTCACAGT TTTTTTCTAC AAAACTGTGA        100

     CACTTCAGTC AGTTTTTC                                           118


 35     (2) INFORMATION FOR SEQ ID :1098:


            (i) SEQUENCE CHARACTERISTICS:
                (A) LENGTH: 138 base pairs
                (B) TYPE: nucleic acid
 40             (C) STRANDEDNESS: double
                (D) TOPOLOGY: linear
```

558

(xi) SEQUENCE DESCRIPTION: SEQ ID :1098:

AAAACTGACT AAAGTCANTG TGTAATACGA AAACCGAACA CTCCAGCAGT   50

CCTATTTTAT NTNTTCCAAC CTAGNNCACC CAGGTGACGC NNGGGACTCG   100

TCNCAGGTGT TTNGNACTTG CCGCCCGACN GGCNAAGG   138

(2) INFORMATION FOR SEQ ID :1099:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 151 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: double
            (D) TOPOLOGY: linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID :1099:

ACTCCACCAC TGGGNCCGCC ATGTTTTGGG TNGGNGCAAT GCGCTGTCTG   50

TGAGCGCCAN TCTAATTGTA TTNGGACTGC ACGGGTCCGT ACACTGACTG   100

ACACTGGGCT ACCTCGCCCG AAAATGNGAA CACCGCTCAA TATCGNTGCG   150

G   151

(2) INFORMATION FOR SEQ ID :1100:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 201 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: double
            (D) TOPOLOGY: linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID :1100:

TAGCAATAGG CTATAACATA AGCCGAGGTA TAGGCTACAC TAGCTAGGTT   50

CGTGTAAGTA CACTCTATAT TGGCACAACA TAAAATTAAC TAGTGACGCA   100

TTTCTCAGAA TGCATCCCCA TCGTTAAGTG ACACAGACTG TCCCTCATAT   150

CACCGGAGGA CTGGNCCAGG ACCTCCTGGC GGCACCAAAA TCCACGAGCG   200

C   201

(2) INFORMATION FOR SEQ ID :1101:

(i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 212 base pairs
    (B) TYPE: nucleic acid
    (C) STRANDEDNESS: double
    (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :1101:

TAGCAATAGG CTATAACATA TACCGAGGTA TAGGCTACAC TAGCTAGGTT   50

CGTGTAAGTA CACTCTATAT TAGCACAACG ATAAAATTAA CTAGTGATGC   100

ATTTTTCAGA ATGCATCCCC ATCGTTAAGT GACACATGAC TGTCCCTCAG   150

TATCACTGGA GGACTGGGNC CAGGACCTGA CCTGGTGGTA CCAAAATCCA   200

TGAGGCNGNA AT   212

(2) INFORMATION FOR SEQ ID :1102:

(i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 218 base pairs
    (B) TYPE: nucleic acid
    (C) STRANDEDNESS: double
    (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :1102:

560

CGGTAGCAAT AGCTATAACA TATAGCCGAG GTATAGGCTA CACTAGCTAG   50

GTTCGTGTAA GCACACTCTA TACNNGCACA ACATAAAATN AACTAGTGAT   100

GCATTTCTCA GAATGCATCC CCATCGTNAA GNGACACATG ACTGTCCCTC   150

AGTATTACTG NAGGACTGGN CCAGGACCTC CCTGGGGTAC CAAAATCCAN   200

GAGTGGAAAT TCCANCAT   218

(2) INFORMATION FOR SEQ ID :1103:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 207 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID :1103:

GTAGCAATAG GCTATAACAT ATACCGAGGT ATAGGCTACA CTAGCTAGGT   50

TCGTGTAAGT ACACTCTATA TTAGCACAAC GATAAAATTA ACTAGTGATG   100

CATTTTTCAG AATGCATCCC CATCGTTAAG TGACACATGA CTGTCCCTCA   150

GTATCACTGG AGGACTGGGN CCAGGACCTG ACCTGGTGGT ACCAAAATCC   200

ATGAGCG   207

(2) INFORMATION FOR SEQ ID :1104:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 259 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

561

(xi) SEQUENCE DESCRIPTION: SEQ ID :1104:

```
GGCGTCAAGT GGCCCAATCT AACAGCTCCA GGGTAGCCAC AACCATCGTG        50

ATGGATTGCC ATTATTGTGT GCTAGTGGCT AGAGGTAGAC CCAATAGAAC       100

TCTGCCCCAA CAGGGCAACA GCCAAGCTCA ATTCTCCAAG CCCCCTGAAC       150

AGACCTTCCA CATCCAGGAG AAGCTGTTGT TGTCTAGAGC TACTTAGTGT       200

CAGAATCCAG GCCAGCTTGG CTGCTTGATG CGACTGGCTA TAGGATTNGN       250

GTGNAGGCC                                                    259
```

(2) INFORMATION FOR SEQ ID :1105:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 230 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: double
            (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :1105:

```
ACATGACCCC TTGGACTGAA GGCGCTCAGT AGTAAAGGAG TGTCATGCAG        50

GTCAACACAT GTCGCACATG GACCACAAAG CCTGCCACCA GCAGGATGCA       100

CGGGGACTTC TGGGAGGGGG TGGACAGGAT ACTTATCTGT GACTGGAATG       150

CAGGCGAGAG GCGGAGAAGA GAGTGAAGGA TAACTCATAG AGGGGGCAGC       200

ATTTGTTTCG NGTTGAAAGA GGCAGAAAAT                             230
```

(2) INFORMATION FOR SEQ ID :1106:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 163 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: double

562

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :1106:

ACATGNCCTG GACTGAAGGT GCTCAGTTAG TAAGGGAGTG TCATGCAGGT   50

CAACACACGT CGCACATGGA CCACAAATGC CTGCCACCAC AGGATGCACA   100

GGACTTTTGG GGGGAGTGGA CAGGTATTAT TGNGACTGGT GAGGTGAGAG   150

GTNAGAGGGG GCT   163

(2) INFORMATION FOR SEQ ID :1107:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 182 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :1107:

ACNTGATGAT TGCCATTATT GTGTGCTAGT GGCTAGAGGT AGACCCAATA   50

GAACTCTGCC CCAACAGGGC AACAGCCAAG CTCAATTCTC CAAGCCCCCT   100

GAACAGACCT TCCACATCCA GGAGAAGCTG TTGTTGTCTA GAGCTACTTA   150

GTGTCAAATC CAGGCCAGCT TGGCTGCTTG AT   182

(2) INFORMATION FOR SEQ ID :1108:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 214 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

563

(xi) SEQUENCE DESCRIPTION: SEQ ID .:1108:

CCCCTGGACT GAAGGCGCTC AGTAGTAAAG AGTGTCATGC AGGTCAACAC   50

ATGTCGCACA TGGACCACAA AGCCTGCCAC CAGCAGGATG CACGGGGACT   100

TCTGGGAGGG GAGTGGACAG GATACTATCT GTGACTGGAA TGCAGGCGAG   150

AGGCGGAGAA GAGAGTGAAG GATAACTCAT AGAGGGGGCA GCATTTGTTT   200

CGNGCCTTGA AAGA   214

(2) INFORMATION FOR SEQ ID :1109:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 133 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :1109:

ACATGGCCCC TGGACTGAAG GTGCTCAGTT AGTAAGGGAG TGTCATGCAG   50

GTCAACACAC GTCGCACATG GACCACAAAT GCCTGCCACC AGCAGGATGC   100

ACAGGACTTT TGGGGGGGGT GGACAGGTAT TAT   133

(2) INFORMATION FOR SEQ ID :1110:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 156 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :1110:

564

GCATGACCCC ATGGCACTGA AGGTGCTCAG GTTAGTAAGG GAGTGTCATG   50

CAGGTCAACA CATGTCGCAC ATGGACCACA AATGCCTGCC ACCAGCAGGA   100

TGCACGGGGG ACTTCTGGGA GGAGAGTGCA TAGGATACTT GTCTGTGACT   150

GGAATG   156

(2) INFORMATION FOR SEQ ID :1111:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 282 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID :1111:

GGCGCTCANT GGATCCAATA CACCAGACTC CCGGGAGCGA AAACGCCCGC   50

AGGTGCCTCA AGAACTTAA AACAGAACTG CCATTAGACC CCACAATCTC   100

ATNAAGGATG TTATAGATAT ATCCAAAAGA AAATAAATCA TTCTTCAAAA   150

AGACACATAC ACTAACACGT TCATGGAGCA CTATTCACAC AGCAAAGACT   200

CGATCAACTC ACACACTCAT GAATGCGGAT CGAAATAGAA GATGTGGTAT   250

GCATACACCA CGAAATACTA CGAGCCATAA AA   282

(2) INFORMATION FOR SEQ ID :1112:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 181 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

565

(xi) SEQUENCE DESCRIPTION: SEQ ID :1112:

TAATTAGTTT AACCACTGTG GAAAGCGTTG TAGGGTCTCA AAGACTNAAA   50

ACAGAACTGC TTAGACCCCA CAATNTTANG AGCGGATGTT ATGATATATT   100

CAAAAGGAAA TAAANNGNCN TGTNAAAGAC CATACACNAT NGTCCATCGG   150

AGCCCGTATN CACGCAGCTT GTCATAACTA T   181

(2) INFORMATION FOR SEQ ID :1113:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 278 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :1113:

ATCCAATGAC ACCAGACTCC CGGGAGCGAA ACGCCCGCAG GTGCTCAAAG   50

AACTTAAAAC AGAACTGCCA TTAGACCCCA CAATCTCATN AAGGATGTTA   100

TAGATATATC CAAAAGAAAA TAAATCATTC TTCAAAAAGA CACATACACT   150

AACACGTTCA TGGAGCACTA TTCACACAGC AAAGACTCGA TCAACTCACA   200

CACTCATGAA TGCGGATCGA AATAGAAGAT GTGGTATGCA TACACCACGA   250

AATACTACGA GCCATAAAAG GCGAAATC   278

(2) INFORMATION FOR SEQ ID :1114:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 125 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

566

(xi) SEQUENCE DESCRIPTION: SEQ ID :1114:

ACCTGCAAAC TTTTTCTGTA AAGACCAGAT AGTAAGTATT TTATGCTTTG   50

TGAGCCATAC AGTTTTTGTT GCAACTAGTC AACTCTCAAC TNACGTGGAC   100

AGCATGTAAA GAACGAGAGT GACTG   125

(2) INFORMATION FOR SEQ ID :1115:

    (i) SEQUENCE CHARACTERISTICS:
       (A) LENGTH: 157 base pairs
       (B) TYPE: nucleic acid
       (C) STRANDEDNESS: double
       (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :1115:

GTAGCGACCG GCGCTCATGG AATTCCGGGA CCTGCAAACT TTTTTGAAAG   50

ACCAGATAGT AAGTATTTTA TGCTTTGTGA GCCATACAGT TTTTGTGCAA   100

CTAGTCAACT CTCAACTCAC CGTGGACAGC ATGTAAATGG ATGGGAGTGG   150

CTGCCGG   157

(2) INFORMATION FOR SEQ ID :1116:

    (i) SEQUENCE CHARACTERISTICS:
       (A) LENGTH: 123 base pairs
       (B) TYPE: nucleic acid
       (C) STRANDEDNESS: double
       (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :1116:

CCTGCAAACT TTTTCTGTAA AGACCAGATA GTAAGTATTT TATGCTTTGT   50

567

GAGCCATACA GTTTTTGTTG CAACTAGTCA ACTCTCAACT NACGTGGACA   100

GCATGTAAAG AACGAGAGTG ACT   123

(2) INFORMATION FOR SEQ ID :1117:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 125 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID :1117:

ACCTGCAAAC TTTTTTTGTA AAGACCAGAT AGTAAGTATT TTATGCTTTG   50

TGAGCCATAC AGTTTTTGTG CAACTAGTCA ACTCTCAACT CACCGTGGAC   100

AGCATGTAAA TGGATGGGAG TGGCT   125

(2) INFORMATION FOR SEQ ID :1118:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 125 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID :1118:

ACCTGCAAAC TTTTTCTGTA AAGGACCAGA TAGTAAGTAT TTTATGCTTT   50

GTGAGCCATA CAGTTTTCGT TGCAACTAGT CAACTCTCAA CTTCACCGTG   100

GACAGCATGT AAATGGATGG GAGTG   125

(2) INFORMATION FOR SEQ ID :1119:

568

(i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 148 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
 .5   (D) TOPOLOGY: linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID :1119:
 10

ATTAAGCTTG ACACATCTGT GTTATCACGC ACTGAAGACA GGAAGCAGTT   50

CACTGAGTCA GCTGGCTTCC AAGCTTACAC AGAAGGCGAT AAGTCACTAT   100

 15   CAAAGAGCCA ATGAGAATCT TCTTATAGAA TAACCTGGGC CCAAGTGA   148

(2) INFORMATION FOR SEQ ID :1120:

        (i) SEQUENCE CHARACTERISTICS:
 20   (A) LENGTH: 240 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: double
            (D) TOPOLOGY: linear

 25

        (xi) SEQUENCE DESCRIPTION: SEQ ID :1120:

AGAATAACAG AGCCAAAGGA CTAATAAAAT CAATGAATCN TGGTGAGACT   50
 30
AATCAAGAAA AAATAGCACC AACAACAATG AGGAGAAAAT GGAAAAAGGG   100

CAGAGTATTT CAP.'GATTAC GAGAGGGCAA ACCAATCAAC GAATGATTCT   150

 35   TAAGCCTTCA GTTTGCCCTG TAAGCAAACT GAAGACGTGC AAGTCATCCT   200

TTGCCCTGGG AGAGTTAACT TAACCCACAG GGACAAٴ゙.3   240

(2) INFORMATION FOR SEQ ID :1121:
 40
        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 254 base pairs

569

        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

5

        (xi) SEQUENCE DESCRIPTION: SEQ ID :1121:

AAATGGGGAG AATCAACAGA GCCAAAGGAC TAATAAAATT AAGAATCCTG   50

10

GTGAGACTAA TAAGAAAAAA TACACCAACA ACAATCCGAG AAAATGGAAA   100

AAGGGCAGAG TATTTAATGA TACGAAGATG GGCAAACCAA TCAATGAATG   150

15

ATTTTTAAGC CTTCACGTCT GCCCTGTAAG CAAACTGAAG ACGTGCAAGT   200

CATCCTTCGG CCCTGGAGAG TTAACGTTNC CCAAGGGGCA ATGAGAAGGG   250

ACAG   254

20

(2) INFORMATION FOR SEQ ID :1122:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 253 base pairs
25   (B) TYPE: nucleic acid
            (C) STRANDEDNESS: double
            (D) TOPOLOGY: linear

30

        (xi) SEQUENCE DESCRIPTION: SEQ ID :1122:

AAACGAGGGG AGAATCAACA GAGCCAAAGG ACTAATAAAA TCAATGAATC   50

35 NTGGTGAGAC TAATCAAGAA AAAATAGCAC CAACAACAAT GAGGAGAAAA   100

TGGAAAAAGG GCAGAGTATT TCAATGATTA CGGAGAGGGC AAACCAATCA   150

ACGAATGATT CTTAAGCCTT CACGTTTGCC CTGTAAGCAA ACTGAAGACG   200

40 TGCAAGTCAT CCTTTGCCCT GGGAGAGTTA ACTTAACCCA CAGGGACAAC   250

570

GAG   253

(2) INFORMATION FOR SEQ ID :1123:

    (i) SEQUENCE CHARACTERISTICS:
       (A) LENGTH: 210 base pairs
       (B) TYPE: nucleic acid
       (C) STRANDEDNESS: double
       (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID :1123:

AAATGGGGAG AATCAACAGA GCCAAAGGAC TAATAAAATT AATGAATCCT   50

GGTGAGACTA ATAAGAAAAA ATACACCAAC AACAATCCGA GAAAATGGAA   100

AAAGGGCAGA GTATTTAATG ATACGAAGAT GGGCAAACCA ATCAATGAAT   150

GATTTTTAAG CCTTCACGTC TGCCCTGTAA GCAAACTGAA GACGTGCAAG   200

TCATCCTTTG   210

(2) INFORMATION FOR SEQ ID :1124:

    (i) SEQUENCE CHARACTERISTICS:
       (A) LENGTH: 231 base pairs
       (B) TYPE: nucleic acid
       (C) STRANDEDNESS: double
       (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID :1124:

AAATGGGGGG AGAATCAACA GAGCCAAAGG ACTAATAAAA TTAATGAATC   50

CTGGTGAGAC TAATCAAGAA AAAATAGCAC CAACAACAAT CAAGAGAAAA   100

TGGAAAAAGG GCAGAGTATT TAAATGATTA CGGAGACGGG CAAACCAATC   150

571

```
AACGAATGAT TCTTAAGCCT TCATGTTTGC CCTGTAAGCA AACTGAAGAC        200

GTGCAAGTCA TCCTTTGGAC CCTGGGAGAG T                          231
```

(2) INFORMATION FOR SEQ ID :1125:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 89 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID :1125:

```
AAGTCCCATC AGCAACCCGT TTTTTACCAG ATGTCACTCA AGAATGCGCC        50

CGTGGCCCTC CAGTTCCTGC GCACTAAGAG CGTCCCGCT                  89
```

(2) INFORMATION FOR SEQ ID :1126:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 205 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID :1126:

```
AAGAAACCCG AGACMCCAAC TAATCCCAGA ACAGCTAAAA CCAATAAAGA        50

ACCAAAACTT CACGACCACT TTCCTGAGGA CCCTGCTGAG TGCTCATGAC       100

ACCAATACTG ACAATTGTAG CGGTAATACA TACAATGATT TAATAAGCCT       150

ATGCTACTGG ACACATGCCC ACACAATAAT ANTCANRTGT NTYGTTAGGC       200

CTACT                                                      205
```

572

(2) INFORMATION FOR SEQ ID :1127:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 151 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: double
            (D) TOPOLOGY: linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID :1127:

GCAAGGCCTG GCCGACAACA CCCTTATTGC TAAAGTAAAT AATGNCGCGC   50

GGGGCCTGGA CCACCCTCTG GAAGAAGATT GTACCTTGGA GCTTCTCAAG   100

TCTGAGGATG AGGAAGCTCA GGCAGTGTAT TGGCGCTTTA GTATCACATA   150

A   151

(2) INFORMATION FOR SEQ ID :1128:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 237 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: double
            (D) TOPOLOGY: linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID :1128:

GAGCACCCCA GCCCATAACA CAGAACTCGT CCCCCTACCC CCCTCAGCAA   50

GCCGGAGAGG CTAGCCCAAG TAATCATAAY AACAGCCGCC CGAGAGCAGC   100

CCCAGTAGCA GCCCCATGGC CGGGCGGAAC ACCTACATCG ACAACCTCAT   150

GACAGACGAG ACCTGCCAGG ACGCAGCCAT TGCGGGCTGC AAGGCCTCRC   200

CCTTCGTCTG GGCCGCCGTC CCCGGAGAAA CGCTCGT   237

573

(2) INFORMATION FOR SEQ ID :1129:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 126 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID :1129:

GCCTCGTGGA AGTGACATAG CCTTTAAACC CTGCGTGGCA ATCCCTGACG   50

CACCACGTGA CGCCCAGGAA AGACAGGGCG ACCTGGAAGT CCAACTACTT   100

CCTTAAGATC ATCCAACTAT AGGATG   126

(2) INFORMATION FOR SEQ ID :1130:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 246 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID :1130:

GCCATCTTCT GTAACAAAAT AAATAGTGTC AAGCACTAAA TATATGCATG   50

AATGCATCAG CAATAAGATG ACAATCAAAG AATGCTGTGA AGATTGGCAT   100

CAAGATGTTA GCAGCATACT GCAGGACTAG GCTTAGAAGC CTACCTGCAG   150

TTTATTTGCA AGGATTTTTC TTTCGRGGGC GGAGGGGAGA GAAAAGTAAA   200

TGTGCTAACT TCGGATACTT GCCCTTATAA AGAATTCCTT YGTATC   246

(2) INFORMATION FOR SEQ ID :1131:

574

```
            (i) SEQUENCE CHARACTERISTICS:
                (A) LENGTH: 273 base pairs
                (B) TYPE: nucleic acid
                (C) STRANDEDNESS: double
 5              (D) TOPOLOGY: linear




            (xi) SEQUENCE DESCRIPTION: SEQ ID :1131:
10
            CGAGGATCCG GGTACCATGG CAAGTCTCAT GAGGCTATTT ACCGAATTTA        50

            TCCTCTGTCT GACCATGATT TTTTCCCTCA AATACAACCA CTCCTCGACT       100

15          TTTCACCCTC AAAGTATAAA AAGTATGAAA NATAAACAAG CTCTTGCACT       150

            GTACACTTAG AAGTGTACAA TTAAAGCATT ATAGAGCTAT CTACACACCG       200

            ATAAATCCCA TCGAATCTTG AATAATCCAT CAATACGTAG AACGCAAGGG       250
20
            TGCAGACAGA ACTAAAACCA ACT                                   273


        (2) INFORMATION FOR SEQ ID :1132:


25          (i) SEQUENCE CHARACTERISTICS:
                (A) LENGTH: 329 base pairs
                (B) TYPE: nucleic acid
                (C) STRANDEDNESS: double
                (D) TOPOLOGY: linear
30



            (xi) SEQUENCE DESCRIPTION: SEQ ID :1132:

35          GAGGATCCGG GTACCATGGT CTGTATATCT GTGCTTCCAC TTCTCGGAGG        50

            TGGTAGAGGG GAGGCTGTCC TCTGGTCAGG AGAATCCTAT TCAGTGCTCC       100

            CTTAGACATT CTTCCAGGCA GGATCAAACT CAAAGGAAAA GGAATTTGTG       150
40
            AAGCAAACCA TGGCTTTGTC ACAGTAAAGT AATTGTCACT CTCAACCCAG       200
```

575

AATGTGTGAA GCGCTGCAGG GAGAAGCTTC TCTTCCAGGA GAGCAATANA   250

AGCCAATGTA TCTGACCCTT GCTTYGATGA GAGTTAATAA TAAGTATTAT   300

5   ATTTCTGTTT GTTAAAAAGT TCAGAATTT   329

(2) INFORMATION FOR SEQ ID :1133:

      (i) SEQUENCE CHARACTERISTICS:
10   (A) LENGTH: 24 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: double
            (D) TOPOLOGY: linear

15

      (xi) SEQUENCE DESCRIPTION: SEQ ID :1133:

CCCCGAGCTA GTTGTCCCGA CCTG   24
20
(2) INFORMATION FOR SEQ ID :1134:

      (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 297 base pairs
25   (B) TYPE: nucleic acid
            (C) STRANDEDNESS: double
            (D) TOPOLOGY: linear

30
      (xi) SEQUENCE DESCRIPTION: SEQ ID :1134:

GAGGATCCAC AAACCATGGA ACACTCTCGC GGCTGCCACT CCCCCATGAC   50

35   CACCCTACAG GCCCTAACCC CAGCCCCTCA CGTTATCGTC CAGCCACAAA   100

TAGCTGCCGC CCTGAGATCT CCACCTCAGA CCCTCTCCCG AAGCCCACAG   150

CGGCCCCTGC CGGGCACCCC AGCTTCCTCG CAGGCACCAA AAGCGCAGTT   200
40
CCAGGAATCT CTACCCTAGA GTGATCCGGC GCCAGTTGCC AGTTAAGGGA   250

576

CCAAACCTCG CCAGAAGGCT TCTTTTCGGG TTGATCGCCA TCTATTY   297

(2) INFORMATION FOR SEQ ID :1135:

5   (i) SEQUENCE CHARACTERISTICS:
                   (A) LENGTH: 93 base pairs
                   (B) TYPE: nucleic acid
                   (C) STRANDEDNESS: double
                   (D) TOPOLOGY: linear
10

              (xi) SEQUENCE DESCRIPTION: SEQ ID :1135:

15   GCCGCTTTAC TGCTCAGTTC GGAGCTACCG CTTCGAAAGC AACAAAAAAG   50

        CNTTTGCAAA TGAAACGAGA TTGCTGAATT GCGTACACCG AGA   93

        (2) INFORMATION FOR SEQ ID :1136:
20
              (i) SEQUENCE CHARACTERISTICS:
                   (A) LENGTH: 334 base pairs
                   (B) TYPE: nucleic acid
                   (C) STRANDEDNESS: double
25   (D) TOPOLOGY: linear

              (xi) SEQUENCE DESCRIPTION: SEQ ID :1136:
30
        CGAGGATCCG GGTACCATGG AGCTTCACAC GGGTCTTCTT GGTCTCAGGG   50

        TTGTGGGAGA TAACGGTGGC ATAGTTCCCT GATGCCCGGG CCAGCTTGCC   100

35   ACGGTCTCCA GGCTTCTCCT CCAGGCAGCA CACGATTGTA CCCTCAGGCA   150

        TGGTGCCCAC AGGGAGCRCA TTGCCAATGT TGAGCTGGGC CTTCTTGCCG   200

        CAATACACAA ACTGGCCCGT GNGAATGCCC TCGCGGGCAA TGAACAGTTC   250
40
        CGCCCGCTTC TTAAACCAAG ACAGATCCCG GAAGGCCGCC TGGGCAAGGG   300

577

GCCCCTCRAA CCCGGGGCTA TACACGTCAA AATC   334

(2) INFORMATION FOR SEQ ID :1137:

5   (i) SEQUENCE CHARACTERISTICS:
                         (A) LENGTH: 199 base pairs
                         (B) TYPE: nucleic acid
                         (C) STRANDEDNESS: double
                         (D) TOPOLOGY: linear

10

                    (xi) SEQUENCE DESCRIPTION: SEQ ID :1137:

15   CGAGGATCCG CATACCATGG CCCCCATCTT ACGAGCCCTT ACTCCTCATG   50

        ATGAAGAAAC TCCAAACCCT TTGACAGCTC CTCGGGGTNA AACCTGGNAY   100

        AAAGCTGACT GACCAGGCTC CATGAAATCT CCCATCTCCA TRATGTACCT   150

20
        CCTTGRTGCC ATCTCTATAT AAAGMGAACC AGTCCTAAAA TCAAACACT   199

        (2) INFORMATION FOR SEQ ID :1138:

25   (i) SEQUENCE CHARACTERISTICS:
                         (A) LENGTH: 304 base pairs
                         (B) TYPE: nucleic acid
                         (C) STRANDEDNESS: double
                         (D) TOPOLOGY: linear

30

                    (xi) SEQUENCE DESCRIPTION: SEQ ID :1138:

35   CGAGGATCCA AATACCATGG CGCTCCCTCC TCCCGAGCGC CGCTCCGCGT   50

        GGCACCCGGC TCGCTCCGAG TTTCAGGCTC GTGCTAAGCT AGCGCCGTCG   100

        TCGTCTCCCT TCAGTCGCCA TCATGATTAT CTACCGGGAC CTCATCAGCC   150

40
        ACGATGAGAT GTTCTCCAAC ATCTACAAGA TCCGGGAGAT CGCGGACGGG   200

578

TTGTGCCTGG AGGTGAAGGG GAAGATGATC AGTAGGACAG AAGGTAACAT   250

TGMTGACTTG CTCATTGGTG GAAATGCTTC CTCTGAAGGC CCCGAGGAAG   300

5   AAGG   304

        (2) INFORMATION FOR SEQ ID :1139:

            (i) SEQUENCE CHARACTERISTICS:
10   (A) LENGTH: 277 base pairs
                (B) TYPE: nucleic acid
                (C) STRANDEDNESS: double
                (D) TOPOLOGY: linear

15

        (xi) SEQUENCE DESCRIPTION: SEQ ID :1139:

GAGGATCCGG GTACCATGAG AAACTTTGAA GCCAGAGATT TTAAACAATC   50
20
AAGGCACTTG AAAACATTAA GTATATGTAC AAATGTGCAA GTAAAACAAA   100

CAGCTGTACC AACGAGTAAC AAAGAAACAG TAAATCTTCA TCTTAACAAC   150

25   CTTTAATAGT TATCTAAATG CAGAGTTTGT TTATGAAATG AACCAAAGCA   200

GTTTGTCATT TCTTACTATA AAATACCGAA AATAAAGTGC AAAACTTAGC   250

CACTACTGGC TAAAGAAACT AAGTAAA   277
30
        (2) INFORMATION FOR SEQ ID :1140:

            (i) SEQUENCE CHARACTERISTICS:
                (A) LENGTH: 208 base pairs
35   (B) TYPE: nucleic acid
                (C) STRANDEDNESS: double
                (D) TOPOLOGY: linear

40
        (xi) SEQUENCE DESCRIPTION: SEQ ID :1140:

```
        CGAGATCCGG GTACCATGGC CTCCTACAGG TGCCGTGGAG CCACGCCCAA          50

        AAGAGAGCTC CCTGAGAAAC TCGTTGATGC CTTGCTCACT GAAGGAGCCT         100

        TTTAGCAGAG CAAATTTCAT CTTGCGTGCA TTGATGGCGG CCATGGCGGG         150

        GTACCCAAAC CCTCCAATTC CCAACGCGGT CTCAAGTTCA GACTGGGCTC         200

        CAGCTTCT                                                       208
```

(2) INFORMATION FOR SEQ ID :1141:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 274 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID :1141:

```
        CGAGGATCCG AGTACCATGG CCTCGAACTG AGCATCAATA TATTCTACTG          50

        CCAGCTTATA ACTGTCATCT TTATTCATAT GGTCTCCAAA TCCCACGATG         100

        TCAACAATGG TTAACTTCAG CCGTACATTG CTTTCCTGAA GCTCATAACT         150

        TCTGGCTTTT AACCGAACAC CTGGTTCATT GTGAGTAGCT GGGTCACTTT         200

        TAAATTTGGT GTTGAACAAA GTGTCCATTA ACGTGGATTT GCCAATGCCT         250

        GTCTCACCAA TACAAAGGAT GTTG                                     274
```

(2) INFORMATION FOR SEQ ID :1142:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 226 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

580

(xi) SEQUENCE DESCRIPTION: SEQ ID .:1142:

GCCTGCACAT TGACTGTGGG AAACTCGGAA ACAAGCTCAC ATCTCCCCGT   50

GGGAAACCTT CTAGCAACAG GATGAGTCTG CAGTGAACTG CAGTTGCCAC   100

CTTCCTCTAT GCGGAGGTCT TTGTTGTGTT GCTTCTCTGC ATTCCCTTCA   150

TTTCTCCTAA AAGATGGCAG AAGATTTTAA AGTCCCGGCT GATGGAGTTG   200

TTAGTGTCCT ATGGTAACAC CTTCTT   226

(2) INFORMATION FOR SEQ ID :1143:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 168 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: double
            (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :1143:

RGGRTCCRNG TGCCRTGGGG YNTNNCTAGR CRGCRGGYAA GGTCCACCRC   50

TGRCRCGNTG NCNGTGAGGR CRTGNRGGNC CRTGCGAGTG GGCTTACCGN   100

TAGGTTCGGG AATGACCTTG CYMACGNCNN YGACAGCTAA GTRGRNGCRG   150

GNANGRTGNN GTGGAGRG   168

(2) INFORMATION FOR SEQ ID :1144:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 256 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: double
            (D) TOPOLOGY: linear

581

(xi) SEQUENCE DESCRIPTION: SEQ ID :1144:

CGAGGATCCA AATACCATGG AGCTGACAAT GTCAGCTCAA TTTGAAGTAT   50

5   TCTTGAGGGA CCTTTTGCTC ATAGGCTTTA ATTCTGTCTG TGACTTTTGC   100

CAGGATTTGA GGAAATCGAC TGCCTTCACT CTTCCCTGAA ACTTTGAAGT   150

CCACATAAGG GCTTTCTCAT CAAATGGCAG AAATTATAAT TTATAAACCT   200

10   AAACAACCTT ATAGTGTTTT CGCTTTGAAT TGTATGAATT CTTAGAACTG   250

AGAAGT   256

15   (2) INFORMATION FOR SEQ ID :1145:

(i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 184 base pairs
    (B) TYPE: nucleic acid
20   (C) STRANDEDNESS: double
    (D) TOPOLOGY: linear

25   (xi) SEQUENCE DESCRIPTION: SEQ ID :1145:

AAACACAAGG CTAAAAGTCA CTAAAGGTGA CACAGTACCA ACCCCGGGAA   50

GGTTGAGTTC TGTGCTGCTA CCTTCTACTG ATGGCGAATA GACTATTCTG   100

30   TACCCTGTGA TGGGAGCCTG GGGTCTGCTC CAGCAAACAA CAATCGAGGT   150

GTAATCAACT TGGTCCACAG TCGGGTCAGG AGGG   184

35   (2) INFORMATION FOR SEQ ID :1146:

(i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 221 base pairs
    (B) TYPE: nucleic acid
40   (C) STRANDEDNESS: double
    (D) TOPOLOGY: linear

582

(xi) SEQUENCE DESCRIPTION: SEQ ID :1146:

CGAGGATCCG GGTACCATGG CCCAAAGAGT GAATGATGTA TCCCAGGGCG   50

CAGTCCACAA CTTGCGCAGT ACCTTCCCAG ATGACAGCCT CACTGGACCG   100

ATTTCCATCC ACGAAGATGA TGCTAAGAAG CACCATGAGC AGACCCAGCT   150

TGGGTGAGTC CTTAGTCGTT CCCAGTATGC CTGCATCAGT GGGCTCTAAG   200

GTGCTGAGAA GAATGCACAA G   221

(2) INFORMATION FOR SEQ ID :1147:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 255 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: double
            (D) TOPOLOGY: linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID :1147:

CGAGGATCCA AATACCATGG GAGTCAAGCA TGCCTCGATA GCCACAGATT   50

TACAAGAATT ACCTACAGTT TGCTTCTTNG AATCGACATG CAAATCTGCT   100

TAAGGATTCT CACATTCAGG ACAGAGAACA AATTTTTTAA TGAATCCATC   150

CAACAGGTCT TGNAGTTTAT TCGCCTCATG AGATCCATTG ATAATGGAAC   200

RRTMATTCTT AACANCAAAC NGMGMCTGNN NTCCCRNCTT ATAACCMAAA   250

GATNT   255

(2) INFORMATION FOR SEQ ID :1148:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 230 base pairs
            (B) TYPE: nucleic acid

```
                        (C) STRANDEDNESS: double
                        (D) TOPOLOGY: linear


  5

                   (xi) SEQUENCE DESCRIPTION: SEQ ID :1148:


          CGAGGATCCA GGTACCATGG ACGATTCACA GCCCCTGGCC ACTGGCCATT          50

 10       TCCAGTGGTA GGGAGCACAC TGRTCACATT CGAGACCCAC CACGTTGAGC         100

          AGACAAAGGC AGCCTCCACT CTCCTCGTCA CTCAACATGT ACCTCCGTCC         150

          CCCAGGATGT TGTAGTTATA GCAATAGCAG CCCTGCGGTT GACGTAGGTG         200
 15
          AGTCGGTGAC GCCCGATTTG GATCGGGTGT                              230


         (2) INFORMATION FOR SEQ ID :1149:

 20            (i) SEQUENCE CHARACTERISTICS:
                   (A) LENGTH: 223 base pairs
                   (B) TYPE: nucleic acid
                   (C) STRANDEDNESS: double
                   (D) TOPOLOGY: linear
 25


                   (xi) SEQUENCE DESCRIPTION: SEQ ID :1149:

 30       GTGCCGTTGG TCCTGTGCGG TCACTTAACC AAGATGCCTG AGGAAACCCA          50

          GACCCAAGAC CAACCAATGG AGGAGGAGGA GGTTGAGACG TTCTCCTTTC         100

          AGGCAGAAAT CGCCCAGTTG ATGTCATTGA TCATCAATAT TACCNACTAG         150
 35
          AACAAAGAGA TCTTTCTGAG AGAGCTTATT CAAAATACAT TAAATGTATT         200

          GGACAAAATT CGATATAAAA GCT                                     223

 40      (2) INFORMATION FOR SEQ ID :1150:

               (i) SEQUENCE CHARACTERISTICS:
```

584

```
              (A) LENGTH: 272 base pairs
              (B) TYPE: nucleic acid
              (C) STRANDEDNESS: double
              (D) TOPOLOGY: linear
```

```
         (xi) SEQUENCE DESCRIPTION: SEQ ID :1150:
```

```
CGAGGATCCG AGCACCATGG AGAGACTATG ACGCTCAACA AGAATCACTC          50

GGAGGGCGAC GGAGTGATCG TCAATAACAC CGAGA. .TC CTAATGCCCT          100

ATGATCACGT GGAACTAACA T CAATGACA TGAAGAACGT GCCAGAAGCC          150

TTCAAAGAGA CCAAGAAAGG CGCTGTCTAC CTTACTTCTC ATTGAACCAT          200

CTTTATGTCC AAGAACAAGG ATGCGATGGG TATTTCGTGA NGCTATTTGA          250

NMTRAGGRMA GNCTGNAAGG TM                                        272
```

```
    (2) INFORMATION FOR SEQ ID :1151:
```

```
         (i) SEQUENCE CHARACTERISTICS:
              (A) LENGTH: 140 base pairs
              (B) TYPE: nucleic acid
              (C) STRANDEDNESS: double
              (D) TOPOLOGY: linear
```

```
        (xi) SEQUENCE DESCRIPTION: SEQ ID :1151:
```

```
TGAGGATTTA TAGATTANAG CTAGAGTTCA CATTTTATGG ATTACAACCA          50

AAAAAAACCT GAAAAAGAAA AAAAACAAAA AAGCTCAAAA GCAATCACAA          100

GGATAGTTGA ATCCCTCTTT AAACCCCCAA AGCAACCCCC                     140
```

```
    (2) INFORMATION FOR SEQ ID :1152:
```

```
         (i) SEQUENCE CHARACTERISTICS:
```

585

```
                    (A)  LENGTH: 208 base pairs
                    (B)  TYPE: nucleic acid
                    (C)  STRANDEDNESS: double
                    (D)  TOPOLOGY: linear
```

```
            (xi) SEQUENCE DESCRIPTION: SEQ ID :1152:
```

```
        AAGGATCCGG GTACCATGTA TTCCCCCGGT ATCAGCAGAG GCGTGTACGG          50

        GCACTGCTTT AAAACTGGGA AGGAGGAAGA CGAGGCCAGG GAGCCGGAGG          100

        GTCACCAAGG TAGATTTCCA GCAGCCTAGT CCAGCTGAAC GCTTTCCAGC          150

        CTTGCTTTTT AGCAGCTTTG AGGAAAAGTA TAGTGATCCG GATGTGAAAC          200

        TTTCATTG                                                        208
```

```
        (2) INFORMATION FOR SEQ ID :1153:
```

```
            (i) SEQUENCE CHARACTERISTICS:
                    (A)  LENGTH: 274 base pairs
                    (B)  TYPE: nucleic acid
                    (C)  STRANDEDNESS: double
                    (D)  TOPOLOGY: linear
```

```
            (xi) SEQUENCE DESCRIPTION: SEQ ID :1153:
```

```
        CGAGGATCCA GGTACCATGG GGTGGATCCG CCGGGCATAG CCACCCTGGA          50

        TGGTGGCCAT GGTGAGGCCG ATGAGGAAAA ACATCTTCCC CTGCTGTAGG          100

        CTACTGAACT GGAAGCGCTG GTGTGTGAGG AAGCTCAACG TGCACTCCAG          150

        GCCCAAGAAC AGGAAGAGGT AGAGGAAGTA GACTMGGCCC AGGCGGCCAG          200

        GCTGATGAAT TGTCTCCAAA GGGTGAGACC TGGCCACGAG CCATANCCCA          250

        GAMGCCNMAC AGGGCTRGGG ACTG                                      274
```

586

(2) INFORMATION FOR SEQ ID :1154:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 267 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID :1154:

GAGGATCCAC CGACCATGGA ACACTCTCAA TGGCTGCAAC CACCCCGTGG   50

CCCCCCTACC AGCCCCAATC TCCAAACCCC GCACGTCGAT CATGACGCCA   100

CCAACAGCTG CAGCCCCTGA GATCTTCACC TTAGACCCTC TCCCGAAGCC   150

CGCAGCCGCC CCTGCGAACC CTCCAACTCG TTCACACGCG CCGAAAGCCT   200

ATTCCCAGGA CTCTCTGCCC CTACGTGACC GNCCCTAGCT GCTAGTCGAG   250

AATCCGAACT CCGCTCC   267

(2) INFORMATION FOR SEQ ID :1155:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 231 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID :1155:

CTCAAACCCC GNTTCCCCCC TAATAAGAGC AACTAAAAAA CTTCTGATAA   50

CCACAATAAA AGCGTGCATT TGAGCACAAT TCAAAAGCCA ACCCCTTCGA   100

AGGNGCTTCT GATGNAAAAG GAGTTATGTT GAACGAAGCA GGAGTTAACG   150

```
· CTACACAGTC AAATTGTGGC ATTAGGACGC GCGAGCGGGC TAGCTGCGGC          200

  CGTCTANCAA GGCAACGGCC GCCTTTGAAT T                              231
```

5   (2) INFORMATION FOR SEQ ID :1156:

            (i) SEQUENCE CHARACTERISTICS:
                (A) LENGTH: 128 base pairs
                (B) TYPE: nucleic acid
10   (C) STRANDEDNESS: double
                (D) TOPOLOGY: linear

15   (xi) SEQUENCE DESCRIPTION: SEQ ID :1156:

```
  GCGCGAGCAC AGAGCCTCGC CTTTGCCGAT CCGCCGCCCA TCCACACCTG           50

  CCGCCAGCTC ACCGTGTATG ATGATATCAC CNCGCTCGCC ACCAACRACG          100
20
  GCTCYAACMT GTGCAAGGCC GCCTTCAA                                  128
```

        (2) INFORMATION FOR SEQ ID :1157:

25   (i) SEQUENCE CHARACTERISTICS:
                (A) LENGTH: 126 base pairs
                (B) TYPE: nucleic acid
                (C) STRANDEDNESS: double
                (D) TOPOLOGY: linear
30

            (xi) SEQUENCE DESCRIPTION: SEQ ID :1157:

```
35  GCCGCAACAC AACCCAGGGA GACTCAAGNC CACAGGGGCC CCCCGGCTCT           50

  GAGGGATTCA CCGTCGCCTC CCGGTCCCCG AAGGCCCACA AGGGCAGAAA          100

  GGTGAGCCTT ATGCACTGCC TAAAGA                                    126
```
40
        (2) INFORMATION FOR SEQ ID :1158:

588

(i)´ SEQUENCE CHARACTERISTICS:

      (A) LENGTH: 101 base pairs

      (B) TYPE: nucleic acid

      (C) STRANDEDNESS: double

5   (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :1158:

10

AATAACCATA ACTGCAAAAA CCCAAMCAAA AAAAAAGGGG GAACAAAAAA   50

CCCCAAACCC CCAAAAAAAC CAGAAAAAAC CACAAAAAAA AACCCCTCCT   100

15   T   101

(2) INFORMATION FOR SEQ ID :1159:

(i) SEQUENCE CHARACTERISTICS:

20   (A) LENGTH: 172 base pairs

      (B) TYPE: nucleic acid

      (C)´ STRANDEDNESS: double

      (D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :1159:

GAGGATCCGG GTACGGGCAG GGTGAGAGCC TGGGGTCCAC CGATAACCGG   50

30

GAGGGAGATG GCGTTCTTGA GCAGAGGGGA TGGGCCGTCC GGGAGCTCCC   100

CCCACACACG GTGGCGGTGC GGGTGAACTG GAAGGGGAGG TCGAAGGTGC   150

35   CATCTTCTTC AGGCCCCTCC AC   172

(2) INFORMATION FOR SEQ ID :1160:

(i) SEQUENCE CHARACTERISTICS:

40   (A) LENGTH: ·235 base pairs

      (B) TYPE: nucleic acid

      (C) STRANDEDNESS: double

589

        (D) TOPOLOGY: linear

    5   (xi) SEQUENCE DESCRIPTION: SEQ ID :1160:

        GAGGATCCAC ATACCATGGA ACAGCACCAC AAAAATAGCC ATTTTGATCA   50

        TGGTTATTTC CCAGGACCAC ACGATTTGCC TACGTCACTG GAAGGCTATG   100
   10
        TGTCTGTTCT GAGCCTTCCC ACTCTCCTAA AGGGCAGATG AAGATCAGAG   150

        CTTTGACCCT .GTGATGCCAT TTTAATCAAC CCTGCTTGGT TTTAGAGGAT   200

   15   TGCTCCCGTG GGTCACTTGA GGCAGGCTCC ACCTT   235

        (2) INFORMATION FOR SEQ ID :1161:

            (i) SEQUENCE CHARACTERISTICS:
   20   (A) LENGTH: 284 base pairs
                (B) TYPE: nucleic acid
                (C) STRANDEDNESS: double
                (D) TOPOLOGY: linear

   25

        (xi) SEQUENCE DESCRIPTION: SEQ ID :1161:

        GAGGATCCAC CAACCATAGA AAGTAAATAC TGTATAAAAA GCTCCAGCTG   50
   30
        TTAGATACAA ATGCAAAACG CTTCCTAAAA AACGGCCTGA AAAAAAACTC   100

        ACAGACAATG CCAAACTTTA TAGGTCTGTA TTTTCCTTTA TACAAAATGC   150

   35   CCTCAAATTA AAAAGTAATT CCCATATAGC AATAAAGTCC ACATCTCTGG   200

        ATTACCTATA ACCGGTATTA TGGGGTGTGT TTATACTGCC TAGAATGTTA   250

        ACCCTCATAA AGCCTTAAAA GTACATTTGT GAAA   284

   40
        (2) INFORMATION FOR SEQ ID :1162:

590

(i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 287 base pairs
    (B) TYPE: nucleic acid
    (C) STRANDEDNESS: double
    (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :1162:

GCTCACATAA ATTTCTTCAC CGACCCTTTT CCTTCCAGCT TCCTTACTAT   50

AAAAAACCCC ACA   AATA TGTTCATCAT CATCCATACT AACCAACCCC   100

GTCACCATCT CAATCAGCAG CAAGTCCTAC TCTCTGTGGG TGAAACCTTG   150

TTACCACCTC TAGGGGCAGA CCCCTTTTCA GATATATTCA AGAGTTTAAT   200

ATCCTCCCAC TATAGCGCTT CGACTTTGTA TCTTCCTCTA TGGCTACCAA   250

ATTCTGTCCG TTGATAAGTA CTGGCTCTAA ACCATGC   287

(2) INFORMATION FOR SEQ ID :1163:

(i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 122 base pairs
    (B) TYPE: nucleic acid
    (C) STRANDEDNESS: double
    (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :1163:

GAGGATCCAA AAACCATAAA ATTCATCATC CCCAGCAGGT GCNCTAGCTA   50

TACTTTATTA CAGCAAARCA CAACCACACG CTGAMCTANM TCGTATAGAT   100

AAACACCAAT CATGGGTCGG CC   122

(2) INFORMATION FOR SEQ ID :1164:

     (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 142 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
5   (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID :1164:
10

GCGCGGGTCT GTCTCTTGCT TCAACAGTGT TTGGACGGAA CAGATCCGGG   50

GACTCTCTTC CAGCCTCCGA CCGCCCTCCG ATTNCCTCTC CACTTGCAAC   100

15 CTCCAAGACC ATCTTCTCGG CCATCTCCTG CTTCTGAAGC CT   142

(2) INFORMATION FOR SEQ ID :1165:

     (i) SEQUENCE CHARACTERISTICS:
20   (A) LENGTH: 219 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

25

    (xi) SEQUENCE DESCRIPTION: SEQ ID :1165:

TATTCCCCCG GTATCAGCAG AGGCGTGTAC GGGCACTGCT TTAAAACTGG   50
30
GAAGGAGGAA GACGAGGCCA GGGAGCCGGA GGGTCACCAA GGTAGATTTC   100

CAGCAGCCCT AGTCCAGCTG AACACTTTCC AGCCTTGCTT TTCAGCAGCT   150

35 TTGAGGAAAA GTATAGTGAT CCGTATGTGA AATTTTCATC GCACGTAGCG   200

GATGAGAATA GAGAACTCA   219

(2) INFORMATION FOR SEQ ID :1166:
40
     (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 202 base pairs

592

```
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: double
            (D) TOPOLOGY: linear
```

```
        (xi) SEQUENCE DESCRIPTION: SEQ ID :1166:
```

```
GAGGATCCAC CAACCATAGA AAGGAAACAA CACTTGGAGT GAACCCGACC        50

CAAGCCACTA CACCCCAGCC TAACCGACAG GTGCTAGACT AATNGTNAAA        100

AACAACCGGA AAATAGACCC GGACGAAGAT CAAAGNTTNT CAATCCAAAC        150

ATTTTAGGGG GACCAAGACC CMGGGATCAA AAACAAGGTC CACCACACCC        200

AA                                                            202
```

```
    (2) INFORMATION FOR SEQ ID :1167:
```

```
            (i) SEQUENCE CHARACTERISTICS:
                (A) LENGTH: 159 base pairs
                (B) TYPE: nucleic acid
                (C) STRANDEDNESS: double
                (D) TOPOLOGY: linear
```

```
        (xi) SEQUENCE DESCRIPTION: SEQ ID :1167:
```

```
GAGAAACCTA CCCAACCAAG AGGCGCCCTG CTTTGTAATG ACCTTTACGA        50

AGACACGTCT GATACCCAAC CTGACAGAGG AAACAACAGT AGTCTGAAAG        100

GGACAGAATG AGAGAGGGGG CTGGAGAAAG AAATGAATAA ACATGAATGC        150

ATCTGGAGA                                                     159
```

```
    (2) INFORMATION FOR SEQ ID :1168:
```

```
            (i) SEQUENCE CHARACTERISTICS:
                (A) LENGTH: 211 base pairs
```

593

```
              (B) TYPE: nucleic acid
              (C) STRANDEDNESS: double
              (D) TOPOLOGY: linear


    5


         (xi) SEQUENCE DESCRIPTION: SEQ ID :1168:


    CCCTAGACAA GCCACCTGAG GAGAGGCTCG GAGCCGGGCC CGGACCCCGG        50
   10
    CGATTGCCAC CGCTTCTCTC TAGTCTCACG AGGGGTTTCC CGCCTCGCAC       100


    CCCCACCTCT GGACTTGCCT TTCCTTCTCT TCTCCGCGTG TGGAGGGAGC       150


   15    CAGCGCTTAG GTCGGAGCGA GCCTGGGGCC ACCGCCGTGA AGACATCGCG      200


    GGGACCGATT C                                                 211


         (2) INFORMATION FOR SEQ ID :1169:
   20
              (i) SEQUENCE CHARACTERISTICS:
                   (A) LENGTH: 211 base pairs
                   (B) TYPE: nucleic acid
                   (C) STRANDEDNESS: double
   25              (D) TOPOLOGY: linear




         (xi) SEQUENCE DESCRIPTION: SEQ ID :1169:
   30
    GGATTTCCGG TCCTGGCTTT CTGATATTTC TAAAATCGAC CTGGAATCAA        50


    CCATTGACAT GTCCTGTGCT AAATATGAAT TCACTGATGC CCTGCTGTGC       100


   35    CATGATGATG AGCTGGAAGG GCGCCGGATT GCCTTCATCC TGTACCTGGT      150


    TCCTCCCTGG GACAGGAGCA TGGGTGGTAC CCTGGACCTG TACAGCATTG       200


    ATGAACACTT T                                                 211
   40
         (2) INFORMATION FOR SEQ ID :1170:
```

594

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 266 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
5   (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID :1170:

10

GAGGATCCGC GCAACCATAG AACTCACAAC CCAGCCATAT ACCTCAGACA   50

CAATGGAATG GGCGGAGGTC GAGGTNGACA AACCCTGAGT AATGTTGGGC   100

15
ACTTCCGCAC CGGAGCTGTT CTTACCTTTG ATAAAGTGGA TGTTATTGCT   150

ATTAATGATC TCTTAACGGA CTTCAACTGT AAAATTNGCA TGATCTAGTC   200

CTATCCACCA ACGNCGAACA ATATGCTGTT GCCAMGATTG AGCACGAGCC   250
20
GTTTGGGCTC AACGGC   266

(2) INFORMATION FOR SEQ ID :1171:

25   (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 167 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear
30

    (xi) SEQUENCE DESCRIPTION: SEQ ID :1171:

35
GGCACAACCC ACTTTGAACA ATCATGCTTC AGAAATCTGC CTGACCTTAG   50

CTGCTGCTGC TGCTCACTTT ATTATAGTAT AACTTCGGTA GGCATACTTG   100

GAGAACATAT CCCACATTAG GAATTGATTT AAGCCTGAGA GTTTGAGGGC   150
40
TTTAATCCTT TAAAACT   167

595

(2) INFORMATION FOR SEQ ID :1172:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 232 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID :1172:

```
AATAAACCTC CCTATCACAG TGACCTACTA CCCGCGTGTG CTTATATAAC          50

TAATCCAGGA CAACCCACAA AAATTATAGC AACACACAAA CACACCGCTG         100

ACCATAACAT GTGCGTCTTT CAAAGATGCC TTATCAACCA GAGCGATGAT         150

TACTGAGGAT ACGCAACTCA TAAAACTCTA CTTAAAGCAA CAGGGCAGAC         200

GTGCGTCTGT GCCAGTCGTG AATGTGGTGA AC                            232
```

(2) INFORMATION FOR SEQ ID :1173:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 93 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID :1173:

```
GAGGATCCAC CAACCATAGC CCGAAAATGT GGTAAGGGAC CCTCATCTAT          50

CACACAACNC AGGTAAGAAG GCACCCAGCC CCATGGGCCA TAC                 93
```

(2) INFORMATION FOR SEQ ID :1174:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 200 base pairs

596

        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID :1174:

GCCTTTTTTT ACCCGCCGGA AGCTACAGCT TTTGCCCCCC CAAAAAAACC   50

CCACCCTTTT ACCCACCGCG GACCCAAAAA CAGCAAAAAC CAAGGACCTC   100

TCCCAACCCC AACCCCTCCT TTTTGGCCCT TCCTTCCCCC CCTCCCAGCC   150

CACCCCCAGA CACCTCAATC CCCCAAAAGG ATGCCCTAAA CCTCTCCTAA   200

    (2) INFORMATION FOR SEQ ID :1175:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 121 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: double
            (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID :1175:

GAGGATCCAA AAACCATGGC ATTCATCACG CCCAGCAGGT GTCCCAGCCA   50

TGACTTACCA TAGCAAAACA CAACCACACA CTAACCTGCA TCGCCTAGCT   100

TACTGATGAT GATGTCCTGG T   121

    (2) INFORMATION FOR SEQ ID :1176:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 26 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: double
            (D) TOPOLOGY: linear

597

(xi) SEQUENCE DESCRIPTION: SEQ ID :1176:

AACCAGACAC GCCGACCCGC TGAATC   26

(2) INFORMATION FOR SEQ ID :1177:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 178 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID :1177:

GAATCGATCT TGACCTGGCT GCCAGGAATA TCCAGCTTGT TACCGACTGG   50

TAAAGAATAA GACCGCTGAT CATAGAGTGA AGCTCCAGGA ATCAGAGAGT   100

CTCATAGCAA ACCTCGAAAC TGAGGATGAG ATGGTTACAG ATAAAGCCTT   150

TCAGGATGGA TTMAAGNAMG CAGAGAGG   178

(2) INFORMATION FOR SEQ ID :1178:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 144 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID :1178:

GGTTAAGTTT TTCATCAAAG ACTCAGGTAC CTATTATCGT TCCCTGGCGA   50

AACTGAGGAG AAAAGTTAAT CAACCAGGTT ACTCCCACAG TTTGCCCGTG   100

TGTTATGCAT CAGTTATACA GGTATCCCAC CAAGTTCAAG TCAA   144

598

(2) INFORMATION FOR SEQ ID :1179:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 233 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID :1179:

GACCAGGGAG GAGGTTTAAT CAACTTGGAC CCCCTCCGGC CTAGCCGCCG   50

AGGAGGTGCA TTCGGGACAA CCACTAGGTC AGAACGCAGC CTCTCCAGAG   100

TCCTCAGGCT CGACAACGAT TATCCTGCTG CTATCACGCT TTGATTTACT   150

GATCTCGCTG AAAAGACAGA CGCTTTTAGA TACCGAGTCG ATAGGGGGTC   200

TGCGGTACTT TTCAGTAGAT AGGTGGTGCT TGT   233

(2) INFORMATION FOR SEQ ID :1180:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 225 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID :1180:

CGAGGATCCG GGTACCATGG GCCGGATACA ACGAGCTATC ATTACTGCTC   50

CCATGGCCAA AACCAGCAGT CCCACAATCC CCGTGAAAGG GATGAGGTAA   100

TAGCCCAAGG GGAAGGTATT GTCTGGAACC AGAAGCGCCC GAGCCCCCTT   150

CTTGTAGRCA AAGAGGGCGC CCAGGTGCTT GGAGCTNCTN TCCCCAATGG   200

599

AGGTAGACGG GACCAAGATC TGCTG   225

(2) INFORMATION FOR SEQ ID :1181:

5   (i) SEQUENCE CHARACTERISTICS:
                     (A) LENGTH: 293 base pairs
                     (B) TYPE: nucleic acid
                     (C) STRANDEDNESS: double
                     (D) TOPOLOGY: linear

10

               (xi) SEQUENCE DESCRIPTION: SEQ ID :1181:

15   TGAGGATTTA AAAATTCTGG AATATCTATG ATTGATCGTC AACTTTATTC   50

         GATGAATAAG CTTGATGTGG CCTAGTTTTN NGNNNNNTGG NYATGGTNNA   100

         TCNNNTTANT TTTTTGGTTG TTGTGNATAT TATNGAATAR AMGAATRGNG   150
20
         TTTAGAGTTT GGAAGCGGCN RNGCGTARMG NNACTCYACG CTCGCNNCTN   200

         TTGNNNNACA GMRGGNTCTC TNGGRTGAGT GGRTNCMGTT GGMGGNNTCN   250

25   NNNTAGCTGN NGNGAGRATC AGCTRGCTTN CTTTGNGCTN GCT   293

         (2) INFORMATION FOR SEQ ID :1182:

               (i) SEQUENCE CHARACTERISTICS:
30   (A) LENGTH: 252 base pairs
                     (B) TYPE: nucleic acid
                     (C) STRANDEDNESS: double
                     (D) TOPOLOGY: linear

35

               (xi) SEQUENCE DESCRIPTION: SEQ ID :1182:

         GAGGATCCGG GTACCATGGC TCTCTCTTTC TTTTTTTTCT TTTTCTTGGC   50
40
         GGATGTGAGA GCTGCCTGAG ATTCAAGGTC ATCCGGCAGC TCAGTCCCCA   100

600

```
CCACCTCTGT CTCTGGCTCC ACTGTGGCAT CTTGCTGTTT TTCTTTCTCA          150

GTCTTCTCTT AGGGAGCTGC CAGAGCTGCC TGGACCTGAG AATTCATTCC          200

TTCTGGCTGT TGAGACCCCG TGGACTCCCC TGGATTCCAG AGNNTNATTT          250

NG                                                             252
```

(2) INFORMATION FOR SEQ ID :1183:

        (i) SEQUENCE CHARACTERISTICS:
             (A) LENGTH: 202 base pairs
             (B) TYPE: nucleic acid
             (C) STRANDEDNESS: double
             (D) TOPOLOGY: linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID :1183:

```
ACGAGGATCT GAATACTCTG GCCTGCAAGT AGAGGCTAAT TCGATGTGTG           50

AAACTGTAGA TTCGGCTTAA GGTAATAGTC ATTTATAGAC TATTCAATAG          100

AGTCAGACTG GTCGAGGCTG GTAAGTGTAG CGGAACGGTT GCTGACTGAT          150

ATTGTTAGAG TGAGGCTTGT ACTGGTGTGT ATCCGTAGGT GGTCTGCAGT          200

GT                                                             202
```

(2) INFORMATION FOR SEQ ID :1184:

        (i) SEQUENCE CHARACTERISTICS:
             (A) LENGTH: 43 base pairs
             (B) TYPE: nucleic acid
             (C) STRANDEDNESS: double
             (D) TOPOLOGY: linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID :1184:

601

CAGATCCTCA GCTTTCGTGG TTCACAATTT CTTCAGTCTC TTA   43

(2) INFORMATION FOR SEQ ID :1185:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 48 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID :1185:

ACCGTCCTTC TGGTTCATCC TAGCAAAAAT CTCACCATCT TCTATCAC   48

(2) INFORMATION FOR SEQ ID :1186:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 104 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID :1186:

ACATCATCCG AGTCCCCTCT ACAGTGTTCA TTGTGATCGT TGCATCCCCC   50

TGGTTTGGAA ATAAAATATA AACTGCCCGG CAAGAGATAA AATTGTATTT   100

TTTA   104

(2) INFORMATION FOR SEQ ID :1187:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 76 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

602

(xi) SEQUENCE DESCRIPTION: SEQ ID :1187:

CTGGTTCTGT TTCTCGCAGG TGGTAGAGGG GAGGCTGTCC TCTGGTCAGG   50

AGAATCCTAT TCAGTGCTCC CTTAGA   76

(2) INFORMATION FOR SEQ ID :1188:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 42 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: double
            (D) TOPOLOGY: linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID :1188:

AATAGGGCGC GATCAACTCT TAACTTTGAG GAGAACCAAC AA   42

(2) INFORMATION FOR SEQ ID :1189:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 253 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: double
            (D) TOPOLOGY: linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID :1189:

GGCGGACGTG CGCGCCTTGT CTTCGCGGCA CCTGGGCCTG AGGTGCGTGC   50

CTCCCGGGCC CTCGCCAGCT CCAGATGCGT GAGGAGGACT TCAGAAACCC   100

GACTGAGAAG TGGAGCAACC CCCAGGAAGG GCCGGACCTG CCTAAATGCC   150

GCCAAGGCCT TTTATTTATG GCTAGTTTGC TCTCGTGAAA TACTAACATC   200

GTTTTAATGG CACTCATCAA GTACGCAAAT GATATGATTT AACCTCGCGC   250

603

AAT   253

(2) INFORMATION FOR SEQ ID :1190:

5   (i) SEQUENCE CHARACTERISTICS:
                (A) LENGTH: 252 base pairs
                (B) TYPE: nucleic acid
                (C) STRANDEDNESS: double
                (D) TOPOLOGY: linear
10

            (xi) SEQUENCE DESCRIPTION: SEQ ID :1190:

15   GAGGATCCAC CAACCATAGA ACGGCCCTAC TAATGAACCA CACAAGCTAG   50

       TTGCACCACT ATAGAAACAC AAAACTACAC ATCTATACCA ATAAAAATAA   100

       CAACTACTCC AATTGCCCAT GTGGTATTGT CGCAGACTGA AATGAATTAT   150
20
       GAATTTAGGT TGGTTACCAA TATCGGCATA AAATAAACTR TGTAAGGCTC   200

       AMTATGTTGA CAGTAAGCTC TTGTCAGGTG TCTAATGAGG TAAAAGCATT   250

25   TT   252

       (2) INFORMATION FOR SEQ ID :1191:

            (i) SEQUENCE CHARACTERISTICS:
30   (A) LENGTH: 178 base pairs
                (B) TYPE: nucleic acid
                (C) STRANDEDNESS: double
                (D) TOPOLOGY: linear

35

            (xi) SEQUENCE DESCRIPTION: SEQ ID :1191:

       GAGGATCCAA CAACCATAGA GCACATAAAA ACCGCCCAAC GATCTAACTA   50
40
       ATATACAACG GCTAACCGGG CCATTCAAAA GCTCGCCCAG ATTAAATGCC   100

604

TGCCGANAGC AAGTACATGG GGAGGATTAC TACTTCCTGG TTGCCAACCA   150

CCCTTCCGGC TGCCCTTGTG TTGACTTG   178

5   (2) INFORMATION FOR SEQ ID :1192:

              (i) SEQUENCE CHARACTERISTICS:
                  (A) LENGTH: 156 base pairs
                  (B) TYPE: nucleic acid
10   (C) STRANDEDNESS: double
                  (D) TOPOLOGY: linear

15   (xi) SEQUENCE DESCRIPTION: SEQ ID :1192:

GGATCGGCGG TAATCGGTGA GCTCGGTGTC GGGTAAGGGA CCCAGTCCAT   50

CGCCACCAAG CGCCAGGAAT GGGCAGCATA AGGGAAGGCT AAGGAGGACT   100
20
GCAACAGGTT AGGGCCCTGG AGATTGTATT TAGCAAGGGT ACCTGCGNNG   150

NGGGCA   156

25   (2) INFORMATION FOR SEQ ID :1193:

              (i) SEQUENCE CHARACTERISTICS:
                  (A) LENGTH: 99 base pairs
                  (B) TYPE: nucleic acid
30   (C) STRANDEDNESS: double
                  (D) TOPOLOGY: linear

35   (xi) SEQUENCE DESCRIPTION: SEQ ID :1193:

ATTCTGAATC TTTAATGAAA ATCAGCCCAG AGCTTGTTGT AATACAGACA   50

TAACTGCAAG AGCATGCCCA CAGCTTAGAG AGGTTGTACC AAATTTAGA   99
40

605

(2) INFORMATION FOR SEQ ID NO: 1194

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 24 base pairs
5   (B) TYPE: nucleic acid
            (C) STRANDEDNESS: single
            (D) TOPOLOGY: linear

10
        (xi) SEQUENCE DESCRIPTION: SEQ ID : 1194:

    NNNNTCCTTC TCCTGCGACA GACA   24

15 (2) INFORMATION FOR SEQ ID NO: 1195

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 20 base pairs
            (B) TYPE: nucleic acid
20   (C) STRANDEDNESS: single
            (D) TOPOLOGY: linear

25   (xi) SEQUENCE DESCRIPTION: SEQ ID : 1195:

    TGTCTGTCGC AGGAGAAGGA   20

    (2) INFORMATION FOR SEQ ID NO: 1196
30
        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 26 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: single
35   (D) TOPOLOGY: linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID : 1196:
40
    AANNTCTCGG ACAGTGCTCC GAGAAC   26

606

(2) INFORMATION FOR SEQ ID NO: 1197

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 26 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID : 1197:

TTNNTCTCGG ACAGTGCTCC GAGAAC   26

(2) INFORMATION FOR SEQ ID NO: 1198

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 22 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID : 1198:

GTTCTCGGAG CACTGTCCGA GA   22

(2) INFORMATION FOR SEQ ID NO: 1199

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 23 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID : 1199:

GTTCTCGGAG CACTGTCCGA GAG   23

607

(2) INFORMATION FOR SEQ ID NO: 1200

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 23 base pairs
    5   (B) TYPE: nucleic acid
            (C) STRANDEDNESS: single
            (D) TOPOLOGY: linear

    10
            (xi) SEQUENCE DESCRIPTION: SEQ ID : 1200:

GTTCTCGGAG CACTGTCCGA GAC   23

    15 (2) INFORMATION FOR SEQ ID NO: 1201

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 22 base pairs
            (B) TYPE: nucleic acid
    20   (C) STRANDEDNESS: single
            (D) TOPOLOGY: linear

    25   (xi) SEQUENCE DESCRIPTION: SEQ ID : 1201:

CTGTCTGTCG CAGGAGAAGG AA   .   22

        (2) INFORMATION FOR SEQ ID NO: 1202
    30
        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 22 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: single
    35   (D) TOPOLOGY: linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID : 1202:
    40
CTGTCTGTCG CAGGAGAAGG AG   22

608

(2) INFORMATION FOR SEQ ID NO: 1203

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 17 base pairs
5   (B) TYPE: nucleic acid
            (C) STRANDEDNESS: single
            (D) TOPOLOGY: linear

10
        (xi) SEQUENCE DESCRIPTION: SEQ ID : 1203:

AGCTCGGCTC GAGTCTG   17

15   (2) INFORMATION FOR SEQ ID NO: 1204

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 24 base pairs
            (B) TYPE: nucleic acid
20   (C) STRANDEDNESS: single
            (D) TOPOLOGY: linear

25   (xi) SEQUENCE DESCRIPTION: SEQ ID : 1204:

GCGACAGACA GCAGACTCGA GCCG   24

        (2) INFORMATION FOR SEQ ID NO: 1205
30
        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 14 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: single
35   (D) TOPOLOGY: linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID : 1205:
40
GATCCGGCTC GAGT   14

609

(2) INFORMATION FOR SEQ ID NO: 1206

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 18 base pairs
5   (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

10

    (xi) SEQUENCE DESCRIPTION: SEQ ID : 1206:

CCGAGAACAC TCGAGCCG   18

15   (2) INFORMATION FOR SEQ ID NO: 1207

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 17 base pairs
        (B) TYPE: nucleic acid
20   (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

25   (xi) SEQUENCE DESCRIPTION: SEQ ID : 1207:

GTAAAACGAC GGCCAGT   17

    (2) INFORMATION FOR SEQ ID NO: 1208
30

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 17 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
35   (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID : 1208:
40

CGAGGTCGAC GGTATCG   17

610

(2) INFORMATION FOR SEQ ID NO: 1209

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 17 base pairs
5   (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

10

    (xi) SEQUENCE DESCRIPTION: SEQ ID : 1209:

CGAGGTCGAC GGTATCG   17

15   (2) INFORMATION FOR SEQ ID NO: 1210

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 56 base pairs
        (B) TYPE: nucleic acid
20   (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

25   (xi) SEQUENCE DESCRIPTION: SEQ ID : 1210:

TACGTTCGAC AAGCTTGAAT TCGCGGCCGC TTTTTTTTTT TTTTTTTTTT   50

TTTTTT   56
30
(2) INFORMATION FOR SEQ ID NO: 1211

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 11 base pairs
35   (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

40

    (xi) SEQUENCE DESCRIPTION: SEQ ID : 1211:

611

GCCWSCGCCG A   11

(2) INFORMATION FOR SEQ ID NO: 1212

5   (i) SEQUENCE CHARACTERISTICS:
                (A) LENGTH: 24 base pairs
                (B) TYPE: nucleic acid
                (C) STRANDEDNESS: single
                (D) TOPOLOGY: linear

10

          (xi) SEQUENCE DESCRIPTION: SEQ ID : 1212:

15   GGTGGCGACG ACTCCTGGAG CCCG   24

       (2) INFORMATION FOR SEQ ID NO: 1213

          (i) SEQUENCE CHARACTERISTICS:
20   (A) LENGTH: 24 base pairs
                (B) TYPE: nucleic acid
                (C) STRANDEDNESS: single
                (D) TOPOLOGY: linear

25

          (xi) SEQUENCE DESCRIPTION: SEQ ID : 1213:

       TTGACACCAG ACCAACTGGT AATG   24
30

       In the above SEQUENCE LISTINGS, some sequences are preferred because
35   they fall into the category of sequences referred to hereinbefore which
       exhibit no more than 90% homology to a human sequence known per se.
       The preferred sequences in these terms are all of sequences SEQ ID Nos
       1 to 1193, EXCEPT FOR SEQ ID Nos:

40   85, 117, 177, 197, 223, 248, 317, 354, 355, 483, 829, 1057, 594, 595,
       597, 164, 427, 420, 58, 67, 374, 373, 501, 569, 188, 550, 904, 932, 97,
       89, 134, 433, 434, 357, 4, 6, 11, 336, 529, 544, 545, 549, 1037, 847,

612

870, 871, 872, 873, 875, 876, 579, 199, 524, 544, 513, 380, 276, 291,
615, 623, 627, 634, 635, 648, 652, 617, 619, 684, 697, 718, 720, 1127,
1145, 1148, 1164, 938, 587, 589, 588, 241, 243, 335, 61.

5

10

15

613

CLAIMS:

1.   A nucleic acid fragment encoding a gene product or portion thereof and comprising any one of:-

5

(a)   a sequence selected from SEQ ID Nos 1 to 1193;

(b)   an allelic variation of a sequence as defined in (a); or

10   (c)   a sequence complementary to (a) or (b).

2.   A nucleic acid sequence as set out in any one of SEQ ID Nos 1 to 1193, or a complement or allelic variation thereof.

15   3.   A sequence as claimed in claim 2 and which exhibits no more than 90% homology to a human sequence known per se.

4.   A nucleic acid fragment comprising a portion of a sequence as defined in claim 2 or claim 3 of sufficient size such that a probe of 20   the same size and exhibiting complementarity to said portion can hybridize to said sequence as defined in claim 2 or claim 3.

5.   A fragment as claimed in claim 4, wherein said portion is at least 15 bases in length.

25

6.   A fragment as claimed in any one of claims 1, 4 or 5 and encoding at least a portion of a biologically active polypeptide.

7.   A nucleic acid sequence as claimed in claim 2 or claim 3 and 30   encoding at least a portion of a biologically active polypeptide.

8.   A DNA construct comprising a fragment as defined in any one of claims 1, 4, 5 or 6 or a sequence as defined in any one of claims 2, 3 or 7, together with a control or regulatory sequence.

35

9.   A construct as claimed in claim 8 which encodes a fusion protein comprising a known protein and the polypeptide encoded by said fragment or sequence.

40   10.   A construct as claimed in claim 9, wherein the fusion protein encoded is a cleavable fusion protein having an endopeptidase recognition site positioned between codons corresponding to said known

protein and said fragment or sequence.

11. The use of a fragment as defined in any one of claims 1, 4, 5 or 6 or a sequence as defined in any one of claims 2, 3 or 7 to produce a gene.

12. A DNA fragment comprising a gene obtainable by the use defined in claim 11.

13. An expression vector comprising a fragment as defined in any one of claims 1, 3, 5 or 6, a sequence as defined in any one of claims 2, 3 or 7, a DNA construct as defined in any one of claims 8 to 10, or a DNA fragment as claimed in claim 12, positioned such that that nucleic acid sequence which encodes the polypeptide corresponding to said fragment, sequence or DNA fragment is in operable reading frame with a control or regulatory sequence.

14. A vector as claimed in claim 13, wherein said vector control or regulatory sequence comprises a regulatable promoter.

15. Host cells which incorporate as a heterologous part of their expressible genetic information a fragment as defined in any one of claims 1, 3, 5 or 6, a sequence as defined in any one of claims 2, 3 or 7, or a DNA fragment as defined in claim 12.

16. A process for the production of a polypeptide comprising cultivating host cells as defined in claim 15.
17. An antibody directed against a polypeptide obtainable by the performance of a process as defined in claim 16.

18. An antibody as claimed in claim 17 and which is monoclonal.

19. A novel gene product or portion thereof encoded by a fragment as defined in any one of claims 1, 3, 5 or 6, or encoded by a sequence as defined in any one of claims 2, 3 or 7, or encoded by the gene comprised in a DNA fragment as defined in claim 12.